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OM nucleic - nucleic search, using sw model

Run on: June 10, 2006, 15:46:40 ; Search time 9.72504 Seconds
(without alignments)
7321.729 Million cell updates/sec

Title: US-10-821-670A-101
Perfect score: 561
Sequence: 1 gggatgttccagtgcctcaa.....tgagctatctgaatgcttcc 561

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 253354 seqs, 63461778 residues

Total number of hits satisfying chosen parameters: 506708

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	35	6.2	2487	6	US-10-471-571A-3681	Sequence 3681, Ap
	2	33.2	5.9	1710	7	US-11-217-529-79541	Sequence 79541, A
	3	32.4	5.8	2338	7	US-11-293-697-1600	Sequence 1600, Ap
	4	32.2	5.7	1287	7	US-11-217-529-80999	Sequence 80999, A
c	5	31.4	5.6	654	6	US-10-488-619-2605	Sequence 2605, Ap
c	6	31.2	5.6	1532	6	US-10-196-749-121	Sequence 121, App
	7	30.8	5.5	1212	6	US-10-471-571A-4253	Sequence 4253, Ap
c	8	30.8	5.5	2920	7	US-11-293-697-683	Sequence 683, App
	9	30.4	5.4	6826	6	US-10-505-928-330	Sequence 330, App
c	10	30.2	5.4	1422	6	US-10-953-349-31587	Sequence 31587, A
	11	30.2	5.4	1491	6	US-10-953-349-10993	Sequence 10993, A
c	12	29.8	5.3	2267	7	US-11-293-697-2354	Sequence 2354, Ap
c	13	29.6	5.3	1336	6	US-10-953-349-23670	Sequence 23670, A
	14	29.2	5.2	588	6	US-10-953-349-2851	Sequence 2851, Ap
	15	29.2	5.2	1384	6	US-10-953-349-17610	Sequence 17610, A
c	16	29.2	5.2	10735	6	US-10-839-442A-3	Sequence 3, Appli
c	17	29	5.2	657	7	US-11-217-529-4785	Sequence 4785, Ap
c	18	29	5.2	2184	7	US-11-217-529-166643	Sequence 166643,
c	19	28.8	5.1	841	6	US-10-953-349-30929	Sequence 30929, A
	20	28.6	5.1	822	6	US-10-953-349-8031	Sequence 8031, Ap
	21	28.6	5.1	1947	7	US-11-217-529-4699	Sequence 4699, Ap
	22	28.6	5.1	3869	6	US-10-511-937-2853	Sequence 2853, Ap
	23	28.4	5.1	1614	6	US-10-953-349-12483	Sequence 12483, A
c	24	28.2	5.0	414	7	US-11-217-529-191170	Sequence 191170,
	25	28.2	5.0	26850	7	US-11-318-813-41	Sequence 41, Appl
	26	28	5.0	1287	7	US-11-328-070-5	Sequence 5, Appli
	27	28	5.0	1463	6	US-10-953-349-31591	Sequence 31591, A
	28	28	5.0	1704	6	US-10-953-349-11021	Sequence 11021, A
	29	28	5.0	1846	7	US-11-293-697-2144	Sequence 2144, Ap
	30	27.8	5.0	648	7	US-11-217-529-842	Sequence 842, App
	31	27.8	5.0	1321	6	US-10-953-349-20187	Sequence 20187, A
	32	27.8	5.0	1497	6	US-10-953-349-14136	Sequence 14136, A
c	33	27.8	5.0	1529	6	US-10-953-349-33663	Sequence 33663, A
	34	27.8	5.0	1587	7	US-11-217-529-223	Sequence 223, App
c	35	27.6	4.9	672	7	US-11-251-466-47	Sequence 47, Appl
c	36	27.6	4.9	672	7	US-11-264-784-74	Sequence 74, Appl
c	37	27.6	4.9	672	7	US-11-264-737-115	Sequence 115, App
c	38	27.6	4.9	672	7	US-11-265-761-87	Sequence 87, Appl
	39	27.6	4.9	1442	6	US-10-953-349-21635	Sequence 21635, A
c	40	27.6	4.9	12918	6	US-10-501-834-4	Sequence 4, Appli
	41	27.4	4.9	1299	7	US-11-217-529-77793	Sequence 77793, A
	42	27.4	4.9	1314	7	US-11-217-529-190	Sequence 190, App
c	43	27.4	4.9	1517	6	US-10-953-349-5491	Sequence 5491, Ap
c	44	27.4	4.9	3624	7	US-11-217-529-80041	Sequence 80041, A
c	45	27.2	4.8	785	6	US-10-953-349-33659	Sequence 33659, A

ALIGNMENTS

RESULT 1
US-10-471-571A-3681
; Sequence 3681, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 3681
; LENGTH: 2487
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-471-571A-3681

Query Match 6.2%; Score 35; DB 6; Length 2487;
Best Local Similarity 46.2%; Pred. No. 0.12;
Matches 116; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

```
Qy        298 AAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGG 357
              || ||  | | | || |   || |    ||||   |||| | ||| | | | ||  |
Db       2144 AATATAAAACGGTTGAATCACAGGAATCTGAAGCTAAAGATAGTAAGGAAACATACGACA 2203

Qy        358 CAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAAT 417
              ||    ||  | ||   ||| | ||  |   ||  ||        |  ||   | |
Db       2204 CAACCTTTAAAGTATATCCACAAGGTGCAACAAATGTATCGAAACATCAAGATGCACATG 2263

Qy        418 GTCAACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACT 477
              | ||| |   ||    | | | || |||     | -||  |  | ||| |   || |
Db       2264 GGCAAGATGATGCACATTCAATAGTACTAGATGATAAAACGATGGCATTGTACCAAGAAG 2323

Qy        478 AAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGA 537
                || ||          | ||| |  | |||  |  ||.| |  |  ||  |||| | |
Db       2324 TGAAACAGCAATCAGCAAGTTCATTGTTCTTATATGATGCTTTAATAGATTATCAAAACA 2383

Qy        538 ATGATGAGCTA 548
              |  || | |||
Db       2384 AGCATCAACTA 2394
```

RESULT 2
US-11-217-529-79541
; Sequence 79541, Application US/11217529

; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79541
; LENGTH: 1710
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1692)..(1692)
; OTHER INFORMATION: a, c, g, t, unknown, or other
US-11-217-529-79541

Query Match 5.9%; Score 33.2; DB 7; Length 1710;
Best Local Similarity 55.1%; Pred. No. 0.38;
Matches 65; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

Qy 47 TCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAG 106
Db 290 TCAAGAACGATCTTCAAAATTTCATGAAGAATGTAGGATTTGACCAACACAAACTCGAAG 349

Qy 107 AGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACC 164
Db 350 ATGTAGACGATGACGATATAGAAGAAGAATCCACTAGCTCCAAAGAATCTAAAATACC 407

RESULT 3
US-11-293-697-1600
; Sequence 1600, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1600
; LENGTH: 2338
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-1600

Query Match 5.8%; Score 32.4; DB 7; Length 2338;
Best Local Similarity 49.4%; Pred. No. 0.83;
Matches 84; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

Qy 274 CTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCA 333
Db 1001 CTCAGGCGGAGCAAAGTGTCCATTGAGATGTACCAGTCGCAGGTGGCAAAGCTGGAGGAT 1060

Qy 334 AAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATT 393
Db 1061 GATATCTACAAAGAGGCCGAAGAGAAGGCCCTGCTGAAGGAGGCCCTGGAGCGCATGGAG 1120

Qy 394 GATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAA 443
Db 1121 CACCAGCTGTGCCAGGAGAAGAGGGTCAACAGGGCCATCCGGCAGCAGAA 1170

RESULT 4
US-11-217-529-80999
; Sequence 80999, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80999
; LENGTH: 1287
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-80999

Query Match 5.7%; Score 32.2; DB 7; Length 1287;
Best Local Similarity 52.6%; Pred. No. 0.69;
Matches 70; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Qy 408 GGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTT 467
Db 327 GCCCATGAATAGATCAGATGTGGATTTAACAATATACTACTCTTTTAATGAAACGGTTTT 386

Qy 468 TTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGAC 527
Db 387 AGAGAACCCAAATATAGGTCAAAGTGCAGTTTTTCAGGATGGCTACATCCAAGCATTAGC 446

Qy 528 CATCAATAGAATG 540
Db 447 CATCAGTCCAGTG 459

RESULT 5
US-10-488-619-2605/c
; Sequence 2605, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2605
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2605

Query Match 5.6%; Score 31.4; DB 6; Length 654;
Best Local Similarity 51.0%; Pred. No. 0.85;
Matches 74; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

Qy 197 CTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTT 256
Db 476 CTTCAAAAGTCACCTTCACGATCTCCTCTCTGCCTTCCCGGGCCACGTAAAGGGCGACTC 417

Qy 257 TTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGT 316

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                |   |    || ||||||  || ||  ||| || | | |||| |  |   |   || |
Db        416 TGTCGTTCTCCTTGTGCCGCAGGAGGTTCTCTGCGTAGTTGAGGCGGCTGCCTCTGAACC 357

Qy        317 TCAAGGCCATGAATGCAAAGCTGTT 341
              |  ||  |    ||||| |  ||
Db        356 ACTCGGGGACATCTGCAATCCCTTT 332


RESULT 6
US-10-196-749-121/c
; Sequence 121, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C340
;  CURRENT APPLICATION NUMBER: US/10/196,749
;  CURRENT FILING DATE:  2002-07-16
;  PRIOR APPLICATION NUMBER: 10/052586
;  PRIOR FILING DATE: 2002-01-15
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059266
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063120
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063121
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063486
;  PRIOR FILING DATE: 1997-10-21
;  PRIOR APPLICATION NUMBER: 60/063540
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063541
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063544
;  PRIOR FILING DATE: 1997-10-28
;  Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 121
;   LENGTH: 1532
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-196-749-121

  Query Match             5.6%;  Score 31.2;  DB 6;  Length 1532;
  Best Local Similarity   49.4%;  Pred. No. 1.6;
  Matches   81;  Conservative    0;  Mismatches   83;  Indels    0;  Gaps    0;

Qy        140 CCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTT 199
              |||  |  || | |   |  |||  ||     ||  ||| ||     ||   || ||||
Db        633 CCAACGGAGGGTACATCGACTTCACAACATCATCCACCCTGGGGCTGATCCGCTTGGCCA 574

Qy        200 CCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTA 259
              |||  |  ||| || |||| |     ||     | | |     ||  | || ||  | | |
Db        573 CCACAATGATGTCGCTGACACTGGCTGAAGTCTTCATCTTGGCCCCAGAGCCCATTGTCA 514

Qy        260 TGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              || | ||    | |  |  |||  | |   |   ||| ||||||
Db        513 TGGCAACAAGCTTCTCTGTCAGAGTGTGACAAATCTTCAAGATG 470


RESULT 7
US-10-471-571A-4253
; Sequence 4253, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 4253
;   LENGTH: 1212
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-4253

  Query Match             5.5%;  Score 30.8;  DB 6;  Length 1212;
  Best Local Similarity   50.7%;  Pred. No. 1.9;
  Matches   74;  Conservative    0;  Mismatches   72;  Indels    0;  Gaps    0;

Qy        297 GAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAG 356
              | |||||  |  ||||    ||   |   ||| | |  ||  ||||   | | | | || |
Db         25 GCAGATGAATTAGGTTTCTTTGGTGAATATGGAGGGCAATATGTTCCAGAAACATTAATG 84

Qy        357 GCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAA 416
              |||   ||  ||  |  ||| | ||| | |   |   |  ||| |   |||    | ||
Db         85 CCAGCAATTATTGAGTTGAAAAAAGCTTATAAAGAGGCAAAAGCAGACCCAGAGTTTCAA 144

Qy        417 TGTCAACAGTGTGACTGTGCCACAGA 442
              |  ||| |    ||| |    ||||
Db        145 AGAGAACTGGAATACTATTTATCAGA 170


RESULT 8
US-11-293-697-683/c
; Sequence 683, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 683
;   LENGTH: 2920
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-683

  Query Match             5.5%;  Score 30.8;  DB 7;  Length 2920;
  Best Local Similarity   53.3%;  Pred. No. 3.1;
  Matches   65;  Conservative    0;  Mismatches   57;  Indels    0;  Gaps    0;

Qy         55 ACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGAT 114
              | | || ||| |   || | ||  |  |   | || ||| | ||||     |  || |||
Db       1411 AGGATTGAGACGCTGAGCCCAATGCAGGTGATGTAGTCCAGAACTTTGTCGGTCATCGAT 1352

Qy        115 CATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 174
              || || || | ||  || |||  || |||      ||  |  ||||  | | | ||
Db       1351 TTGGAGGACATGAGAATGGAAAAAGACATCACCACACTGGTGTAGTTACAGCGGCATTTC 1292

Qy        175 AC 176
              ||
Db       1291 AC 1290
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RESULT 9
US-10-505-928-330
; Sequence 330, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
;  APPLICANT: Ludwig Institute for Cancer Research et al.
;  TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
;  FILE REFERENCE: 28967/39178
;  CURRENT APPLICATION NUMBER: US/10/505,928
;  CURRENT FILING DATE:  2004-08-27
;  PRIOR APPLICATION NUMBER: US 60/363,019
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: PatentIn 3.2
; SEQ ID NO 330
;   LENGTH: 6826
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-505-928-330

  Query Match             5.4%;  Score 30.4;  DB 6;  Length 6826;
  Best Local Similarity   53.3%;  Pred. No. 6.8;
  Matches   64;  Conservative    0;  Mismatches   56;  Indels    0;  Gaps    0;

Qy        381 GCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACA 440
              ||  || |  |||| ||||  |      ||  |  |||   |   |   ||   || | ||
Db       3630 GCCTACGGTCATTGGTGAGAGGAAGTGGGGACAAAATTGAAGGGGGTGGAGCATGACTCA 3689

Qy        441 GAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCT 500
               | || |||||||||   |  || | |||| |  |   |   | ||| ||| | | | ||
Db       3690 AAGCTTCTCCCTGGAGAGAGAGGGTATTTAGACCAGGCATTCCTAGCCCTGAAAATTCCT 3749


RESULT 10
US-10-953-349-31587/c
; Sequence 31587, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31587
;   LENGTH: 1422
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-10-953-349-31587

  Query Match             5.4%;  Score 30.2;  DB 6;  Length 1422;
  Best Local Similarity   49.7%;  Pred. No. 3.2;
  Matches   77;  Conservative    0;  Mismatches   78;  Indels    0;  Gaps    0;

Qy        217 ATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTT 276
              || || |  | ||| ||| | | |  |||||  ||||| || | |  ||   |||
Db        430 ATGACGATGGCGAGATGCGTCGGCGTCAGAATAACCTCCTTGAAGCGGATGATGTTGGGA 371

Qy        277 AGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAG 336
              || | | | |   |  ||||  ||| |  |       ||||    | ||      |   |
Db        370 TGCCGCAGCGACCTGTGGTTGATGATCTCTCTCTGCACGTTCTCATCGATCTTCTCGCCG 311

Qy        337 CTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGA 371
              | ||  ||| |    | |  |  || ||  | |||
Db        310 CGGTCGATGTACTTGACAGCGACGAGCTCGCCGGA 276


RESULT 11
US-10-953-349-10993
; Sequence 10993, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10993
;   LENGTH: 1491
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-10993

  Query Match             5.4%;  Score 30.2;  DB 6;  Length 1491;
  Best Local Similarity   51.9%;  Pred. No. 3.3;
  Matches   68;  Conservative    0;  Mismatches   63;  Indels    0;  Gaps    0;

Qy        274 CTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCA 333
              || |  || |   | | ||   ||||| | |  | || ||   || |  || |||| |
Db        929 CTGAAGAGGAAAGAGGCGGCAAAGAAGAGGAAGAAAGTCGATCCCATGATCAAGAATCCT 988

Qy        334 AAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATT 393
              ||   |   | |||  |   | | | |||  | | ||   |||| ||  ||      |
Db        989 GAGAGATACCTCGATGATCCTAAGAATATCCATTTCGAGACAAACGTGAAGAATAGGTTA 1048

Qy        394 GATGAGCTGTT 404
               | ||||||||
Db       1049 TACGAGCTGTT 1059


RESULT 12
US-11-293-697-2354/c
; Sequence 2354, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2354
;   LENGTH: 2267
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-2354

  Query Match             5.3%;  Score 29.8;  DB 7;  Length 2267;
  Best Local Similarity   49.7%;  Pred. No. 5.7;
  Matches   76;  Conservative    0;  Mismatches   77;  Indels    0;  Gaps    0;

Qy        235 CTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGAC 294
              | ||||  ||       | |||  | ||     | ||| | |  ||  |||| |   |
Db        963 CCGGCCATCAAGTTCCCTTCTGATCTGGGCTGCTTGTTCATCTGCGTTATCCAGCTGACA 904

Qy        295 TTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAA 354
              |  |  ||  |  || ||| |||| ||    | ||| |  ||    |  || | | |
Db        903 TGCATTATAAAGGAGCTGGTGTTCTAGTTTTTTAATACCCAGAATCTGCTGAAACATTTC 844

Qy        355 AGGCAGATCTTTCTGGATCAAAACATGCTGACA 387
              |   || | ||  || | ||| || | | | | |
Db        843 ATAGAGTTGTTCCTTGCTCAGAATAAGTTCAGA 811


RESULT 13
US-10-953-349-23670/c
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; Sequence 23670, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23670
;   LENGTH: 1336
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-23670

  Query Match             5.3%;  Score 29.6;  DB 6;  Length 1336;
  Best Local Similarity   52.4%;  Pred. No. 4.9;
  Matches   65;  Conservative    0;  Mismatches   59;  Indels    0;  Gaps    0;

Qy        210 CTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCT 269
              |||| | ||||  | ||| | | ||  ||    |      |||||  | | |  |    ||
Db        640 CTCTGTAATAAGCACTGGTAATGGCACGGTACCGCTCTTGACCTGCTGTGTCCCAGATCT 581

Qy        270 GTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAA 329
              |||| ||  |||| | |       || ||||||  |      |  ||  ||||  ||   |
Db        580 GTGCTTTCACAGTCTTTCCCTCTACCTGAAGAGTTCTGGTGGCGAACTCAACTCCGATAG 521

Qy        330 TGCA 333
              || |
Db        520 TGGA 517


RESULT 14
US-10-953-349-2851
; Sequence 2851, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2851
;   LENGTH: 588
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-2851

  Query Match             5.2%;  Score 29.2;  DB 6;  Length 588;
  Best Local Similarity   43.3%;  Pred. No. 4.1;
  Matches  136;  Conservative    0;  Mismatches  178;  Indels    0;  Gaps    0;

Qy        201 CAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTAT 260
              | |  |||||  |||   ||  |      |   | | | |  || |||| |    | |
Db        161 CCGCAAGATCCATCTCCGAATCAGGATCTGAACCGGGACGTGAAGCAAGATCAGAATCTT 220

Qy        261 GACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAA 320
              |  |   | |||    ||||  |   |  || |   ||||  | |   |||||||  |  |
Db        221 CAACAGAATCTGCAGATGCAGAAGGAAGAAGAAGAGGAAGGAGAAGGTGGTGGAGGTGGA 280

Qy        321 GGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACAT 380
              |    ||    | ||| | |  ||       | | |      | ||| | | |  |
Db        281 GAGTTTGTGAACGAAGATACTGGTGAGATTGGAGGGCCTAGAGGTCCTGAACCGACTCGG 340

Qy        381 GCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACA 440
              | |   |    |  | || |  | || |||| |    | ||  |   |||  | ||
Db        341 TACGGCGATTGGGAACAACGTGGTCGATGCTCTGATTTCTGAGAGGATTCATGTATCCCT 400

Qy        441 GAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCT 500
              |   |    | ||      |      || |   |||| |  ||  ||  ||    || | |
Db        401 GTGTTTTAGCTTGTTCTTATATATTTCTGGGAAAAATGGAAATAAATTCGTTTTATGTGT 460

Qy        501 TCATGCTTTCAGAA 514
              | |||  ||   ||
Db        461 TTATGTATTTGCAA 474


RESULT 15
US-10-953-349-17610
; Sequence 17610, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17610
;   LENGTH: 1384
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-17610

  Query Match             5.2%;  Score 29.2;  DB 6;  Length 1384;
  Best Local Similarity   48.8%;  Pred. No. 6.7;
  Matches   79;  Conservative    0;  Mismatches   83;  Indels    0;  Gaps    0;

Qy        288 TGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGA 347
              | || |   ||| |  |    ||   |  |||  |  |||| |   ||   ||
Db        828 TCAGAATCAAAAGCTAGAGTCAGTTATGGCCAAACCTCTGAAGGATCAGGCTTTTGCTAC 887

Qy        348 TCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACA 407
              |||  | | |  |       || | ||||||  |   ||| ||||||  | ||||   | |
Db        888 TCCAGATAAGGTGGCTGAACTTGTTCAAAAGGTCAGGACTGCTATTCAGGAGCAACTGCC 947

Qy        408 GGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTC 449
              ||   |||  |  || |     |  |      |||||| || ||
Db        948 GGTGGTGATAGAAAAGATGAAGCTTTATTTACAGAATTCATC 989


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OM nucleic - nucleic search, using sw model

Run on: June 9, 2006, 22:33:03 ; Search time 3553.79 Seconds
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Title: US-10-821-670A-101
Perfect score: 561
Sequence: 1 gggatgttccagtgcctcaa.....tgagctatctgaatgcttcc 561

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 6366136 seqs, 31973710525 residues

Word size : 1

Total number of hits satisfying chosen parameters: 12730834

Minimum DB seq length: 0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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c 2	561	100.0	561	2	AR596008	AR596008 Sequence
3	558	99.5	666	2	AR595952	AR595952 Sequence
c 4	558	99.5	666	2	AR595953	AR595953 Sequence
5	510	90.9	1533	2	AR595959	AR595959 Sequence
c 6	510	90.9	1533	2	AR595960	AR595960 Sequence
7	510	90.9	1599	2	AR595956	AR595956 Sequence
c 8	510	90.9	1599	2	AR595957	AR595957 Sequence
9	507	90.4	591	2	AR595954	AR595954 Sequence
c 10	507	90.4	591	2	AR595955	AR595955 Sequence
11	507	90.4	669	14	FCIL12P35	Y07761 Felis catus
12	494	88.1	591	2	AR242439	AR242439 Sequence
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14	494	88.1	591	2	AR322422	AR322422 Sequence
15	494	88.1	1441	2	AR242438	AR242438 Sequence
16	494	88.1	1441	2	AR280206	AR280206 Sequence
17	494	88.1	1441	2	AR322421	AR322421 Sequence
18	450	80.2	669	14	FCU83185	U83185 Felis catus
19	253	45.1	285	14	AF054605	AF054605 Felis cat
20	221	39.4	689	2	AR242451	AR242451 Sequence
21	221	39.4	689	2	AR280219	AR280219 Sequence
22	221	39.4	689	2	AR322434	AR322434 Sequence
23	195	34.8	669	2	AX076201	AX076201 Sequence
24	195	34.8	669	2	AX076483	AX076483 Sequence
25	195	34.8	4201	2	AX076477	AX076477 Sequence
26	178	31.7	660	2	AX154615	AX154615 Sequence
27	120	21.4	660	2	AX154616	AX154616 Sequence
28	115	20.5	660	2	AX154614	AX154614 Sequence
29	115	20.5	660	2	AX154621	AX154621 Sequence
30	102	18.2	660	2	AX154619	AX154619 Sequence
31	98	17.5	657	8	AY191828	AY191828 Synthetic
32	98	17.5	660	2	AX154617	AX154617 Sequence
33	84	15.0	660	2	AX154620	AX154620 Sequence
34	81	14.4	591	2	BD171284	BD171284 Novel can
35	81	14.4	591	2	AR595963	AR595963 Sequence
c 36	81	14.4	591	2	AR595964	AR595964 Sequence
37	81	14.4	666	2	AR595961	AR595961 Sequence
c 38	81	14.4	666	2	AR595962	AR595962 Sequence
39	81	14.4	669	2	AR151062	AR151062 Sequence
40	81	14.4	669	2	AR151072	AR151072 Sequence
41	81	14.4	669	2	BD014654	BD014654 Process f
42	81	14.4	669	2	BD014664	BD014664 Process f
43	81	14.4	669	2	E15018	E15018 Canine mRNA
44	81	14.4	669	2	AR316461	AR316461 Sequence
45	81	14.4	669	2	AR316471	AR316471 Sequence
46	81	14.4	669	14	CFU49085	U49085 Canis famil
47	81	14.4	1282	2	BD171283	BD171283 Novel can
48	81	14.4	1455	2	AR596009	AR596009 Sequence
c 49	81	14.4	1455	2	AR596010	AR596010 Sequence
50	81	14.4	1533	2	AR595973	AR595973 Sequence
c 51	81	14.4	1533	2	AR595974	AR595974 Sequence
52	81	14.4	1599	2	AR595971	AR595971 Sequence
c 53	81	14.4	1599	2	AR595972	AR595972 Sequence
54	71	12.7	71	2	AX076207	AX076207 Sequence
55	65	11.6	660	2	AR008951	AR008951 Sequence
56	65	11.6	660	2	BD007071	BD007071 IL-12 gen
57	65	11.6	660	2	BD007079	BD007079 Gene expr
58	65	11.6	660	2	BD136037	BD136037 Interfero
59	65	11.6	660	2	I28592	I28592 Sequence 3
60	65	11.6	660	2	AX154618	AX154618 Sequence
61	65	11.6	660	2	AX154634	AX154634 Sequence
62	65	11.6	702	2	CQ829447	CQ829447 Sequence
63	65	11.6	721	2	AR052862	AR052862 Sequence
64	65	11.6	721	2	AR288174	AR288174 Sequence
65	65	11.6	721	2	AR567161	AR567161 Sequence
66	65	11.6	762	2	BD105971	BD105971 Animal mo
67	65	11.6	762	2	CQ803343	CQ803343 Sequence
68	65	11.6	762	2	AR533401	AR533401 Sequence
69	65	11.6	762	5	AF101062	AF101062 Homo sapi
70	65	11.6	780	5	MMU19842	U19842 Macaca mula
71	65	11.6	823	5	AF180562	AF180562 Homo sapi
72	65	11.6	856	2	BD165801	BD165801 Antibody
73	65	11.6	1020	2	CQ716168	CQ716168 Sequence
74	65	11.6	1021	5	BC104982	BC104982 Homo sapi
75	65	11.6	1021	5	BC104984	BC104984 Homo sapi
76	65	11.6	1026	2	AR091390	AR091390 Sequence
77	65	11.6	1026	2	AR380496	AR380496 Sequence
78	65	11.6	1026	5	HUMCLMF35	M65271 Human cytot
79	65	11.6	1287	2	AR393790	AR393790 Sequence
80	65	11.6	1287	2	AX084108	AX084108 Sequence
81	65	11.6	1316	2	AR050785	AR050785 Sequence
82	65	11.6	1316	2	AR212036	AR212036 Sequence
83	65	11.6	1316	5	HUMNKSFP35	M65291 Human natur
84	65	11.6	1364	2	AR082685	AR082685 Sequence
85	65	11.6	1364	2	AR122961	AR122961 Sequence
86	65	11.6	1364	2	I28326	I28326 Sequence 3
87	65	11.6	1364	2	I89771	I89771 Sequence 3
88	65	11.6	1395	2	AR309637	AR309637 Sequence
89	65	11.6	1444	2	CS032085	CS032085 Sequence
90	65	11.6	1444	2	CS041037	CS041037 Sequence
91	65	11.6	1444	2	CS143811	CS143811 Sequence

92	65	11.6	1560	2	AR091395	AR091395 Sequence
93	65	11.6	1623	2	AR091394	AR091394 Sequence
94	65	11.6	1645	2	A92078	A92078 Sequence 2
95	65	11.6	1645	2	AR230689	AR230689 Sequence
96	65	11.6	3205	2	CS131489	CS131489 Sequence
97	65	11.6	5686	2	BD136048	BD136048 Interfero
98	65	11.6	6139	2	AR091393	AR091393 Sequence
99	65	11.6	11792	5	AF404773	AF404773 Homo sapi
100	65	11.6	157079	5	AC010370	AC010370 Homo sapi
101	65	11.6	176108	5	AC026118	AC026118 Homo sapi
102	65	11.6	300140	12	AC129109	AC129109 Homo sapi
103	60	10.7	666	2	AX154612	AX154612 Sequence
104	60	10.7	666	2	AX154613	AX154613 Sequence
105	55	9.8	786	5	CTU19835	U19835 Cercocebus
106	50	8.9	669	14	ECIL12P35	Y11130 Equus cabal
107	50	8.9	817	14	AY686642	AY686642 Equus cab
108	50	8.9	1626	8	AF401989	AF401989 Synthetic
c 109	45	8.0	76	2	AX076205	AX076205 Sequence
c 110	45	8.0	76	2	AX076208	AX076208 Sequence
111	45	8.0	669	14	AB107653	AB107653 Lama glam
112	45	8.0	669	14	AB246672	AB246672 Camelus b
113	43	7.7	79	2	AR242449	AR242449 Sequence
114	43	7.7	79	2	AR280217	AR280217 Sequence
115	43	7.7	79	2	AR322432	AR322432 Sequence
116	41	7.3	690	14	AB246272	AB246272 Bubalus c
117	41	7.3	690	14	AB246359	AB246359 Bubalus b
118	41	7.3	690	14	BTU14416	U14416 Bos taurus
119	41	7.3	703	2	E35793	E35793 Process for
120	38	6.8	1426	14	PIGIL12PSU	L35765 Sus scrofa
121	37	6.6	785	5	AY234219	AY234219 Papio anu
c 122	34	6.1	559	7	BV429425	BV429425 S237P6482
123	30	5.3	39	2	AR595997	AR595997 Sequence
124	30	5.3	672	6	AF288520	AF288520 Marmota m
125	30	5.3	672	6	MMIL12P35	X97018 M.monax mRN
126	29	5.2	618	14	AY603407	AY603407 Capra hir
127	29	5.2	666	14	AF173557	AF173557 Ovis arie
128	29	5.2	666	14	AY232819	AY232819 Bubalus b
129	29	5.2	666	14	CEU57751	U57751 Cervus elap
130	29	5.2	690	14	AB246352	AB246352 Bubalus b
131	29	5.2	690	14	AF003542	AF003542 Capra hir
132	29	5.2	711	14	BTA271034	AJ271034 Bos tauru
133	29	5.2	714	14	OAR271035	AJ271035 Ovis arie
c 134	27	4.8	322	7	BV094414	BV094414 RPAMMSEQ0
135	27	4.8	582	2	AR393785	AR393785 Sequence
136	27	4.8	582	2	AX084103	AX084103 Sequence
137	27	4.8	660	2	E26662	E26662 Improved me
138	27	4.8	700	6	S82412S4	S82418 interleukin
139	27	4.8	713	2	AR069652	AR069652 Sequence
140	27	4.8	713	6	AF128212	AF128212 Mus muscu
141	27	4.8	713	6	AF128213	AF128213 Mus muscu
142	27	4.8	786	6	AF128210	AF128210 Mus muscu
143	27	4.8	786	6	AF128211	AF128211 Mus muscu
144	27	4.8	793	6	AF177031	AF177031 Rattus no
145	27	4.8	827	6	AF421396	AF421396 Sigmodon
146	27	4.8	1265	6	MUSIL35A	M86672 Mus musculu
147	27	4.8	1278	2	AR393789	AR393789 Sequence
148	27	4.8	1278	2	AX084107	AX084107 Sequence
149	27	4.8	1569	2	AR393796	AR393796 Sequence
150	27	4.8	1569	2	AX084114	AX084114 Sequence
151	27	4.8	1669	8	AF411293	AF411293 Synthetic
152	27	4.8	2013	2	AR393795	AR393795 Sequence
153	27	4.8	2013	2	AX084113	AX084113 Sequence
154	27	4.8	2438	2	CQ812173	CQ812173 Sequence
155	27	4.8	2709	2	AR393797	AR393797 Sequence
156	27	4.8	2709	2	AX084115	AX084115 Sequence
157	27	4.8	5252	2	CQ803341	CQ803341 Sequence
158	27	4.8	5966	2	BD136050	BD136050 Interfero
159	27	4.8	9049	2	CQ803350	CQ803350 Sequence
160	27	4.8	10633	2	CQ803349	CQ803349 Sequence
161	27	4.8	11746	2	CQ803348	CQ803348 Sequence
162	27	4.8	38246	2	CQ803351	CQ803351 Sequence
c 163	27	4.8	195059	6	AC121306	AC121306 Mus muscu
c 164	27	4.8	223879	12	AC111877	AC111877 Rattus no
165	26	4.6	660	2	BD007080	BD007080 Gene expr
166	26	4.6	660	2	BD007081	BD007081 Gene expr
167	26	4.6	660	2	BD136038	BD136038 Interfero
168	26	4.6	660	2	BD136039	BD136039 Interfero
169	25	4.5	1239	6	AB085791	AB085791 Mesocrice
c 170	24	4.3	27	2	AR595996	AR595996 Sequence
c 171	24	4.3	36	2	AR242450	AR242450 Sequence
c 172	24	4.3	36	2	AR280218	AR280218 Sequence
c 173	24	4.3	36	2	AR322433	AR322433 Sequence
c 174	24	4.3	41	2	AR595998	AR595998 Sequence
c 175	24	4.3	144	14	AY388980S3	AY388982 Sus scrof
176	23	4.1	666	6	AB025723	AB025723 Cavia por
177	22	3.9	146	14	AY575615	AY575615 Ovis arie
178	22	3.9	146	14	AY575616	AY575616 Ovis arie
179	22	3.9	586	7	BV209307	BV209307 IL12A_306
180	22	3.9	221805	6	AC105515	AC105515 Rattus no
c 181	22	3.9	225611	12	AC111446	AC111446 Rattus no
c 182	22	3.9	237532	6	AC094950	AC094950 Rattus no
183	21	3.7	32	2	AR090263	AR090263 Sequence
184	21	3.7	32	2	AR197298	AR197298 Sequence
185	21	3.7	32	2	AR259452	AR259452 Sequence
c 186	21	3.7	733	7	BV616987	BV616987 S216P6464
187	21	3.7	60511	5	HS618F1	AL023878 Human DNA
188	21	3.7	114233	5	AP000783	AP000783 Homo sapi
c 189	21	3.7	136388	14	AC146679	AC146679 Felis cat
c 190	21	3.7	143814	12	AC151632	AC151632 Felis cat
c 191	21	3.7	158375	12	AC080039	AC080039 Homo sapi
c 192	21	3.7	163846	5	AC136619	AC136619 Homo sapi
193	21	3.7	168721	5	AC136431	AC136431 Homo sapi
194	21	3.7	173912	12	AC141075	AC141075 Homo sapi
195	21	3.7	175785	12	AC138897	AC138897 Homo sapi
c 196	21	3.7	179245	5	HUAC002492	AC002492 Human Chr
197	21	3.7	185030	5	AC008785	AC008785 Homo sapi
c 198	21	3.7	186535	12	AL589793	AL589793 Homo sapi
c 199	21	3.7	187721	5	AC126763	AC126763 Homo sapi
c 200	21	3.7	188256	12	AC160269	AC160269 Bos tauru

ALIGNMENTS

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RESULT 1
AR596007
LOCUS       AR596007                561 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 101 from patent US 6818444.
ACCESSION   AR596007
VERSION     AR596007.1  GI:56646988
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 561)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 101 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .561
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 561;  DB 2;  Length 561;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-294;
  Matches  561;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
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Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540

Qy        541 ATGAGCTATCTGAATGCTTCC 561
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Db        541 ATGAGCTATCTGAATGCTTCC 561
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RESULT 2
AR596008/c
LOCUS AR596008 561 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 103 from patent US 6818444.
ACCESSION AR596008
VERSION AR596008.1 GI:56646989
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 561)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 103 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .561
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 100.0%; Score 561; DB 2; Length 561;
Best Local Similarity 100.0%; Pred. No. 1.2e-294;
Matches 561; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1
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RESULT 3
AR595952
LOCUS AR595952 666 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 32 from patent US 6818444.
ACCESSION AR595952
VERSION AR595952.1 GI:56646933
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 666)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 32 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .666
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 99.5%; Score 558; DB 2; Length 666;
Best Local Similarity 100.0%; Pred. No. 5.2e-293;
Matches 558; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648

Qy        544 AGCTATCTGAATGCTTCC 561
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Db        649 AGCTATCTGAATGCTTCC 666


RESULT 4
AR595953/c
LOCUS       AR595953                666 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 34 from patent US 6818444.
ACCESSION   AR595953
VERSION     AR595953.1  GI:56646934
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 34 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             99.5%;  Score 558;  DB 2;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 5.2e-293;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        544 AGCTATCTGAATGCTTCC 561
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Db         18 AGCTATCTGAATGCTTCC 1


RESULT 5
AR595959
LOCUS       AR595959                1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 43 from patent US 6818444.
ACCESSION   AR595959
VERSION     AR595959.1  GI:56646940
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 43 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
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ORIGIN

  Query Match             90.9%;  Score 510;  DB 2;  Length 1533;
  Best Local Similarity   99.8%;  Pred. No. 8.2e-267;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1032

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1092

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1093 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1152

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
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Db       1153 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1212

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1213 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1272

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1273 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1332

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1333 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1392

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1393 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1452

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1453 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1512
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Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db       1513 ATGAGCTATCTGAATGCTTCC 1533


RESULT 6
AR595960/c
LOCUS       AR595960                1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 45 from patent US 6818444.
ACCESSION   AR595960
VERSION     AR595960.1  GI:56646941
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 45 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             90.9%;  Score 510;  DB 2;  Length 1533;
  Best Local Similarity   99.8%;  Pred. No. 8.2e-267;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1


RESULT 7
AR595956
LOCUS       AR595956                1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 38 from patent US 6818444.
ACCESSION   AR595956
VERSION     AR595956.1  GI:56646937
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 38 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             90.9%;  Score 510;  DB 2;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 8.2e-267;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1098

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1158

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1218

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1219 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1278

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1338

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1398

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1458

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1459 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1518

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1519 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1578

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db       1579 ATGAGCTATCTGAATGCTTCC 1599


RESULT 8
AR595957/c
LOCUS       AR595957                1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 40 from patent US 6818444.
ACCESSION   AR595957
VERSION     AR595957.1  GI:56646938
KEYWORDS    .
SOURCE      Unknown.
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  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 40 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             90.9%;  Score 510;  DB 2;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 8.2e-267;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1


RESULT 9
AR595954
LOCUS       AR595954                591 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 35 from patent US 6818444.
ACCESSION   AR595954
VERSION     AR595954.1  GI:56646935
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 35 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             90.4%;  Score 507;  DB 2;  Length 591;
  Best Local Similarity   99.8%;  Pred. No. 3.8e-265;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573

Qy        544 AGCTATCTGAATGCTTCC 561
              ||||||||||||||||||
Db        574 AGCTATCTGAATGCTTCC 591


RESULT 10
AR595955/c
LOCUS       AR595955                591 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 37 from patent US 6818444.
ACCESSION   AR595955
VERSION     AR595955.1  GI:56646936
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 37 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             90.4%;  Score 507;  DB 2;  Length 591;
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  Best Local Similarity   99.8%;  Pred. No. 3.8e-265;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        544 AGCTATCTGAATGCTTCC 561
              ||||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1


RESULT 11
FCIL12P35
LOCUS       FCIL12P35                669 bp    mRNA    linear   MAM 18-APR-2005
DEFINITION  Felis catus mRNA for interleukin-12 p35 chain.
ACCESSION   Y07761
VERSION     Y07761.1  GI:2102662
KEYWORDS    interleukin-12 subunit p35.
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1
  AUTHORS   Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
  TITLE     Molecular cloning of cat interleukin-12
  JOURNAL   Immunogenetics 45 (6), 462-463 (1997)
   PUBMED   9089110
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Schijns,V.E.C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
            Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
            Utrecht, NETHERLANDS
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Felis catus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
                     /cell_type="lymphocyte"
                     /tissue_type="peripheral blood"
     gene            1. .669
                     /gene="IL-12.p35"
     CDS             1. .669
                     /gene="IL-12.p35"
                     /function="heterodimer with IL-12 p40 chain"
                     /codon_start=1
                     /product="interleukin-12 p35 chain"
                     /protein_id="CAA69067.1"
                     /db_xref="GI:2102663"
                     /db_xref="GOA:O02743"
                     /db_xref="InterPro:IPR004281"
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                     /db_xref="UniProtKB/Swiss-Prot:O02743"
                     /translation="MCPPRGLLLVTILVLLNHLDHLSLARNLPTPTPSPGMFQCLNHS
                     QTLLRAISNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
                     REISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAMNAKLLMDPKRQIFLDQ
                     NMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSY
                     LNAS"
ORIGIN

  Query Match             90.4%;  Score 507;  DB 14;  Length 669;
  Best Local Similarity   99.8%;  Pred. No. 3.8e-265;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        529 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 588

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648

Qy        544 AGCTATCTGAATGCTTCC 561
              ||||||||||||||||||
Db        649 AGCTATCTGAATGCTTCC 666


RESULT 12
AR242439
LOCUS       AR242439                 591 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 9 from patent US 6472509.
ACCESSION   AR242439
VERSION     AR242439.1  GI:27288856
KEYWORDS    .
```

```
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 9 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             88.1%;  Score 494;  DB 2;  Length 591;
  Best Local Similarity   99.8%;  Pred. No. 4.9e-258;
  Matches  544;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
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Db        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
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Db        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
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Db        454 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATC 513

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573

Qy        544 AGCTA 548
              |||||
Db        574 AGCTA 578


RESULT 13
AR280207
LOCUS       AR280207                591 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 9 from patent US 6518045.
ACCESSION   AR280207
VERSION     AR280207.1  GI:29715597
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 9 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             88.1%;  Score 494;  DB 2;  Length 591;
  Best Local Similarity   99.8%;  Pred. No. 4.9e-258;
  Matches  544;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
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Db         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
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Db         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
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Db        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
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Db        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
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Db        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
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Db        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
              ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        454 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATC 513

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573

Qy        544 AGCTA 548
              |||||
Db        574 AGCTA 578


RESULT 14
AR322422
LOCUS       AR322422                591 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 9 from patent US 6566097.
ACCESSION   AR322422
VERSION     AR322422.1  GI:33708175
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 9 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
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FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match           88.1%;  Score 494;  DB 2;  Length 591;
  Best Local Similarity   99.8%;  Pred. No. 4.9e-258;
  Matches  544;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
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Db         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
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Db         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
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Db        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
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Db        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        454 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATC 513

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573

Qy        544 AGCTA 548
              |||||
Db        574 AGCTA 578


RESULT 15
AR242438
LOCUS       AR242438                1441 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 8 from patent US 6472509.
ACCESSION   AR242438
VERSION     AR242438.1  GI:27288855
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1441)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 8 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .1441
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match           88.1%;  Score 494;  DB 2;  Length 1441;
  Best Local Similarity   99.8%;  Pred. No. 4.6e-258;
  Matches  544;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 310

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 370

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 430

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 490

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 550

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        551 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 610

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 670

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        671 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATC 730

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        731 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 790

Qy        544 AGCTA 548
              |||||
Db        791 AGCTA 795


RESULT 16
AR280206
LOCUS       AR280206                1441 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 8 from patent US 6518045.
ACCESSION   AR280206
VERSION     AR280206.1  GI:29715596
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1441)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 8 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .1441
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match           88.1%;  Score 494;  DB 2;  Length 1441;
  Best Local Similarity   99.8%;  Pred. No. 4.6e-258;
  Matches  544;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 310

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 370

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 430

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 490

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 550

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        551 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 610

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 670

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
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Db        671 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATC 730

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
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Db        731 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 790

Qy        544 AGCTA 548
              |||||
Db        791 AGCTA 795
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RESULT 17
AR322421
LOCUS       AR322421                1441 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 8 from patent US 6566097.
ACCESSION   AR322421
VERSION     AR322421.1  GI:33708174
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1441)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 8 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .1441
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             88.1%;  Score 494;  DB 2;  Length 1441;
  Best Local Similarity   99.8%;  Pred. No. 4.6e-258;
  Matches  544;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 310

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 370

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 430

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 490

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 550

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        551 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 610

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 670

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
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Db        671 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATC 730

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        731 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 790

Qy        544 AGCTA 548
              |||||
Db        791 AGCTA 795
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RESULT 18
FCU83185
LOCUS       FCU83185                669 bp    mRNA    linear   MAM 16-JUL-1999
DEFINITION  Felis catus interleukin-12 p35 subunit (IL-12) mRNA, complete cds.
ACCESSION   U83185
VERSION     U83185.1  GI:2735052
KEYWORDS    .
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Nucleotide and predicted peptide sequence of feline interleukin-12
            (IL-12)
  JOURNAL   DNA Seq. 8 (1-2), 77-82 (1997)
   PUBMED   9522125
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal
            Veterinary Medicine, University of Zurich, Winterthurerstrasse 260,
            Zurich, ZH 8057, Switzerland
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Felis catus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
     CDS             1. .669
                     /note="cytokine"
                     /codon_start=1
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ORIGIN

  Query Match             80.2%;  Score 450;  DB 14;  Length 669;
  Best Local Similarity   99.6%;  Pred. No. 5.3e-234;
  Matches  550;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
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Db        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        169 AAGGCCAGACAAACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        529 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 588

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648

Qy        544 AGCTATCTGAAT 555
              ||||||||||||
Db        649 AGCTATCTGAAT 660


RESULT 19
AF054605
LOCUS       AF054605                 285 bp    mRNA    linear   MAM 26-JUL-2000
DEFINITION  Felis catus interleukin 12 p35 subunit mRNA, partial cds.
ACCESSION   AF054605
VERSION     AF054605.1  GI:3126818
KEYWORDS    .
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Harley,R., Helps,C.R., Harbour,D.A., Gruffydd-Jones,T.J. and
            Day,M.J.
  TITLE     Cytokine mRNA expression in lesions in cats with chronic
            gingivostomatitis
  JOURNAL   Clin. Diagn. Lab. Immunol. 6 (4), 471-478 (1999)
   PUBMED   10391845
REFERENCE   2  (bases 1 to 285)
  AUTHORS   Harley,R., Helps,C.R., Gruffydd-Jones,T.J., Day,M.J. and
            Harbour,D.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-1998) Clinical Veterinary Science, University of
            Bristol, Langford House, Langford, Bristol BS40 7DU, U.K.
FEATURES             Location/Qualifiers
     source          1. .285
                     /organism="Felis catus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
                     /cell_line="FL4"
                     /cell_type="T cell"
                     /note="persistant FIV infection"
     CDS             <1. .>285
                     /codon_start=3
                     /product="interleukin 12 p35 subunit"
                     /protein_id="AAC15978.1"
                     /db_xref="GI:3126819"
                     /translation="LLRAISNTLHKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLP
                     LELTMNESCLASREISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVE"
ORIGIN

  Query Match             45.1%;  Score 253;  DB 14;  Length 285;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-126;
  Matches  253;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 92

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 152

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 212

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 272

Qy        304 TACCAGGTGGAGT 316
              |||||||||||||
Db        273 TACCAGGTGGAGT 285


RESULT 20
AR242451
LOCUS       AR242451                 689 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 26 from patent US 6472509.
ACCESSION   AR242451
VERSION     AR242451.1  GI:27288868
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 26 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .689
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             39.4%;  Score 221;  DB 2;  Length 689;
  Best Local Similarity   99.2%;  Pred. No. 6.8e-109;
  Matches  371;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
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Qy        175 ACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGC 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 ACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGC 345

Qy        235 CTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGAC 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 CTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGAC 405

Qy        295 TTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAA 354
              |||||||||||||||||||||||||||||||||||||||||||| | ||||||||||||
Db        406 TTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAA 465

Qy        355 AGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTG 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 AGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTG 525

Qy        415 AATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAA 474
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        526 AATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAA 585

Qy        475 ACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAAT 534
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAAT 645

Qy        535 AGAATGATGAGCTA 548
              ||||||||||||||
Db        646 AGAATGATGAGCTA 659
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RESULT 21
AR280219
LOCUS       AR280219                689 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 26 from patent US 6518045.
ACCESSION   AR280219
VERSION     AR280219.1  GI:29715609
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 26 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .689
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             39.4%;  Score 221;  DB 2;  Length 689;
  Best Local Similarity   99.2%;  Pred. No. 6.8e-109;
  Matches  371;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        175 ACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGC 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 ACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGC 345

Qy        235 CTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGAC 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 CTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGAC 405

Qy        295 TTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAA 354
              |||||||||||||||||||||||||||||||||||||||||||| | ||||||||||||
Db        406 TTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAA 465

Qy        355 AGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTG 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 AGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTG 525

Qy        415 AATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAA 474
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Db        526 AATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAA 585

Qy        475 ACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAAT 534
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAAT 645

Qy        535 AGAATGATGAGCTA 548
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Db        646 AGAATGATGAGCTA 659
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RESULT 22
AR322434
LOCUS       AR322434                689 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 26 from patent US 6566097.
ACCESSION   AR322434
VERSION     AR322434.1  GI:33708187
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 26 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .689
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             39.4%;  Score 221;  DB 2;  Length 689;
  Best Local Similarity   99.2%;  Pred. No. 6.8e-109;
  Matches  371;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        175 ACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGC 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 ACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGC 345

Qy        235 CTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGAC 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 CTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGAC 405

Qy        295 TTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAA 354
              |||||||||||||||||||||||||||||||||||||||||||| | ||||||||||||
Db        406 TTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAA 465

Qy        355 AGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTG 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 AGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTG 525

Qy        415 AATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAA 474
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        526 AATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAA 585

Qy        475 ACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAAT 534
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAAT 645

Qy        535 AGAATGATGAGCTA 548
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Db        646 AGAATGATGAGCTA 659
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RESULT 23
AX076201
LOCUS       AX076201                669 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 2 from Patent WO0104155.
ACCESSION   AX076201
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VERSION     AX076201.1  GI:12710826
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 2 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="feline IL-12 p35"
ORIGIN

  Query Match             34.8%;  Score 195;  DB 2;  Length 669;
  Best Local Similarity   99.0%;  Pred. No. 1.1e-94;
  Matches  395;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
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Db        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        169 AAGGCCAGACAAACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAAT 288

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              |||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCC 348

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 402
              |||||||||||||||||||||||||||||||||||||||
Db        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 507


RESULT 24
AX076483
LOCUS       AX076483                669 bp    DNA     linear   PAT 07-FEB-2001
DEFINITION  Sequence 9 from Patent WO0104280.
ACCESSION   AX076483
VERSION     AX076483.1  GI:12711035
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 9 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Sequence coding for SEQ ID NO 3, IL-12 p35"
ORIGIN

  Query Match             34.8%;  Score 195;  DB 2;  Length 669;
  Best Local Similarity   99.0%;  Pred. No. 1.1e-94;
  Matches  395;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
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Db        169 AAGGCCAGACAAACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAAT 288

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              |||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCC 348

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 402
              |||||||||||||||||||||||||||||||||||||||
Db        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 507


RESULT 25
AX076477
LOCUS       AX076477                4201 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 3 from Patent WO0104280.
ACCESSION   AX076477
VERSION     AX076477.1  GI:12711029
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 3 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .4201
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="IL-12p35 (pMOLfIL-12p35 (e-,_e31-)clone61)"
ORIGIN

  Query Match             34.8%;  Score 195;  DB 2;  Length 4201;
  Best Local Similarity   99.0%;  Pred. No. 9.7e-95;
  Matches  395;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3155 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 3214

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
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Db       3215 AAGGCCAGACAAACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGAT 3274

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db       3275 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAAT 3334

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db       3335 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCC 3394

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3395 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 3454

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3455 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 3514

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 402
              |||||||||||||||||||||||||||||||||||||||
Db       3515 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 3553


RESULT 26
AX154615
LOCUS       AX154615                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 19 from Patent WO0140257.
ACCESSION   AX154615
VERSION     AX154615.1  GI:14536190
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 19 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match            31.7%;  Score 178;  DB 2;  Length 660;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-85;
  Matches  178;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        207 GATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGAC 266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 GATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGAC 362

Qy        267 CCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCAT 326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 CCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCAT 422

Qy        327 GAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 384
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 GAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480


RESULT 27
AX154616
LOCUS       AX154616                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 20 from Patent WO0140257.
ACCESSION   AX154616
VERSION     AX154616.1  GI:14536191
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 20 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match            21.4%;  Score 120;  DB 2;  Length 660;
  Best Local Similarity  100.0%;  Pred. No. 1e-53;
  Matches  120;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        265 ACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCC 324
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCC 420

Qy        325 ATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 384
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480


RESULT 28
AX154614
LOCUS       AX154614                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 18 from Patent WO0140257.
ACCESSION   AX154614
VERSION     AX154614.1  GI:14536189
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 18 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match            20.5%;  Score 115;  DB 2;  Length 660;
  Best Local Similarity  100.0%;  Pred. No. 5.6e-51;
  Matches  115;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 216

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAA 175
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        217 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAA 271


RESULT 29
AX154621
LOCUS       AX154621                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 25 from Patent WO0140257.
ACCESSION   AX154621
VERSION     AX154621.1  GI:14536196
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
```

```
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 25 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match           20.5%;  Score 115;  DB 2;  Length 660;
  Best Local Similarity  100.0%;  Pred. No. 5.6e-51;
  Matches  115;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 216

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAA 175
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        217 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAA 271


RESULT 30
AX154619
LOCUS       AX154619                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 23 from Patent WO0140257.
ACCESSION   AX154619
VERSION     AX154619.1  GI:14536194
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 23 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match           18.2%;  Score 102;  DB 2;  Length 660;
  Best Local Similarity  100.0%;  Pred. No. 7.1e-44;
  Matches  102;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        283 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 438

Qy        343 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 384
              |||||||||||||||||||||||||||||||||||||||||||
Db        439 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480


RESULT 31
AY191828
LOCUS       AY191828                657 bp    mRNA    linear   SYN 04-FEB-2003
DEFINITION  Synthetic construct evolved IL-12 p35 precursor, mRNA, partial cds.
ACCESSION   AY191828
VERSION     AY191828.1  GI:27729523
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 657)
  AUTHORS   Leong,S.R., Chang,J.C.C., Ong,R., Dawes,G., Stemmer,W.P.C. and
            Punnonen,J.
  TITLE     Optimized expression and specific activity of IL-12 by directed
            molecular evolution
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (3), 1163-1168 (2003)
  PUBMED    12529500
REFERENCE   2  (bases 1 to 657)
  AUTHORS   Leong,S.R., Chang,J.C.C., Ong,R., Dawes,G., Stemmer,W.P.C. and
            Punnonen,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-DEC-2002) Vaccines, Maxygen, Inc., 515 Galveston
            Drive, Redwood City, CA 94063, USA
FEATURES             Location/Qualifiers
     source          1. .657
                     /organism="synthetic construct"
                     /mol_type="mRNA"
                     /db_xref="taxon:32630"
     CDS             1. .>657
                     /codon_start=1
                     /transl_table=11
                     /product="evolved IL-12 p35 precursor"
                     /protein_id="AAO19111.1"
                     /db_xref="GI:27729524"
                     /translation="MCPARSLLLVATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNL
                     LRAVSNMLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASRGI
                     SLITNGSCLASRKTSFMTTLCLGSIYEDLKMYQVEFKTMNAKLLMNPKRQIFLDQNML
                     TAIDELLQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNS
                     S"
     sig_peptide     1. .66
     mat_peptide     67. .657
                     /product="evolved IL-12 p35"
ORIGIN

  Query Match           17.5%;  Score 98;  DB 8;  Length 657;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-41;
  Matches   98;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 216

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 158
              |||||||||||||||||||||||||||||||||||||||
Db        217 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 254


RESULT 32
AX154617
LOCUS       AX154617                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 21 from Patent WO0140257.
ACCESSION   AX154617
VERSION     AX154617.1  GI:14536192
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 21 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match           17.5%;  Score 98;  DB 2;  Length 660;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-41;
  Matches   98;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 216

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 158
                ||||||||||||||||||||||||||||||||||||||
Db        217 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 254


RESULT 33
AX154620
LOCUS       AX154620                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 24 from Patent WO0140257.
ACCESSION   AX154620
VERSION     AX154620.1  GI:14536195
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 24 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match             15.0%;  Score 84;  DB 2;  Length 660;
  Best Local Similarity   99.3%;  Pred. No. 4.9e-34;
  Matches  134;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        207 GATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGAC 266
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 GATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGAC 362

Qy        267 CCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCAT 326
                |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        363 CCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCAT 422

Qy        327 GAATGCAAAGCTGTT 341
                |||||||||||||||
Db        423 GAATGCAAAGCTGTT 437


RESULT 34
BD171284
LOCUS       BD171284                591 bp    DNA     linear   PAT 18-FEB-2003
DEFINITION  Novel canine cytokine protein.
ACCESSION   BD171284
VERSION     BD171284.1  GI:28412574
KEYWORDS    JP 2002241398-A/4.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Imamura,T., Maeda,H., Tokiyoshi,Y. and Eda,Y.
  TITLE     Novel canine cytokine protein
  JOURNAL   Patent: JP 2002241398-A 4 28-AUG-2002;
            CHEMO SERO THERAPEUT RES INST
COMMENT     OS   Canine splenocyte
            PN   JP 2002241398-A/4
            PD   28-AUG-2002
            PF   03-JUN-1997 JP 1997161936
            PI   TAKAYUKI IMAMURA,HIROAKI MAEDA,YUKIO TOKIYOSHI,YASUYUKI EDA PC
              C07K14/52,A61K38/00,A61K39/395,C07K16/24,C12N5/10,C12N15/09, PC
            C12P21/02//
            PC   C12P21/08,(C12P21/02,C12R1:91),A61K37/02,C12N5/00,C12N15/00 CC
              Strandedness: Double;
            CC   Topology: Linear;
```

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            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             14.4%;  Score 81;  DB 2;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
                |||||||||||||||||||||
Db        223 CTGGCTTCCAGAGAGATCTCT 243


RESULT 35
AR595963
LOCUS       AR595963                591 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 49 from patent US 6818444.
ACCESSION   AR595963
VERSION     AR595963.1  GI:56646944
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 49 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             14.4%;  Score 81;  DB 2;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
                |||||||||||||||||||||
Db        223 CTGGCTTCCAGAGAGATCTCT 243


RESULT 36
AR595964/c
LOCUS       AR595964                591 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 51 from patent US 6818444.
ACCESSION   AR595964
VERSION     AR595964.1  GI:56646945
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 51 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
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                     /mol_type="genomic DNA"
ORIGIN

  Query Match            14.4%;  Score 81;  DB 2;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 37
AR595961
LOCUS       AR595961                 666 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 46 from patent US 6818444.
ACCESSION   AR595961
VERSION     AR595961.1  GI:56646942
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 46 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match            14.4%;  Score 81;  DB 2;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 38
AR595962/c
LOCUS       AR595962                 666 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 48 from patent US 6818444.
ACCESSION   AR595962
VERSION     AR595962.1  GI:56646943
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 48 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match            14.4%;  Score 81;  DB 2;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 39
AR151062
LOCUS       AR151062                 669 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 2 from patent US 6231850.
ACCESSION   AR151062
VERSION     AR151062.1  GI:15117112
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12
  JOURNAL   Patent: US 6231850-A 2 15-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            14.4%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 40
AR151072
LOCUS       AR151072                 669 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 12 from patent US 6231850.
ACCESSION   AR151072
VERSION     AR151072.1  GI:15117122
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12
  JOURNAL   Patent: US 6231850-A 12 15-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            14.4%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
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                    ||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 41
BD014654
LOCUS       BD014654                669 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy.
ACCESSION   BD014654
VERSION     BD014654.1  GI:22555437
KEYWORDS    JP 2001161378-A/2.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F.
  TITLE     Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy
  JOURNAL   Patent: JP 2001161378-A 2 19-JUN-2001;
            TORAY INDUSTRIES INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 2001161378-A/2
            PD   19-JUN-2001
            PF   26-SEP-2000 JP 2000292946
            PI   FUMIYOSHI OKANO
            PC   C12N15/09,A61K38/00,A61P17/00,A61P17/00,A61P31/04,A61P31/04,
            PC   A61P35/00,
            PC   A61P37/00,C07K1/18,C07K1/22,C07K14/54,C12P21/02//(C12P21/02,
            PC   C12R1:91),
            PC   (C12P21/02,C12R1:93),C12N15/00,A61K37/02
            CC   Process for producing highly pure protein, interleukin 12,  CC
                 protein
            CC   inhibiting interleukin-12 activity, remedies for mammalian  CC
                 immunopathy and
            CC   method of treating immunopathy
            FH   Key             Location/Qualifiers
            FT   CDS             (1). .(666)
            FT   mat_peptide     (76). .(666).
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Canis sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9616"
ORIGIN

  Query Match            14.4%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              ||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 42
BD014664
LOCUS       BD014664                669 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy.
ACCESSION   BD014664
VERSION     BD014664.1  GI:22555447
KEYWORDS    JP 2001161378-A/12.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F.
  TITLE     Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy
  JOURNAL   Patent: JP 2001161378-A 12 19-JUN-2001;
            TORAY INDUSTRIES INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 2001161378-A/12
            PD   19-JUN-2001
            PF   26-SEP-2000 JP 2000292946
            PI   FUMIYOSHI OKANO
            PC   C12N15/09,A61K38/00,A61P17/00,A61P17/00,A61P31/04,A61P31/04,
            PC   A61P35/00,
            PC   A61P37/00,C07K1/18,C07K1/22,C07K14/54,C12P21/02//(C12P21/02,
            PC   C12R1:91),
            PC   (C12P21/02,C12R1:93),C12N15/00,A61K37/02
            CC   Process for producing highly pure protein, interleukin 12,  CC
                 protein
            CC   inhibiting interleukin-12 activity, remedies for mammalian  CC
                 immunopathy and
            CC   method of treating immunopathy
            FH   Key             Location/Qualifiers
            FT   CDS             (1). .(666)
            FT   mat_peptide     (76). .(666).
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Canis sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9616"
ORIGIN

  Query Match            14.4%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              ||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 43
E15018
LOCUS       E15018                  669 bp    DNA     linear   PAT 28-JUL-1999
DEFINITION  Canine mRNA for interleukin 12 35kDa subunit,complete cds.
ACCESSION   E15018
VERSION     E15018.1  GI:5709701
KEYWORDS    JP 1998036397-A/2.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F.
  TITLE     CANINE INTERLEUKIN 12 AND ITS PRODUCTION
  JOURNAL   Patent: JP 1998036397-A 2 10-FEB-1998;
            TORAY IND INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 1998036397-A/2
            PD   10-FEB-1998
            PF   08-NOV-1996 JP 1996296789
            PR   08-NOV-1995 JP 95P   289729, 23-MAY-1996 JP 96P   128104 PI
            OKANO FUMIYOSHI
            PC   C07K14/54,C07H21/04,C12N5/10,C12N15/09,C12P21/02,(C12N5/10, PC
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            C12R1:91),
            PC   (C12P21/02,C12R1:91);
            CC   strandedness: Double;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .669
            FT                   /organism='Canis sp.'
            FT                   /tissue_type='liver'
            FT   CDS             1. .669
            FT                   /product='interleukin12 35kDa subunit'.
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Canis sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9616"
ORIGIN

  Query Match            14.4%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 44
AR316461
LOCUS       AR316461                669 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 2 from patent US 6562334.
ACCESSION   AR316461
VERSION     AR316461.1  GI:33695289
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12 administration as an immune disease treatment
  JOURNAL   Patent: US 6562334-A 2 13-MAY-2003;
            Toray Industries, Inc.;;
            JPX;
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match            14.4%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 45
AR316471
LOCUS       AR316471                669 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 12 from patent US 6562334.
ACCESSION   AR316471
VERSION     AR316471.1  GI:33695299
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12 administration as an immune disease treatment
  JOURNAL   Patent: US 6562334-A 12 13-MAY-2003;
            Toray Industries, Inc.;;
            JPX;
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match            14.4%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 46
CFU49085
LOCUS       CFU49085                669 bp    mRNA    linear   MAM 13-MAR-1996
DEFINITION  Canis familiaris interleukin-12 p35 subunit mRNA, complete cds.
ACCESSION   U49085
VERSION     U49085.1  GI:1223905
KEYWORDS    .
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Belke-Louis,G.F. and Buettner,M.
  TITLE     Cloning and sequence analysis of the p35 and p40 subunits of canine
            interleukin-12
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Belke-Louis,G.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-FEB-1996) Georg F. Belke-Louis, Institute of Med.
            Microbiology, Veterinaerstr. 13, Muenchen, D-80539, Germany
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Canis familiaris"
                     /mol_type="mRNA"
                     /db_xref="taxon:9615"
     CDS             1. .669
                     /codon_start=1
                     /product="interleukin-12 p35 subunit"
                     /protein_id="AAA92058.1"
                     /db_xref="GI:1223906"
                     /translation="MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHS
                     QNLLRAVSNTLQKARQTLDYIPCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
                     REISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQ
                     NMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSY
                     LNSS"
ORIGIN

  Query Match            14.4%;  Score 81;  DB 14;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 47
BD171283
LOCUS       BD171283               1282 bp    DNA     linear   PAT 18-FEB-2003
DEFINITION  Novel canine cytokine protein.
ACCESSION   BD171283
VERSION     BD171283.1  GI:28412573
KEYWORDS    JP 2002241398-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 1282)
  AUTHORS   Imamura,T., Maeda,H., Tokiyoshi,Y. and Eda,Y.
  TITLE     Novel canine cytokine protein
  JOURNAL   Patent: JP 2002241398-A 3 28-AUG-2002;
            CHEMO SERO THERAPEUT RES INST
COMMENT     OS   Canine splenocyte
            PN   JP 2002241398-A/3
            PD   28-AUG-2002
            PF   03-JUN-1997 JP 1997161936
            PI   TAKAYUKI IMAMURA,HIROAKI MAEDA,YUKIO TOKIYOSHI,YASUYUKI EDA PC
              C07K14/52,A61K38/00,A61K39/395,C07K16/24,C12N5/10,C12N15/09, PC
            C12P21/02//
            PC   C12P21/08,(C12P21/02,C12R1:91),A61K37/02,C12N5/00,C12N15/00 CC
              Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .1282
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
ORIGIN

  Query Match             14.4%;  Score 81;  DB 2;  Length 1282;
  Best Local Similarity   100.0%;  Pred. No. 2e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 362

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        363 CTGGCTTCCAGAGAGATCTCT 383


RESULT 48
AR596009
LOCUS       AR596009               1455 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 104 from patent US 6818444.
ACCESSION   AR596009
VERSION     AR596009.1  GI:56646990
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1455)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 104 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES              Location/Qualifiers
     source           1. .1455
                      /organism="unknown"
                      /mol_type="genomic DNA"
ORIGIN

  Query Match             14.4%;  Score 81;  DB 2;  Length 1455;
  Best Local Similarity   100.0%;  Pred. No. 2e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 528

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        529 CTGGCTTCCAGAGAGATCTCT 549


RESULT 49
AR596010/c
LOCUS       AR596010               1455 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 106 from patent US 6818444.
ACCESSION   AR596010
VERSION     AR596010.1  GI:56646991
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1455)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 106 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES              Location/Qualifiers
     source           1. .1455
                      /organism="unknown"
                      /mol_type="genomic DNA"
ORIGIN

  Query Match             14.4%;  Score 81;  DB 2;  Length 1455;
  Best Local Similarity   100.0%;  Pred. No. 2e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 928

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        927 CTGGCTTCCAGAGAGATCTCT 907


RESULT 50
AR595973
LOCUS       AR595973               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 66 from patent US 6818444.
ACCESSION   AR595973
VERSION     AR595973.1  GI:56646954
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 66 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES              Location/Qualifiers
     source           1. .1533
                      /organism="unknown"
                      /mol_type="genomic DNA"
ORIGIN

  Query Match             14.4%;  Score 81;  DB 2;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 2e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1105 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1164

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db       1165 CTGGCTTCCAGAGAGATCTCT 1185


RESULT 51
AR595974/c
LOCUS       AR595974               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 68 from patent US 6818444.
ACCESSION   AR595974
VERSION     AR595974.1  GI:56646955
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 68 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match            14.4%;  Score 81;  DB 2;  Length 1533;
  Best Local Similarity  100.0%;  Pred. No. 2e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 52
AR595971
LOCUS       AR595971               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 61 from patent US 6818444.
ACCESSION   AR595971
VERSION     AR595971.1  GI:56646952
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 61 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match            14.4%;  Score 81;  DB 2;  Length 1599;
  Best Local Similarity  100.0%;  Pred. No. 2e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1230

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db       1231 CTGGCTTCCAGAGAGATCTCT 1251


RESULT 53
AR595972/c
LOCUS       AR595972               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 63 from patent US 6818444.
ACCESSION   AR595972
VERSION     AR595972.1  GI:56646953
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 63 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match            14.4%;  Score 81;  DB 2;  Length 1599;
  Best Local Similarity  100.0%;  Pred. No. 2e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 54
AX076207
LOCUS       AX076207                 71 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 8 from Patent WO0104155.
ACCESSION   AX076207
VERSION     AX076207.1  GI:12710832
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 8 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .71
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer f12p35-1-lang"
ORIGIN

  Query Match            12.7%;  Score 71;  DB 2;  Length 71;
  Best Local Similarity  100.0%;  Pred. No. 7.2e-27;
  Matches   71;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        380 TGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCAC 439
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCAC 60

Qy        440 AGAACTCCTCC 450
              ||||||||||||
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Db         61 AGAACTCCTCC 71


RESULT 55
AR008951
LOCUS       AR008951                660 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 3 from patent US 5756085.
ACCESSION   AR008951
VERSION     AR008951.1  GI:3967756
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Sykes,M. and Wolf,S.F.
  TITLE     Use of interleukin-12 to prevent graft versus host disease
  JOURNAL   Patent: US 5756085-A 3 26-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            11.6%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        514 ATTCG 518
              |||||
Db        610 ATTCG 614


RESULT 56
BD007071
LOCUS       BD007071                660 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  IL-12 gene expression and delivery systems and uses.
ACCESSION   BD007071
VERSION     BD007071.1  GI:18635442
KEYWORDS    JP 2001503257-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Nodosutoromu,J., Freemark,B. and Dishupande,D.
  TITLE     IL-12 gene expression and delivery systems and uses
  JOURNAL   Patent: JP 2001503257-A 2 13-MAR-2001;
            BARENTISU INC,SYNTEX INC
COMMENT     OS   Unidentified
            PN   JP 2001503257-A/2
            PD   13-MAR-2001
            PF   10-OCT-1997 JP 1998519514
            PR   18-OCT-1996 US    60/028676
            PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
            C12N15/09,A61K31/711,A61K38/00,A61K47/18,A61K47/28,A61K48/00, PC
            A61P11/06,
            PC   C12N15/00,A61K37/02
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .660
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match            11.6%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        514 ATTCG 518
              |||||
Db        610 ATTCG 614


RESULT 57
BD007079
LOCUS       BD007079                660 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Gene expression and delivery systems and uses.
ACCESSION   BD007079
VERSION     BD007079.1  GI:18635450
KEYWORDS    JP 2001503258-A/4.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Nodosutoromu,J., Freemark,B. and Dishupande,D.
  TITLE     Gene expression and delivery systems and uses
  JOURNAL   Patent: JP 2001503258-A 4 13-MAR-2001;
            BARENTISU INC
COMMENT     OS   Unidentified
            PN   JP 2001503258-A/4
            PD   13-MAR-2001
            PF   10-OCT-1997 JP 1998519520
            PR   18-OCT-1996 US    60/028687
            PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
            C12N15/09,A61K48/00,A61P11/06,A61P35/00,A61P43/00//C07K14/54, PC
            C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .660
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match            11.6%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        514 ATTCG 518
              |||||
Db        610 ATTCG 614


RESULT 58
BD136037
LOCUS       BD136037                660 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Interferon alpha plasmid and delivery system and method of
            preparing and using the same.
ACCESSION   BD136037
VERSION     BD136037.1  GI:23230982
KEYWORDS    JP 2002506647-A/4.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
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REFERENCE   1  (bases 1 to 660)
  AUTHORS   Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.
  TITLE     Interferon alpha plasmid and delivery system and method of
            preparing and using the same
  JOURNAL   Patent: JP 2002506647-A 4 05-MAR-2002;
            VALENTIS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002506647-A/4
            PD   05-MAR-2002
            PF   12-MAR-1999 JP 2000536861
            PR   19-MAR-1998 US    60/078654
            PI   JEFF NORDSTROM,FEDERICA PERICLE,ALAIN ROLLAND,ROBERT RALSTON
            PC   C12N15/09,A61K38/21,A61K48/00,A61P35/00,C07K14/54,C07K14/56,
            PC   C12N1/15,
            PC   C12N1/19,C12N1/21,C12N5/10//A61K9/127,C12N15/00,A61K37/66, PC
             C12N5/00
            CC   Interferon alpha plasmid and delivery system and method of  CC
                    preparing and
            CC   using the same
            FH   Key             Location/Qualifiers
            FT   source          1. .660
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             11.6%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        514 ATTCG 518
              |||||
Db        610 ATTCG 614


RESULT 59
I28592
LOCUS       I28592                  660 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 3 from patent US 5573764.
ACCESSION   I28592
VERSION     I28592.1  GI:1819368
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Sykes,M. and Wolf,S.F.
  TITLE     Use of interleukin-12 to prevent graft versus host disease
  JOURNAL   Patent: US 5573764-A 3 12-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             11.6%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        514 ATTCG 518
              |||||
Db        610 ATTCG 614


RESULT 60
AX154618
LOCUS       AX154618                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 22 from Patent WO0140257.
ACCESSION   AX154618
VERSION     AX154618.1  GI:14536193
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 22 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match             11.6%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        111 TGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGA 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 TGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGA 266

Qy        171 ATTAA 175
              |||||
Db        267 ATTAA 271


RESULT 61
AX154634
LOCUS       AX154634                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 38 from Patent WO0140257.
ACCESSION   AX154634
VERSION     AX154634.1  GI:14536198
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 38 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             11.6%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        514 ATTCG 518
              |||||
Db        610 ATTCG 614
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RESULT 62
CQ829447
LOCUS       CQ829447                 702 bp    DNA     linear   PAT 05-JUL-2004
DEFINITION  Sequence 6 from Patent WO2004052929.
ACCESSION   CQ829447
VERSION     CQ829447.1  GI:49732783
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Vandenbroeck,K. and Alloza,I.
  TITLE     Recombinant cell line
  JOURNAL   Patent: WO 2004052929-A 6 24-JUN-2004;
            The Queen's University of Belfast (GB)
FEATURES             Location/Qualifiers
     source          1. .702
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="cDNA for alpha chain of IL-12"
ORIGIN

  Query Match             11.6%;  Score 65;  DB 2;  Length 702;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 624

Qy        514 ATTCG 518
              |||||
Db        625 ATTCG 629


RESULT 63
AR052862
LOCUS       AR052862                 721 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 199 from patent US 5833975.
ACCESSION   AR052862
VERSION     AR052862.1  GI:5977724
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 721)
  AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
  TITLE     Canarypox virus expressing cytokine and/or tumor-associated antigen
            DNA sequence
  JOURNAL   Patent: US 5833975-A 199 10-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .721
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             11.6%;  Score 65;  DB 2;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy        514 ATTCG 518
              |||||
Db        671 ATTCG 675


RESULT 64
AR288174
LOCUS       AR288174                 721 bp    mRNA    linear   PAT 12-JUN-2003
DEFINITION  Sequence 199 from patent US 6537594.
ACCESSION   AR288174
VERSION     AR288174.1  GI:31675453
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 721)
  AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
  TITLE     Vaccina virus comprising cytokine and/or tumor associated antigen
            genes
  JOURNAL   Patent: US 6537594-A 199 25-MAR-2003;
            Virogenetics Corporation; Troy, NY
FEATURES             Location/Qualifiers
     source          1. .721
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             11.6%;  Score 65;  DB 2;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy        514 ATTCG 518
              |||||
Db        671 ATTCG 675


RESULT 65
AR567161
LOCUS       AR567161                 721 bp    mRNA    linear   PAT 08-OCT-2004
DEFINITION  Sequence 199 from patent US 6780407.
ACCESSION   AR567161
VERSION     AR567161.1  GI:53984803
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 721)
  AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
  TITLE     Pox virus comprising DNA sequences encoding CEA and B7 antigen
  JOURNAL   Patent: US 6780407-A 199 24-AUG-2004;
            Aventis Pasteur; Swiftwater, PA
FEATURES             Location/Qualifiers
     source          1. .721
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             11.6%;  Score 65;  DB 2;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy        514 ATTCG 518
              |||||
Db        671 ATTCG 675


RESULT 66
BD105971
LOCUS       BD105971                 762 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Animal model for evaluation of vaccines.
ACCESSION   BD105971
```

```
VERSION     BD105971.1  GI:23200789
KEYWORDS    JP 2002501375-A/21.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Chang,L.J.
  TITLE     Animal model for evaluation of vaccines
  JOURNAL   Patent: JP 2002501375-A 21 15-JAN-2002;
            LUNG JI CHANG
COMMENT     PN   JP 2002501375-A/21
            PD   15-JAN-2002
            PF   09-APR-1998 JP 1998543062
            PR   09-APR-1997 US    08/838702,01-MAY-1997 US    08/848760 PR
            09-DEC-1997 US    60/069163
            PI   LUNG JI CHANG
            PC   A01K67/027,C12N7/01,C12N1/10,C07K14/16,A61K39/008,C12N1/36, PC
              C12N7/04,
            PC   A61K39/21
            CC   Strandedness: Double;
            CC   Topology: Linear;
            CC   /desc = 'DNA'
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .762
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"
ORIGIN

  Query Match             11.6%;  Score 65;  DB 2;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        514 ATTCG 518
              |||||
Db        712 ATTCG 716


RESULT 67
CQ803343
LOCUS       CQ803343                762 bp    DNA     linear   PAT 10-MAY-2004
DEFINITION  Sequence 3 from Patent WO2004035799.
ACCESSION   CQ803343
VERSION     CQ803343.1  GI:47110209
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Waehler,R. and Schnieders,F.
  TITLE     Viral vectors and the use of the same for gene therapy
  JOURNAL   Patent: WO 2004035799-A 3 29-APR-2004;
            Universitaetsklinikum Hamburg-Eppendorf (DE)
FEATURES              Location/Qualifiers
     source           1. .762
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"
ORIGIN

  Query Match             11.6%;  Score 65;  DB 2;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        514 ATTCG 518
              |||||
Db        712 ATTCG 716


RESULT 68
AR533401
LOCUS       AR533401                762 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 21 from patent US 6730512.
ACCESSION   AR533401
VERSION     AR533401.1  GI:53923067
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Chang,L.-J.
  TITLE     Combination immunogene therapy
  JOURNAL   Patent: US 6730512-A 21 04-MAY-2004;
            Amdl, Inc.; Tustin, CA
FEATURES              Location/Qualifiers
     source           1. .762
                      /organism="unknown"
                      /mol_type="unassigned DNA"
ORIGIN

  Query Match             11.6%;  Score 65;  DB 2;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        514 ATTCG 518
              |||||
Db        712 ATTCG 716


RESULT 69
AF101062
LOCUS       AF101062                762 bp    mRNA    linear   PRI 03-MAR-1999
DEFINITION  Homo sapiens interleukin 12 mRNA, complete cds.
ACCESSION   AF101062
VERSION     AF101062.1  GI:4323578
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Liu,y., Guo,Y. and Wu,M.
  TITLE     Human Interleukin-12 (or Natural Killer Cell Stimulatory Factor, or
            Cytotoxic Lymphocyte Maturation Factor) 35kDa subunit mRNA
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 762)
  AUTHORS   Liu,Y., Guo,Y. and Wu,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-OCT-1998) Molecular Biology Department, Cancer
            Institute of Second Military Medical University, 800 XianYin Road,
            Shanghai 200433, P.R. China
FEATURES              Location/Qualifiers
     source           1. .762
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /chromosome="3"
                      /map="3p12-q13.2"
                      /cell_line="lymphoblastoid B-cell line NC37"
                      /note="cells induced by phorbol 12-myristate 13 acetate
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                     (PMA) and ionophore A23187"
     CDS             1. .762
                     /note="natural killer cell stimulatory factor; cytotoxic
                     lymphocyte maturation factor 35kDa subunit; p35"
                     /codon_start=1
                     /product="interleukin 12"
                     /protein_id="AAD16432.1"
                     /db_xref="GI:4323579"
                     /translation="MWPPGSASQPPPSPAAATGLHPAARPVSLQCRLSMCPARSLLLV
                     ATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEE
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.2e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
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Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        514 ATTCG 518
              |||||
Db        712 ATTCG 716


RESULT 70
MMU19842
LOCUS       MMU19842                 780 bp    mRNA    linear   PRI 03-FEB-1996
DEFINITION  Macaca mulatta interleukin-12 beta p35 subunit (IL-12b) mRNA,
            complete cds.
ACCESSION   U19842
VERSION     U19842.1  GI:644801
KEYWORDS    .
SOURCE      Macaca mulatta (rhesus monkey)
  ORGANISM  Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 780)
  AUTHORS   Villinger,F., Brar,S.S., Mayne,A., Chikkala,N. and Ansari,A.A.
  TITLE     Comparative sequence analysis of cytokine genes from human and
            nonhuman primates
  JOURNAL   J. Immunol. 155 (8), 3946-3954 (1995)
   PUBMED   7561102
REFERENCE   2  (bases 1 to 780)
  AUTHORS   Villinger,F.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JAN-1995) Francois J. Villinger, Emory University,
            Pathology, 1327 Clifton Rd, Atlanta, GA 30322, USA
FEATURES             Location/Qualifiers
     source          1. .780
                     /organism="Macaca mulatta"
                     /mol_type="mRNA"
                     /db_xref="taxon:9544"
                     /clone="RNc IL-12b"
                     /cell_type="peripheral blood mononuclear cells"
                     /tissue_type="blood"
     gene            1. .780
                     /gene="IL-12b"
     CDS             10. .771
                     /gene="IL-12b"
                     /function="NK cell stimulatory factor"
                     /codon_start=1
                     /product="interleukin-12 beta p35 subunit"
                     /protein_id="AAA86707.1"
                     /db_xref="GI:644802"
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                     IYEDLKMYQVEFKTMNAKLLRDPKRQIFLDQNILGVIDELMQALNFNSETVPQKSSLE
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ORIGIN

  Query Match             11.6%;  Score 65;  DB 5;  Length 780;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
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Db        661 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 720

Qy        514 ATTCG 518
              |||||
Db        721 ATTCG 725


RESULT 71
AF180562
LOCUS       AF180562                 823 bp    mRNA    linear   PRI 26-SEP-1999
DEFINITION  Homo sapiens interleukin 12, P35 mRNA, complete cds.
ACCESSION   AF180562
VERSION     AF180562.1  GI:5923852
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 823)
  AUTHORS   Hongyuan,J. and Meiyun,Z.
  TITLE     Cloning and sequence analysis of IL-12 cDNA from Chinese
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 823)
  AUTHORS   Hongyuan,J. and Meiyun,Z.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-AUG-1999) Hepatitis, Institute of Virology, CAPM, 100
            Yingxinjie, Xuanwuqu, Beijing 100052, China
FEATURES             Location/Qualifiers
     source          1. .823
                     /organism="Homo sapiens"
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                     /map="3p12-q13.2"
                     /cell_type="peripheral mononuclear"
     CDS             60. .821
                     /note="NKSF/CLMF; IL12p35; 35kD"
                     /codon_start=1
                     /product="interleukin 12, P35"
                     /protein_id="AAD56385.1"
                     /db_xref="GI:5923853"
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ORIGIN

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Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        711 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 770

Qy        514 ATTCG 518
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              |||||
Db        771 ATTCG 775


RESULT 72
BD165801
LOCUS       BD165801                856 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Antibody against cytotoxic lymphocyte maturing factors.
ACCESSION   BD165801
VERSION     BD165801.1  GI:27871613
KEYWORDS    JP 2002167400-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 856)
  AUTHORS   Chizzonite,R.A., Gately,M.K., Gubler,U.A., Hulmes,J.D., Pan,Y.C.E.,
            Podlanski,F.J. and Stern,A.S.
  TITLE     Antibody against cytotoxic lymphocyte maturing factors
  JOURNAL   Patent: JP 2002167400-A 2 11-JUN-2002;
            PROTEIN DESIGN LABS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002167400-A/2
            PD   11-JUN-2002
            PF   14-AUG-2001 JP 2001246031
            PR   22-DEC-1989 US       455708,09-MAY-1990 US       520935 PR
            27-AUG-1990 US       572284
            PI   RICHARD ANTHONY CHIZZONITE,MAURICE KENT GATELY,ULRICH ANDREAS
            PI   GUBLER,
            PI   JEFFREY DAVID HULMES,YU CHING EUGENE PAN,FRANK JOHN PODLANSKI,
            PI   ALVIN SETH STERN
            PC   C07K16/24,C12N15/02,C12N15/02,C12P21/08,C12N15/00,C12N15/00 CC
              Antibody against cytotoxic lymphocyte maturing factors FH   Key
                     Location/Qualifiers
            FT   CDS              (170). .(826).
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ORIGIN

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Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
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Db        719 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 778

Qy        514 ATTCG 518
              |||||
Db        779 ATTCG 783


RESULT 73
CQ716168
LOCUS       CQ716168                1020 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 2102 from Patent WO02068579.
ACCESSION   CQ716168
VERSION     CQ716168.1  GI:42277025
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 2102 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
     source          1. .1020
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ORIGIN

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  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        712 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 771

Qy        514 ATTCG 518
              |||||
Db        772 ATTCG 776


RESULT 74
BC104982
LOCUS       BC104982                1021 bp    mRNA    linear   PRI 19-JAN-2006
DEFINITION  Homo sapiens interleukin 12A (natural killer cell stimulatory
            factor 1, cytotoxic lymphocyte maturation factor 1, p35), mRNA
            (cDNA clone MGC:132642 IMAGE:8143985), complete cds.
ACCESSION   BC104982
VERSION     BC104982.1  GI:85397857
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1021)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
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            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
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            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1021)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (13-SEP-2005) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Mike Brownstein, NIMH
            cDNA Library Preparation: British Columbia Cancer Research Center
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
```

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            Martin Hirst, Thomas Zeng, Ryan Morin, Michelle Moksa, Johnson
            Pang, Diana Mah, Jing Wang, Kieth Fichter, Eric Chuah, Allen
            Delaney, Rob Kirkpatrick, Agnes Baross, Sarah Barber, Mabel
            Brown-John, Steve S. Chand, William Chow, Ryan Babakaiff, Dave
            Wong, Corey Matsuo, Jaclyn Beland, Susan Gibson, Luis delRio, Ruth
            Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
            Kim MacDonald,  Mike R. Mayo, Josh Moran, Diana Palmquist, JR
            Santos, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang,
            Jacquie Schein, Asim Siddiqui,Steven Jones, Rob Holt, Marco Marra.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRCB Plate: 3 Row: j Column: 15.
FEATURES                Location/Qualifiers
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                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone="MGC:132642 IMAGE:8143985"
                        /tissue_type="Brain, cerebral cortex, PCR rescued clones"
                        /clone_lib="NIH_MGC_287"
                        /note="Vector: pCR4-TOPO with reversed insert; Clone
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                        /db_xref="IMGT/GENE-DB:5969"
                        /db_xref="MIM:161560"
     CDS                154. .915
                        /gene="IL12A"
                        /codon_start=1
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ORIGIN

  Query Match             11.6%;  Score 65;  DB 5;  Length 1021;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-23;
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Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
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Db        805 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 864

Qy        514 ATTCG 518
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Db        865 ATTCG 869


RESULT 75
BC104984
LOCUS       BC104984                1021 bp    mRNA    linear   PRI 19-JAN-2006
DEFINITION  Homo sapiens interleukin 12A (natural killer cell stimulatory
            factor 1, cytotoxic lymphocyte maturation factor 1, p35), mRNA
            (cDNA clone MGC:132644 IMAGE:8143987), complete cds.
ACCESSION   BC104984
VERSION     BC104984.1  GI:85397860
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1021)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
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            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
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            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1021)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (13-SEP-2005) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Mike Brownstein, NIMH
            cDNA Library Preparation: British Columbia Cancer Research Center
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
            Martin Hirst, Thomas Zeng, Ryan Morin, Michelle Moksa, Johnson
            Pang, Diana Mah, Jing Wang, Kieth Fichter, Eric Chuah, Allen
            Delaney, Rob Kirkpatrick, Agnes Baross, Sarah Barber, Mabel
            Brown-John, Steve S. Chand, William Chow, Ryan Babakaiff, Dave
            Wong, Corey Matsuo, Jaclyn Beland, Susan Gibson, Luis delRio, Ruth
            Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
            Kim MacDonald,  Mike R. Mayo, Josh Moran, Diana Palmquist, JR
            Santos, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang,
            Jacquie Schein, Asim Siddiqui,Steven Jones, Rob Holt, Marco Marra.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRCB Plate: 3 Row: j Column: 17.
FEATURES                Location/Qualifiers
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                     /product="interleukin 12A, precursor"
                     /protein_id="AAI04985.1"
                     /db_xref="GI:85397861"
                     /db_xref="GeneID:3592"
                     /db_xref="HGNC:5969"
                     /db_xref="IMGT/GENE-DB:5969"
                     /db_xref="MIM:161560"
                     /translation="MWPPGSASQPPPSPAAATGLHPAARPVSLQCRLSMCPARSLLLV
                     ATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEE
                     IDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSS
                     IYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLE
                     EPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS"
ORIGIN

  Query Match             11.6%;  Score 65;  DB 5;  Length 1021;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 864

Qy        514 ATTCG 518
              |||||
Db        865 ATTCG 869


RESULT 76
AR091390
LOCUS       AR091390                1026 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 1 from patent US 5994104.
ACCESSION   AR091390
VERSION     AR091390.1  GI:10018145
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1026)
  AUTHORS   Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
  TITLE     Interleukin-12 fusion protein
  JOURNAL   Patent: US 5994104-A 1 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .1026
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             11.6%;  Score 65;  DB 2;  Length 1026;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 778

Qy        514 ATTCG 518
              |||||
Db        779 ATTCG 783


RESULT 77
AR380496
LOCUS       AR380496                1026 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1041 from patent US 6607879.
ACCESSION   AR380496
VERSION     AR380496.1  GI:40088130
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1026)
  AUTHORS   Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.
  TITLE     Compositions for the detection of blood cell and immunological
            response gene expression
  JOURNAL   Patent: US 6607879-A 1041 19-AUG-2003;
            Incyte Corporation; Palo Alto, CA
FEATURES             Location/Qualifiers
     source          1. .1026
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             11.6%;  Score 65;  DB 2;  Length 1026;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 778

Qy        514 ATTCG 518
              |||||
Db        779 ATTCG 783


RESULT 78
HUMCLMF35
LOCUS       HUMCLMF35               1026 bp    mRNA    linear   PRI 27-APR-1993
DEFINITION  Human cytotoxic lymphocyte maturation factor 35 kDa subunit mRNA,
            complete cds.
ACCESSION   M65271 M38443
VERSION     M65271.1  GI:180623
KEYWORDS    cytotoxic lymphocyte maturation factor 35 kDa subunit; interleukin.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1026)
  AUTHORS   Gubler,U., Chua,A.O., Schoenhaut,D.S., Dwyer,C.M., McComas,W.,
            Motyka,R., Nabavi,N., Wolitzky,A.G., Quinn,P.M., Familletti,P.C.
            and Gately,M.K.
  TITLE     Coexpression of two distinct genes is required to generate secreted
            bioactive cytotoxic lymphocyte maturation factor
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 88 (10), 4143-4147 (1991)
   PUBMED   1674604
COMMENT     Original source text: Human, cDNA to mRNA.
FEATURES             Location/Qualifiers
     source          1. .1026
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     CDS             170. .829
                     /codon_start=1
                     /product="cytotoxic lymphocyte maturation factor 35 kDa
                     subunit"
                     /protein_id="AAA35694.1"
                     /db_xref="GI:180624"
                     /translation="MCPARSLLLVATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNL
                     LRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRET
                     SFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNML
                     AVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVTSYLNA
                     S"
ORIGIN

  Query Match             11.6%;  Score 65;  DB 5;  Length 1026;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 778

Qy        514 ATTCG 518
              |||||
Db        779 ATTCG 783
```

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RESULT 79
AR393790
LOCUS       AR393790               1287 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 6 from patent US 6617135.
ACCESSION   AR393790
VERSION     AR393790.1  GI:40120794
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1287)
  AUTHORS   Gillies,S.D. and Lo,K.-M.
  TITLE     Multiple cytokine protein complexes
  JOURNAL   Patent: US 6617135-A 6 09-SEP-2003;
            EMD Lexigen Research Center Corp.; Billerica, MA
FEATURES             Location/Qualifiers
     source          1. .1287
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match            11.6%;  Score 65;  DB 2;  Length 1287;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1177 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1236

Qy        514 ATTCG 518
              |||||
Db       1237 ATTCG 1241


RESULT 80
AX084108
LOCUS       AX084108               1287 bp    DNA     linear   PAT 28-FEB-2001
DEFINITION  Sequence 6 from Patent WO0110912.
ACCESSION   AX084108
VERSION     AX084108.1  GI:13185658
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Gillies,S.D. and Lo,K.M.
  TITLE     Multiple cytokine-antibody complexes
  JOURNAL   Patent: WO 0110912-A 6 15-FEB-2001;
            Lexigen Pharmaceuticals Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .1287
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="human Fc-p35 fusion protein coding sequence"
ORIGIN

  Query Match            11.6%;  Score 65;  DB 2;  Length 1287;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1177 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1236

Qy        514 ATTCG 518
              |||||
Db       1237 ATTCG 1241


RESULT 81
AR050785
LOCUS       AR050785               1316 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 3 from patent US 5830451.
ACCESSION   AR050785
VERSION     AR050785.1  GI:5974149
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1316)
  AUTHORS   Devergne,O. and Kieff,E.D.
  TITLE     Haematopoietic cytokine Epstein Barr virus-induced protein
  JOURNAL   Patent: US 5830451-A 3 03-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .1316
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            11.6%;  Score 65;  DB 2;  Length 1316;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       753 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 812

Qy        514 ATTCG 518
              |||||
Db       813 ATTCG 817


RESULT 82
AR212036
LOCUS       AR212036               1316 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 3 from patent US 6399379.
ACCESSION   AR212036
VERSION     AR212036.1  GI:21515515
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1316)
  AUTHORS   Baker,B.F. and Freier,S.M.
  TITLE     Antisense modulation of interleukin 12 p35 subunit expression
  JOURNAL   Patent: US 6399379-A 3 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .1316
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            11.6%;  Score 65;  DB 2;  Length 1316;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       753 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 812

Qy        514 ATTCG 518
              |||||
Db       813 ATTCG 817


RESULT 83
HUMNKSFP35
LOCUS       HUMNKSFP35             1316 bp    mRNA    linear   PRI 07-JAN-1995
DEFINITION  Human natural killer cell stimulatory factor (NKSF) mRNA, complete
            cds, clone p35.
ACCESSION   M65291
VERSION     M65291.1  GI:189233
KEYWORDS    cytokine; natural killer cell stimulatory factor.
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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1316)
  AUTHORS   Wolf,S.F., Temple,P.A., Kobayashi,M., Young,D., Dicig,M., Lowe,L.,
            Dzialo,R., Fitz,L., Ferenz,C., Hewick,R.M., Kelleher,K.,
            Herrmann,S.H., Clark,S.C., Azzoni,L., Chan,S.H., Trinchieri,G. and
            Perussia,B.
  TITLE     Cloning of cDNA for natural killer cell stimulatory factor, a
            heterodimeric cytokine with multiple biologic effects on T and
            natural killer cells
  JOURNAL   J. Immunol. 146 (9), 3074-3081 (1991)
   PUBMED   1673147
COMMENT     Original source text: Human EBV-transformed B cell line RPMI 8866,
            cDNA to mRNA, clone p35.
FEATURES             Location/Qualifiers
     source          1. .1316
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /map="Unassigned"
                     /cell_line="EBV-transformed B cell line RPMI 8866"
     gene            1. .1316
                     /gene="NKSF1"
     CDS             102. .863
                     /gene="NKSF1"
                     /codon_start=1
                     /product="natural killer cell stimulatory factor"
                     /protein_id="AAA59937.1"
                     /db_xref="GI:189234"
                     /db_xref="GDB:G00-127-869"
                     /translation="MWPPGSASQPPPSPAAATGLHPAARPVSLQCRLSMCPARSLLLV
                     ATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEE
                     IDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSS
                     IYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLE
                     EPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS"
     sig_peptide     102. .269
                     /gene="NKSF1"
                     /note="G00-127-869"
     mat_peptide     270. .860
                     /gene="NKSF1"
                     /product="natural killer cell stimulatory factor"
                     /note="G00-127-869"
ORIGIN

  Query Match             11.6%;  Score 65;  DB 5;  Length 1316;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 812

Qy        514 ATTCG 518
              |||||
Db        813 ATTCG 817


RESULT 84
AR082685
LOCUS       AR082685                1364 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 3 from patent US 5976539.
ACCESSION   AR082685
VERSION     AR082685.1  GI:10009475
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1364)
  AUTHORS   Scott,P. and Trinchieri,G.
  TITLE     Compositions and methods for use of IL-12 as an adjuvant
  JOURNAL   Patent: US 5976539-A 3 02-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .1364
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             11.6%;  Score 65;  DB 2;  Length 1364;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 811

Qy        514 ATTCG 518
              |||||
Db        812 ATTCG 816


RESULT 85
AR122961
LOCUS       AR122961                1364 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 3 from patent US 6168923.
ACCESSION   AR122961
VERSION     AR122961.1  GI:14107927
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1364)
  AUTHORS   Scott,P. and Trinchieri,G.
  TITLE     Compositions and methods for use of IL-12 as an adjuvant
  JOURNAL   Patent: US 6168923-A 3 02-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .1364
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             11.6%;  Score 65;  DB 2;  Length 1364;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 811

Qy        514 ATTCG 518
              |||||
Db        812 ATTCG 816


RESULT 86
I28326
LOCUS       I28326                  1364 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 3 from patent US 5571515.
ACCESSION   I28326
VERSION     I28326.1  GI:1819102
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1364)
  AUTHORS   Scott,P. and Trinchieri,G.
  TITLE     Compositions and methods for use of IL-12 as an adjuvant
  JOURNAL   Patent: US 5571515-A 3 05-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .1364
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN
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  Query Match            11.6%;  Score 65;  DB 2;  Length 1364;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 811

Qy        514 ATTCG 518
              |||||
Db        812 ATTCG 816


RESULT 87
I89771
LOCUS       I89771                  1364 bp    DNA     linear   PAT 10-AUG-1998
DEFINITION  Sequence 3 from patent US 5723127.
ACCESSION   I89771
VERSION     I89771.1  GI:3409711
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1364)
  AUTHORS   Scott,P. and Trinchieri,G.
  TITLE     Compositions and methods for use of IL-12 as an adjuvant
  JOURNAL   Patent: US 5723127-A 3 03-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .1364
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            11.6%;  Score 65;  DB 2;  Length 1364;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 811

Qy        514 ATTCG 518
              |||||
Db        812 ATTCG 816


RESULT 88
AR309637
LOCUS       AR309637                1395 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 5 from patent US 6555658.
ACCESSION   AR309637
VERSION     AR309637.1  GI:31701688
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1395)
  AUTHORS   Trinchieri,G., Perussia,B., Clark,S.C., Wong,G.G., Hewick,R. and
            Kobayashi,M.
  TITLE     Antibodies to natural killer stimulatory factor
  JOURNAL   Patent: US 6555658-A 5 29-APR-2003;
            Wyeth and The Wistar Institute; Madison, NJ
FEATURES             Location/Qualifiers
     source          1. .1395
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match            11.6%;  Score 65;  DB 2;  Length 1395;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        765 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 824

Qy        514 ATTCG 518
              |||||
Db        825 ATTCG 829


RESULT 89
CS032085
LOCUS       CS032085                1444 bp    DNA     linear   PAT 10-MAR-2005
DEFINITION  Sequence 1591 from Patent WO2005016962.
ACCESSION   CS032085
VERSION     CS032085.1  GI:60731804
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Abbas,A., Clark,H., Ouyang,W., Williams,M.P., Wood,W.I. and Wu,T.D.
  TITLE     Compositions and methods for the treatment of immune related
            diseases
  JOURNAL   Patent: WO 2005016962-A 1591 24-FEB-2005;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1444
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match            11.6%;  Score 65;  DB 2;  Length 1444;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 926

Qy        514 ATTCG 518
              |||||
Db        927 ATTCG 931


RESULT 90
CS041037
LOCUS       CS041037                1444 bp    DNA     linear   PAT 22-MAR-2005
DEFINITION  Sequence 1591 from Patent WO2005019258.
ACCESSION   CS041037
VERSION     CS041037.1  GI:61848609
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Abbas,A., Clark,H., Ouyang,W., Williams,P.M., Wood,W.I. and Wu,T.D.
  TITLE     Compositions and methods for the treatment of immune related
            diseases
  JOURNAL   Patent: WO 2005019258-A 1591 03-MAR-2005;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1444
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
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ORIGIN

  Query Match            11.6%;  Score 65;  DB 2;  Length 1444;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-23;
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Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
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Db        867 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 926

Qy        514 ATTCG 518
              |||||
Db        927 ATTCG 931


RESULT 91
CS143811
LOCUS       CS143811               1444 bp    DNA     linear   PAT 19-AUG-2005
DEFINITION  Sequence 53 from Patent WO2005073411.
ACCESSION   CS143811
VERSION     CS143811.1  GI:73658825
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ried,T.
  TITLE     Composition for detecting the response of rectal adenocarcinomas to
            radiochemotherapy
  JOURNAL   Patent: WO 2005073411-A 53 11-AUG-2005;
            DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
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ORIGIN

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Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
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Db        867 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 926

Qy        514 ATTCG 518
              |||||
Db        927 ATTCG 931


RESULT 92
AR091395
LOCUS       AR091395               1560 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 11 from patent US 5994104.
ACCESSION   AR091395
VERSION     AR091395.1  GI:10018150
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1560)
  AUTHORS   Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
  TITLE     Interleukin-12 fusion protein
  JOURNAL   Patent: US 5994104-A 11 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .1560
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 1.1e-23;
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Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
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Db       1450 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1509

Qy        514 ATTCG 518
              |||||
Db       1510 ATTCG 1514


RESULT 93
AR091394
LOCUS       AR091394               1623 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 9 from patent US 5994104.
ACCESSION   AR091394
VERSION     AR091394.1  GI:10018149
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1623)
  AUTHORS   Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
  TITLE     Interleukin-12 fusion protein
  JOURNAL   Patent: US 5994104-A 9 30-NOV-1999;
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
ORIGIN

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Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
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Db       1513 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1572

Qy        514 ATTCG 518
              |||||
Db       1573 ATTCG 1577


RESULT 94
A92078
LOCUS       A92078                 1645 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 2 from Patent WO9821322.
ACCESSION   A92078
VERSION     A92078.1  GI:6740882
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 1645)
  AUTHORS   Junghans,C. and Wittig,B.
  TITLE     DESIGN PRINCIPLE FOR CONSTRUCTING EXPRESSION CONSTRUCTS FOR GENE
            THERAPY
  JOURNAL   Patent: WO 9821322-A 2 22-MAY-1998;
            JUNGHANS CLAAS (DE); SOFT GENE GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .1645
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
ORIGIN

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Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1284 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1343
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Qy        514 ATTCG 518
              |||||
Db       1344 ATTCG 1348


RESULT 95
AR230689
LOCUS       AR230689               1645 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 2 from patent US 6451593.
ACCESSION   AR230689
VERSION     AR230689.1  GI:27271470
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1645)
  AUTHORS   Wittig,B. and Junghans,C.
  TITLE     Design principle for construction of expression constructs for gene
            therapy
  JOURNAL   Patent: US 6451593-A 2 17-SEP-2002;
            Soft Gene GmbH; Berlin;
            DEX;
FEATURES             Location/Qualifiers
     source          1. .1645
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 1.1e-23;
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Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
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Db       1284 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1343

Qy        514 ATTCG 518
              |||||
Db       1344 ATTCG 1348


RESULT 96
CS131489
LOCUS       CS131489               3205 bp    DNA     linear   PAT 02-AUG-2005
DEFINITION  Sequence 8 from Patent WO2005066348.
ACCESSION   CS131489
VERSION     CS131489.1  GI:71794157
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Gillies,S.
  TITLE     Compounds for targeting
  JOURNAL   Patent: WO 2005066348-A 8 21-JUL-2005;
            Antisoma PLC (GB); EMD Lexigen Research Center Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .3205
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HuBC1 heavy chain fused to huIL12 p35 subunit"
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 1e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3095 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 3154

Qy        514 ATTCG 518
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Db       3155 ATTCG 3159


RESULT 97
BD136048
LOCUS       BD136048               5686 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Interferon alpha plasmid and delivery system and method of
            preparing and using the same.
ACCESSION   BD136048
VERSION     BD136048.1  GI:23230993
KEYWORDS    JP 2002506647-A/15.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 5686)
  AUTHORS   Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.
  TITLE     Interferon alpha plasmid and delivery system and method of
            preparing and using the same
  JOURNAL   Patent: JP 2002506647-A 15 05-MAR-2002;
            VALENTIS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002506647-A/15
            PD   05-MAR-2002
            PF   12-MAR-1999 JP 2000536861
            PR   19-MAR-1998 US    60/078654
            PI   JEFF NORDSTROM,FEDERICA PERICLE,ALAIN ROLLAND,ROBERT RALSTON
            PC   C12N15/09,A61K38/21,A61K48/00,A61P35/00,C07K14/54,C07K14/56,
            PC   C12N1/15,
            PC   C12N1/19,C12N1/21,C12N5/10//A61K9/127,C12N15/00,A61K37/66, PC
             C12N5/00
            CC   Sequence source: synthetic construct
            FH   Key             Location/Qualifiers
            FT   source          1. .5686
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .5686
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

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Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
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Db       2094 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 2153

Qy        514 ATTCG 518
              |||||
Db       2154 ATTCG 2158


RESULT 98
AR091393
LOCUS       AR091393               6139 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 7 from patent US 5994104.
ACCESSION   AR091393
VERSION     AR091393.1  GI:10018148
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 6139)
  AUTHORS   Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
  TITLE     Interleukin-12 fusion protein
  JOURNAL   Patent: US 5994104-A 7 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .6139
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ORIGIN

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Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
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Db       4734 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 4793

Qy        514 ATTCG 518
              |||||
Db       4794 ATTCG 4798


RESULT 99
AF404773
LOCUS       AF404773               11792 bp    DNA     linear   PRI 09-AUG-2001
DEFINITION  Homo sapiens interleukin 12A (natural killer cell stimulatory
            factor 1, cytotoxic lymphocyte maturation factor 1, p35) (IL12A)
            gene, complete cds.
ACCESSION   AF404773
VERSION     AF404773.1  GI:15128214
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 11792)
  AUTHORS   Rieder,M.J., Carrington,D.P., Chung,M.-W., Lee,K.L., Poel,C.L.,
            Yi,Q. and Nickerson,D.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2001) Molecular Biotechnology, University of
            Washington, 1705 NE Pacific, Seattle, WA 98195, USA
COMMENT     To cite this work please use:  SeattleSNPs. NHLBI Program for
            Genomic Applications, UW-FHCRC, Seattle, WA (URL:
            http://pga.mbt.washington.edu).
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                     /db_xref="taxon:9606"
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                     factor 1, cytotoxic lymphocyte maturation factor 1, p35)"
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                     factor 1, cytotoxic lymphocyte maturation factor 1, p35)"
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Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
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Db       8484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 8543

Qy        514 ATTCG 518
              |||||
Db       8544 ATTCG 8548


RESULT 100
AC010370
LOCUS       AC010370              157079 bp    DNA     linear   PRI 23-JAN-2002
DEFINITION  Homo sapiens chromosome 3 clone CTD-2049J23, complete sequence.
ACCESSION   AC010370
VERSION     AC010370.5  GI:14573679
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 157079)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 157079)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE   3  (bases 1 to 157079)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
REFERENCE   4  (bases 1 to 157079)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JAN-2002) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
COMMENT     On Jun 28, 2001 this sequence version replaced gi:12830118.
            Draft Sequence Produced by DOE Joint Genome Institute
            www.jgi.doe.gov
            Finishing Completed at Stanford Human Genome Center
            www-shgc.stanford.edu
            Quality: Phrap Quality >=40 99.7% of Sequence;
            Estimated Total Number of Errors is 0.4.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="3"
                     /clone="CTD-2049J23"
ORIGIN

  Query Match             11.6%;  Score 65;  DB 5;  Length 157079;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
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Qy        514 ATTCG 518
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Db     114382 ATTCG 114386


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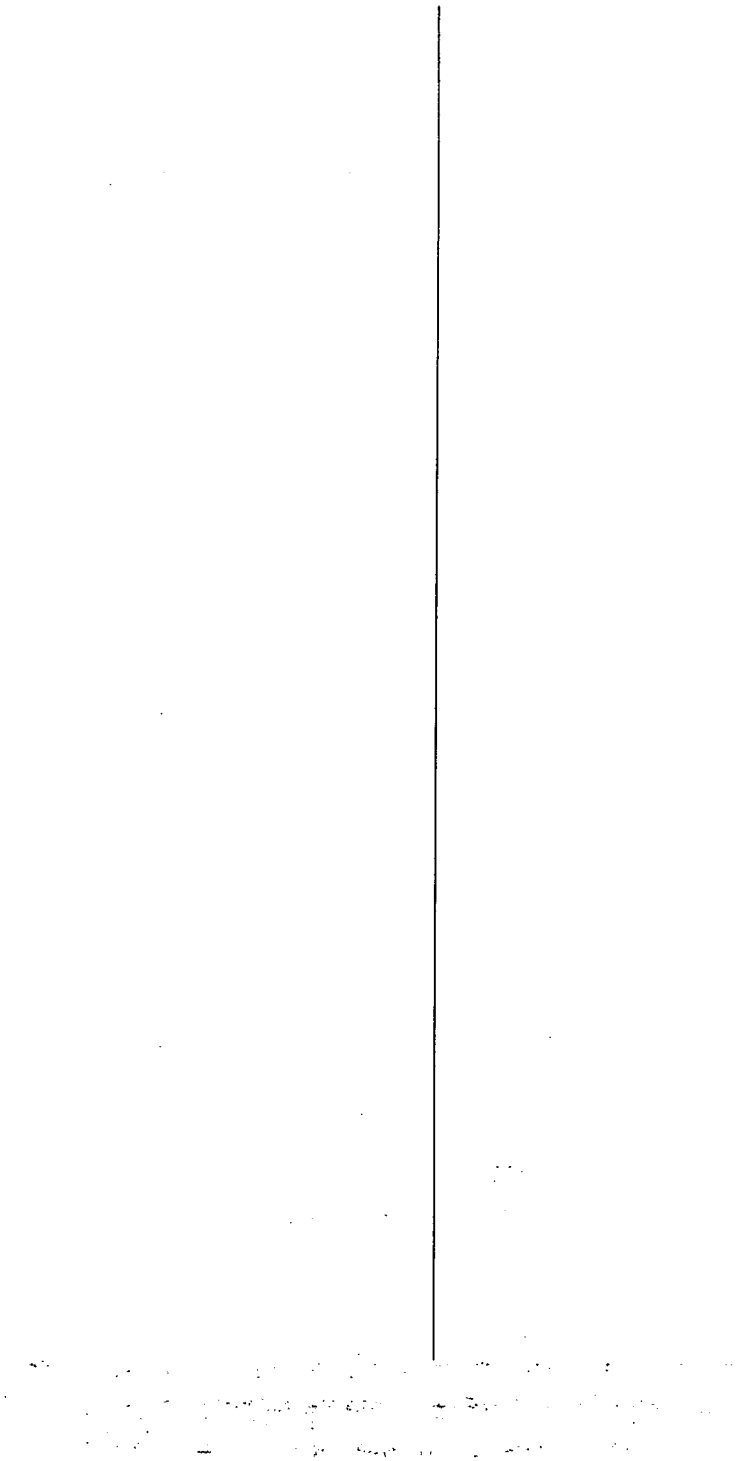

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3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	561	100.0	561	6	ABK99001	Abk99001 Feline in
c	2	561	100.0	561	6	ABK99002	Abk99002 Feline in
	3	561	100.0	561	14	ADV34751	Adv34751 Feline N-
c	4	561	100.0	561	14	ADV34753	Adv34753 Feline N-
c	5	558	99.5	666	6	ABK98947	Abk98947 Feline in
	6	558	99.5	666	6	ABK98946	Abk98946 Feline in
	7	558	99.5	666	14	ADV34685	Adv34685 Feline si
c	8	558	99.5	666	14	ADV34687	Adv34687 Feline si
c	9	510	90.9	1533	6	ABK98954	Abk98954 Feline in
	10	510	90.9	1533	6	ABK98953	Abk98953 Feline in
c	11	510	90.9	1533	14	ADV34697	Adv34697 Feline si
	12	510	90.9	1533	14	ADV34695	Adv34695 Feline si
	13	510	90.9	1599	6	ABK98950	Abk98950 Feline in
c	14	510	90.9	1599	6	ABK98951	Abk98951 Feline in
	15	510	90.9	1599	14	ADV34691	Adv34691 Feline si
c	16	510	90.9	1599	14	ADV34693	Adv34693 Feline si
	17	507	90.4	591	6	ABK98948	Abk98948 Feline in
c	18	507	90.4	591	6	ABK98949	Abk98949 Feline in
	19	507	90.4	591	14	ADV34688	Adv34688 Feline si
c	20	507	90.4	591	14	ADV34690	Adv34690 Feline si
	21	494	88.1	591	2	AAV56629	Aav56629 Feline FL
	22	494	88.1	1441	2	AAV56628	Aav56628 Feline FL
	23	338	60.2	679	4	AAF26097	Aaf26097 Feline fi
	24	221	39.4	689	2	AAV56641	Aav56641 Feline FL
	25	195	34.8	669	4	AAF26083	Aaf26083 Feline IL
	26	195	34.8	669	4	AAF26086	Aaf26086 Feline IL
	27	195	34.8	4201	4	AAF26077	Aaf26077 Feline IL
	28	178	31.7	660	5	AAD15214	Aad15214 Modified
	29	162	28.9	639	4	AAF26098	Aaf26098 Plasmid p
	30	120	21.4	660	5	AAD15215	Aad15215 Modified
	31	115	20.5	660	5	AAD15213	Aad15213 Modified
	32	115	20.5	660	5	AAD15220	Aad15220 Modified
	33	102	18.2	660	5	AAD15218	Aad15218 Modified
	34	98	17.5	660	5	AAD15216	Aad15216 Modified
	35	84	15.0	660	5	AAD15219	Aad15219 Modified
	36	81	14.4	591	2	AAX18179	Aax18179 Canine ma
c	37	81	14.4	591	6	ABK98958	Abk98958 Canine in
	38	81	14.4	591	6	ABK98957	Abk98957 Canine in
	39	81	14.4	591	14	ADV34701	Adv34701 Canine si
c	40	81	14.4	591	14	ADV34703	Adv34703 Canine si
	41	81	14.4	666	6	ABK98955	Abk98955 Canine in
c	42	81	14.4	666	6	ABK98956	Abk98956 Canine in
c	43	81	14.4	666	14	ADV34700	Adv34700 Canine si
	44	81	14.4	666	14	ADV34698	Adv34698 Canine si
	45	81	14.4	669	2	AAV13818	Aav13818 Canine IL
	46	81	14.4	669	2	AAV13819	Aav13819 Canine IL
	47	81	14.4	669	2	AAX03163	Aax03163 Nucleic a
	48	81	14.4	669	2	AAX03153	Aax03153 Nucleic a
	49	81	14.4	669	2	AAX35616	Aax35616 Nucleic a
	50	81	14.4	669	2	AAX35626	Aax35626 Nucleic a
	51	81	14.4	669	4	AAI64389	Aai64389 Canine co
	52	81	14.4	669	4	AAI64379	Aai64379 Canine co
	53	81	14.4	669	11	ADZ25701	Adz25701 Canine in
	54	81	14.4	669	13	ADT04852	Adt04852 Canine in
	55	81	14.4	1282	2	AAX18178	Aax18178 Canine fu
	56	81	14.4	1455	6	ABK99003	Abk99003 Canine in
c	57	81	14.4	1455	6	ABK99004	Abk99004 Canine in
c	58	81	14.4	1455	14	ADV34756	Adv34756 Canine si
	59	81	14.4	1455	14	ADV34754	Adv34754 Canine si
	60	81	14.4	1533	6	ABK98967	Abk98967 Canine in
c	61	81	14.4	1533	6	ABK98968	Abk98968 Canine in
c	62	81	14.4	1533	14	ADV34718	Adv34718 Canine si
	63	81	14.4	1533	14	ADV34716	Adv34716 Canine si
	64	81	14.4	1599	6	ABK98965	Abk98965 Canine in
c	65	81	14.4	1599	6	ABK98966	Abk98966 Canine in
c	66	81	14.4	1599	14	ADV34715	Adv34715 Canine si
	67	81	14.4	1599	14	ADV34713	Adv34713 Canine si
	68	71	12.7	71	4	AAF26092	Aaf26092 Feline IL
	69	71	12.7	71	4	AAF26099	Aaf26099 Feline Il
	70	65	11.6	201	13	ADQ41825	Adq41825 Myocardia
	71	65	11.6	201	13	ADQ41824	Adq41824 Myocardia
	72	65	11.6	201	13	ADQ41835	Adq41835 Myocardia
	73	65	11.6	201	13	ADQ41829	Adq41829 Myocardia
	74	65	11.6	201	13	ADQ41838	Adq41838 Myocardia
	75	65	11.6	201	13	ADQ41833	Adq41833 Myocardia
	76	65	11.6	657	12	ADG39431	Adg39431 Human CLM
	77	65	11.6	660	2	AAQ97485	Aaq97485 Human int
	78	65	11.6	660	2	AAV07274	Aav07274 Human Int
	79	65	11.6	660	2	AAV07218	Aav07218 DNA encod
	80	65	11.6	660	2	AAZ40407	Aaz40407 Human int
	81	65	11.6	660	5	AAD15217	Aad15217 Modified
	82	65	11.6	660	5	AAD15221	Aad15221 Human cyt
	83	65	11.6	660	6	AAL44226	Aal44226 Human int
	84	65	11.6	660	6	ACC47589	Acc47589 Human int
	85	65	11.6	660	12	ADF77244	Adf77244 Human IL-
	86	65	11.6	702	12	ADP88401	Adp88401 Human int
	87	65	11.6	721	2	AAQ67880	Aaq67880 EPV 42 kD
	88	65	11.6	721	2	AAZ08515	Aaz08515 Vaccinia
	89	65	11.6	721	13	ADR21891	Adr21891 Vaccinia
	90	65	11.6	761	10	ADK98708	Adk98708 Human int
	91	65	11.6	761	10	ADK98706	Adk98706 Human int

92	65	11.6	762	2	AAV83207	Aav83207 Interleuk
93	65	11.6	762	3	AAA35201	Aaa35201 Human ade
94	65	11.6	762	3	AAF21323	Aaf21323 Human low
95	65	11.6	762	10	ABZ97017	Abz97017 Human nuc
96	65	11.6	762	11	ABD20866	Abd20866 Human pul
97	65	11.6	762	12	ADO07654	Ado07654 Human int
98	65	11.6	762	13	ADS88021	Ads88021 Tumour tr
99	65	11.6	762	14	ADV42511	Adv42511 Human psy
100	65	11.6	823	10	ACD26420	Acd26420 cDNA enco
101	65	11.6	856	2	AAQ12150	Aaq12150 Cytotoxic
102	65	11.6	856	2	AAT77850	Aat77850 35 kDa su
103	65	11.6	856	2	AAT97970	Aat97970 35 kDa su
104	65	11.6	856	2	AAV00402	Aav00402 35 kDa su
105	65	11.6	856	2	AAV37772	Aav37772 Cytotoxic
106	65	11.6	856	12	ADG39389	Adg39389 Human cyt
107	65	11.6	856	12	ADO03760	Ado03760 Human CLM
108	65	11.6	889	13	ADU04652	Adu04652 Human ext
109	65	11.6	1026	3	AAZ40020	Aaz40020 Human p35
110	65	11.6	1026	8	ACA61266	Aca61266 DNA encod
111	65	11.6	1026	11	ADI31715	Adi31715 Human cDN
112	65	11.6	1026	13	ADS83782	Ads83782 Human lym
113	65	11.6	1172	8	ACC42373	Acc42373 Human ext
114	65	11.6	1200	8	ACF64408	Acf64408 Human IL1
115	65	11.6	1287	4	AAF76882	Aaf76882 DNA encod
116	65	11.6	1289	8	ACC42375	Acc42375 Human ext
117	65	11.6	1316	2	AAT63621	Aat63621 Interleuk
118	65	11.6	1316	6	AAD41639	Aad41639 Human int
119	65	11.6	1364	2	AAT48099	Aat48099 Human int
120	65	11.6	1364	2	AAV42536	Aav42536 Human int
121	65	11.6	1364	2	AAV15228	Aav15228 Heterodim
122	65	11.6	1364	3	AAZ28863	Aaz28863 Human int
123	65	11.6	1364	4	AAF56281	Aaf56281 IL-12 vac
124	65	11.6	1384	15	AEF92723	Aef92723 Human int
125	65	11.6	1396	2	AAQ24371	Aaq24371 Natural k
126	65	11.6	1444	12	ACF57533	Acf57533 Human IL1
127	65	11.6	1444	12	ADJ62891	Adj62891 Human int
128	65	11.6	1444	12	ADN12152	Adn12152 Interleuk
129	65	11.6	1444	14	ADY15785	Ady15785 DNA encod
130	65	11.6	1444	14	ADZ26544	Adz26544 Human IL1
131	65	11.6	1444	14	AEB56478	Aeb56478 Radiochem
132	65	11.6	1494	12	ADQ59495	Adq59495 Human can
133	65	11.6	1526	12	ADQ59549	Adq59549 Human can
134	65	11.6	1532	13	ADQ38388	Adq38388 Human SNP
135	65	11.6	1532	14	ADZ13866	Adz13866 Human can
136	65	11.6	1607	13	ADQ38387	Adq38387 Human SNP
137	65	11.6	1607	14	ADZ13864	Adz13864 Human can
138	65	11.6	2300	3	AAA92406	Aaa92406 Human int
139	65	11.6	2336	14	AEE03207	Aee03207 Human int
140	65	11.6	2390	12	ADM29103	Adm29103 Human int
141	65	11.6	3205	14	AEB48820	Aeb48820 Monoclona
142	65	11.6	4521	3	AAA35204	Aaa35204 Human ade
143	65	11.6	4521	3	AAF21326	Aaf21326 Human low
144	65	11.6	4521	10	ABZ97020	Abz97020 Human nuc
145	65	11.6	4521	11	ABD20869	Abd20869 Human pul
146	65	11.6	5013	14	AEA40941	Aea40941 T-DNA reg
147	65	11.6	5686	2	AAZ40415	Aaz40415 Plasmid p
148	65	11.6	5686	12	ADF77239	Adf77239 Human IL-
149	65	11.6	6139	3	AAZ40023	Aaz40023 Interleuk
150	65	11.6	8578	6	AAD31546	Aad31546 pIRES-hB7
151	65	11.6	8578	6	AAD31545	Aad31545 pIRES-hB7
152	65	11.6	8608	6	AAD31548	Aad31548 pIRES-hB7
153	65	11.6	8623	6	AAD31547	Aad31547 pIRES-hB7
154	65	11.6	8629	6	AAD31552	Aad31552 pIRES-IL1
155	65	11.6	8638	6	AAD31549	Aad31549 pIRES-hB7
156	65	11.6	8644	6	AAD31551	Aad31551 pIRES-IL1
157	65	11.6	8659	6	AAD31550	Aad31550 pIRES-IL1
158	65	11.6	11441	6	AAL44225	Aal44225 Human int
159	65	11.6	11453	10	ADG25152	Adg25152 Vector pS
160	65	11.6	11569	10	ADG25150	Adg25150 Vector pA
161	65	11.6	27277	12	ADQ59494	Adq59494 Human can
162	65	11.6	27277	14	ADZ13863	Adz13863 Human can
163	62	11.1	683	4	AAF26096	Aaf26096 Human pG-
164	60	10.7	666	5	AAD15212	Aad15212 Modified
165	60	10.7	666	5	AAD15211	Aad15211 Modified
166	56	10.0	700	8	ACF64405	Acf64405 Human IL1
167	45	8.0	76	4	AAF26100	Aaf26100 Feline Il
c 168	45	8.0	76	4	AAF26093	Aaf26093 Feline IL
c 169	45	8.0	76	4	AAF26090	Aaf26090 Feline IL
170	43	7.7	79	2	AAV56639	Aav56639 Feline FL
171	41	7.3	703	3	AAA70708	Aaa70708 Bovine in
172	40	7.1	700	8	ACF64406	Acf64406 Human IL1
173	40	7.1	700	8	ACF64407	Acf64407 Human IL1
174	30	5.3	39	6	ABK98991	Abk98991 Synthetic
175	30	5.3	39	14	ADV34741	Adv34741 Feline IL
176	30	5.3	201	13	ADQ41830	Adq41830 Myocardia
177	30	5.3	201	13	ADQ41821	Adq41821 Myocardia
178	29	5.2	554	2	AAT50757	Aat50757 Partial s
179	27	4.8	79	2	AAX18181	Aax18181 Primer fo
180	27	4.8	582	4	AAF76877	Aaf76877 Mature mu
181	27	4.8	660	2	AAX78396	Aax78396 IL-12p35
182	27	4.8	660	2	AAX25946	Aax25946 Interleuk
183	27	4.8	713	2	AAT35199	Aat35199 Mouse int
184	27	4.8	1231	12	ADQ59492	Adq59492 Human can
185	27	4.8	1265	2	AAV28473	Aav28473 Murine in
186	27	4.8	1265	8	ACA61264	Aca61264 DNA encod
187	27	4.8	1273	14	ADZ13861	Adz13861 Murine ca
188	27	4.8	1278	4	AAF76881	Aaf76881 DNA encod
189	27	4.8	1569	4	AAF76888	Aaf76888 Single-ch
190	27	4.8	2013	4	AAF76887	Aaf76887 Murine p3
191	27	4.8	2334	14	AEE03206	Aee03206 Murine in
192	27	4.8	2438	12	ADO43004	Ado43004 DNA encod
193	27	4.8	2709	4	AAF76889	Aaf76889 Coding se
194	27	4.8	5252	12	ADO07652	Ado07652 Tricistro
195	27	4.8	5966	2	AAZ40417	Aaz40417 Plasmid p
196	27	4.8	5966	12	ADF77241	Adf77241 Mouse IL-
197	27	4.8	5985	12	ADQ82718	Adq82718 Anticance
198	27	4.8	6295	2	AAV02043	Aav02043 Plasmid p
199	27	4.8	7287	2	AAV02042	Aav02042 Plasmid p
200	27	4.8	9049	12	ADO07661	Ado07661 Viral vec

ALIGNMENTS

RESULT 1
ABK99001
ID ABK99001 standard; cDNA; 561 BP.
XX
AC ABK99001;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p35-N561 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69315.
XX

PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Disclosure; Page 92-93; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 561 BP; 167 A; 134 C; 120 G; 140 T; 0 U; 0 Other;

Query Match 100.0%; Score 561; DB 6; Length 561;
Best Local Similarity 100.0%; Pred. No. 7.1e-277;
Matches 561; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db        541 ATGAGCTATCTGAATGCTTCC 561
```

RESULT 2
ABK99002/c
ID ABK99002 standard; cDNA; 561 BP.
XX
AC ABK99002;
XX

DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12nFeIL-12p35-N561 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Disclosure; Page 94; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 561 BP; 140 A; 120 C; 134 G; 167 T; 0 U; 0 Other;

Query Match 100.0%; Score 561; DB 6; Length 561;
Best Local Similarity 100.0%; Pred. No. 7.1e-277;
Matches 561; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1


RESULT 3
ADV34751
ID   ADV34751 standard; cDNA; 561 BP.
XX
AC   ADV34751;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline N-terminal single chain IL-12p35 cDNA, nFeIL-12p35-N561.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .561
FT                   /*tag=  a
FT                   /product= "PFeIL-12p35-N187 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34752.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 23; SEQ ID NO 101; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline N-terminal single chain IL-12p35 subunit
CC   protein encoding cDNA.
XX

SQ   Sequence 561 BP; 167 A; 134 C; 120 G; 140 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 561;  DB 14;  Length 561;
  Best Local Similarity  100.0%;  Pred. No. 7.1e-277;
  Matches  561;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db        541 ATGAGCTATCTGAATGCTTCC 561


RESULT 4
ADV34753/c
ID   ADV34753 standard; cDNA; 561 BP.
XX
AC   ADV34753;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline N-terminal IL-12p35 complementary DNA, nFeIL-12p35-N561.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
```

```
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Disclosure; SEQ ID NO 103; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline N-terminal single chain IL-12p35 subunit
CC   protein complementary DNA.
XX
SQ   Sequence 561 BP; 140 A; 120 C; 134 G; 167 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 561;  DB 14;  Length 561;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-277;
  Matches  561;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1


RESULT 5
ABK98947/c
ID   ABK98947 standard; cDNA; 666 BP.
XX
AC   ABK98947;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p35-666 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 3; Page 56; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflamatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 666 BP; 160 A; 138 C; 179 G; 189 T; 0 U; 0 Other;

  Query Match             99.5%;  Score 558;  DB 6;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-275;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        544 AGCTATCTGAATGCTTCC 561
              |||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1


RESULT 6
ABK98946
ID   ABK98946 standard; cDNA; 666 BP.
XX
AC   ABK98946;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p35-666 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69304.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 54-55; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 666 BP; 189 A; 179 C; 138 G; 160 T; 0 U; 0 Other;

  Query Match             99.5%;  Score 558;  DB 6;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-275;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648

Qy        544 AGCTATCTGAATGCTTCC 561
              ||||||||||||||||||
Db        649 AGCTATCTGAATGCTTCC 666


RESULT 7
ADV34685
ID   ADV34685 standard; cDNA; 666 BP.
XX
AC   ADV34685;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12p35 full-length cDNA, nFeIL-12p35 666.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .666
FT                   /*tag=  a
FT                   /product= "PFeIL-12p35 222 protein "
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
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PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34686.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 23; SEQ ID NO 32; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12p35 subunit protein
CC   encoding full-length cDNA.
XX
SQ   Sequence 666 BP; 189 A; 179 C; 138 G; 160 T; 0 U; 0 Other;

  Query Match             99.5%;  Score 558;  DB 14;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-275;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648

Qy        544 AGCTATCTGAATGCTTCC 561
              |||||||||||||||||
Db        649 AGCTATCTGAATGCTTCC 666
```

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RESULT 8
ADV34687/c
ID   ADV34687 standard; DNA; 666 BP.
XX
AC   ADV34687;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12p35 complementary DNA, nFeIL-12p35 666.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 34; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12p35 subunit full-length
CC   complementary DNA.
XX
SQ   Sequence 666 BP; 160 A; 138 C; 179 G; 189 T; 0 U; 0 Other;

  Query Match             99.5%;  Score 558;  DB 14;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-275;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db-       378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
```

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        544 AGCTATCTGAATGCTTCC 561
                ||||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1
```

RESULT 9
ABK98954/c
ID ABK98954 standard; cDNA; 1533 BP.
XX
AC ABK98954;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12-1533 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 66-67; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

```
  Query Match            90.9%;  Score 510;  DB 6;  Length 1533;
  Best Local Similarity  99.8%;  Pred. No. 1e-250;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              ||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1
```

RESULT 10
ABK98953
ID ABK98953 standard; cDNA; 1533 BP.
XX
AC ABK98953;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12-1533 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;

```
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69307.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 63-64; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

  Query Match             90.9%;  Score 510;  DB 6;  Length 1533;
  Best Local Similarity   99.8%;  Pred. No. 1e-250;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1032

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1092

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1093 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1152

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1153 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1212

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1213 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1272

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1273 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1332

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1333 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1392

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1393 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1452

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1453 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1512

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db       1513 ATGAGCTATCTGAATGCTTCC 1533


RESULT 11
ADV34697/c
ID   ADV34697 standard; DNA; 1533 BP.
XX
AC   ADV34697;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 complementary DNA, nFeIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 45; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 complementary DNA.
XX
SQ   Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

  Query Match             90.9%;  Score 510;  DB 14;  Length 1533;
  Best Local Similarity   99.8%;  Pred. No. 1e-250;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202
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Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1
```

RESULT 12
ADV34695
ID ADV34695 standard; cDNA; 1533 BP.
XX
AC ADV34695;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1533.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; gene; ss.
XX
OS Felis catus.
XX
FH Key Location/Qualifiers
FT CDS 1. .1533
FT /*tag= a
FT /product= "PFeIL-12 511 protein"
FT /partial
FT /note= "No start and stop codon"
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
DR P-PSDB; ADV34696.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Claim 24; SEQ ID NO 43; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

Query Match 90.9%; Score 510; DB 14; Length 1533;
Best Local Similarity 99.8%; Pred. No. 1e-250;
Matches 560; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1032

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1092

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1093 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1152

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1153 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1212

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1213 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1272

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1273 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1332

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1333 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1392

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1393 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1452

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1453 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1512

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db       1513 ATGAGCTATCTGAATGCTTCC 1533
```

RESULT 13
ABK98950
ID ABK98950 standard; cDNA; 1599 BP.
XX
AC ABK98950;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12-1599 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX

DR WPI; 2002-573554/61.
DR P-PSDB; ABG69306.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 58-60; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

Query Match 90.9%; Score 510; DB 6; Length 1599;
Best Local Similarity 99.8%; Pred. No. 1e-250;
Matches 560; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1098

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1158

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1218

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1219 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1278

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1338

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1398

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1458

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1459 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1518

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1519 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1578

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db       1579 ATGAGCTATCTGAATGCTTCC 1599
```

RESULT 14
ABK98951/c
ID ABK98951 standard; cDNA; 1599 BP.
XX
AC ABK98951;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12-1599 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 61-62; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

Query Match 90.9%; Score 510; DB 6; Length 1599;
Best Local Similarity 99.8%; Pred. No. 1e-250;
Matches 560; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262
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Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1


RESULT 15
ADV34691
ID   ADV34691 standard; cDNA; 1599 BP.
XX
AC   ADV34691;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1599
FT                   /*tag=  a
FT                   /product= "PFeIL-12p533 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34692.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 38; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

  Query Match            90.9%;  Score 510;  DB 14;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 1e-250;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1098

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1158

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1218

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1219 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1278

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1338

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1398

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1458

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1459 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1518

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1519 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1578

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db       1579 ATGAGCTATCTGAATGCTTCC 1599


RESULT 16
ADV34693/c
ID   ADV34693 standard; DNA; 1599 BP.
XX
AC   ADV34693;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 complementary DNA, nFeIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
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PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 40; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 complementary DNA.
XX
SQ   Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

  Query Match             90.9%;  Score 510;  DB 14;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 1e-250;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1


RESULT 17
ABK98948
ID   ABK98948 standard; cDNA; 591 BP.
XX
AC   ABK98948;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p35-591 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69305.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 56-57; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 591 BP; 178 A; 149 C; 122 G; 142 T; 0 U; 0 Other;

  Query Match             90.4%;  Score 507;  DB 6;  Length 591;
  Best Local Similarity   99.8%;  Pred. No. 3.4e-249;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
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Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573

Qy        544 AGCTATCTGAATGCTTCC 561
              |||||||||||||||||
Db        574 AGCTATCTGAATGCTTCC 591
```

```
RESULT 18
ABK98949/c
ID   ABK98949 standard; cDNA; 591 BP.
XX
AC   ABK98949;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p35-591 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Disclosure; Page 58; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 591 BP; 142 A; 122 C; 149 G; 178 T; 0 U; 0 Other;
```

```
  Query Match             90.4%;  Score 507;  DB 6;  Length 591;
  Best Local Similarity   99.8%;  Pred. No. 3.4e-249;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        544 AGCTATCTGAATGCTTCC 561
              |||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1
```

```
RESULT 19
ADV34688
ID   ADV34688 standard; cDNA; 591 BP.
XX
AC   ADV34688;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain mature IL-12p35 protein cDNA, nFeIL-12p35 591.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .591
FT                   /*tag=  a
FT                   /product= "PFeIL-12p35 197 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
```

```
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34689.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 23; SEQ ID NO 35; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain mature IL-12p35 subunit
CC   protein encoding cDNA.
XX
SQ   Sequence 591 BP; 178 A; 149 C; 122 G; 142 T; 0 U; 0 Other;

  Query Match             90.4%;  Score 507;  DB 14;  Length 591;
  Best Local Similarity   99.8%;  Pred. No. 3.4e-249;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573

Qy        544 AGCTATCTGAATGCTTCC 561
              |||||||||||||||||
Db        574 AGCTATCTGAATGCTTCC 591
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RESULT 20
ADV34690/c
ID   ADV34690 standard; DNA; 591 BP.
XX
AC   ADV34690;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain mature IL-12p35 complementary DNA, nFeIL-12p35 591.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 37; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain mature IL-12p35 subunit
CC   complementary DNA.
XX
SQ   Sequence 591 BP; 142 A; 122 C; 149 G; 178 T; 0 U; 0 Other;

  Query Match             90.4%;  Score 507;  DB 14;  Length 591;
  Best Local Similarity   99.8%;  Pred. No. 3.4e-249;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259
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Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        544 AGCTATCTGAATGCTTCC 561
              ||||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1
```

RESULT 21
AAV56629
ID AAV56629 standard; cDNA; 591 BP.
XX
AC AAV56629;
XX
DT 23-NOV-1998 (first entry)
XX
DE Feline FLAFp35 cDNA mature transcript.
XX
KW Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW T lymphocyte cell; autoimmune disease; ds.
XX
OS Felis catus.
XX
PN WO9746583-A1.
XX
PD 11-DEC-1997.
XX
PF 29-MAY-1997; 97WO-JP001824.
XX
PR 04-JUN-1996; 96JP-00165249.
XX
PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI Imamura T, Maeda H, Fujiyasu T, Imagawa Y, Tokiyoshi S;
XX
DR WPI; 1998-042118/04.
DR P-PSDB; AAW76176.
XX
PT Novel feline cytokine protein - useful for treating feline auto:immune
PT diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS Claim 23; Page 59; 94pp; Japanese.
XX
CC This sequence encodes a novel feline cytokine mature protein, FLAFp35.
CC This protein can be used in the production of a FLAFp35/FLAFp40
CC heterodimer which can potentiate the cytotoxic activity of feline
CC cytotoxic T lymphocyte cells. Such proteins are used for treatment of
CC feline autoimmune diseases e.g. as caused by feline herpes virus or
CC feline calcivirus
XX
SQ Sequence 591 BP; 179 A; 151 C; 120 G; 141 T; 0 U; 0 Other;

Query Match 88.1%; Score 494; DB 2; Length 591;
Best Local Similarity 99.8%; Pred. No. 1.6e-242;
Matches 544; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        454 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATC 513

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573

Qy        544 AGCTA 548
              |||||
Db        574 AGCTA 578
```

RESULT 22
AAV56628
ID AAV56628 standard; cDNA; 1441 BP.
XX
AC AAV56628;
XX
DT 23-NOV-1998 (first entry)
XX
DE Feline FLAFp35 cDNA.
XX
KW Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW T lymphocyte cell; autoimmune disease; ds.
XX
OS Felis catus.
XX
FH Key Location/Qualifiers
FT CDS 133. .811
FT /*tag= a
FT sig_peptide 133. .217
FT /*tag= b
FT mat_peptide 218. .808
FT /*tag= c
FT /product= "FLAFp35"
FT /note= "feline cytokine"
XX
PN WO9746583-A1.
XX
PD 11-DEC-1997.
XX
PF 29-MAY-1997; 97WO-JP001824.
XX
PR 04-JUN-1996; 96JP-00165249.
XX
PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI Imamura T, Maeda H, Fujiyasu T, Imagawa Y, Tokiyoshi S;

```
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76175.
XX
PT   Novel feline cytokine protein - useful for treating feline auto:immune
PT   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS   Claim 22; Page 57-58; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine protein, FLAFp35. This
CC   protein can be used in the production of a FLAFp35/FLAFp40 heterodimer
CC   which can potentiate the cytotoxic activity of feline cytotoxic T
CC   lymphocyte cells. Such proteins are used for treatment of feline
CC   autoimmune diseases e.g. as caused by feline herpes virus or feline
CC   calcivirus
XX
SQ   Sequence 1441 BP; 451 A; 325 C; 258 G; 407 T; 0 U; 0 Other;

  Query Match            88.1%;  Score 494;  DB 2;  Length 1441;
  Best Local Similarity   99.8%;  Pred. No. 1.6e-242;
  Matches  544;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 310

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 370

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 430

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 490

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 550

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        551 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 610

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 670

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        671 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATC 730

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        731 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 790

Qy        544 AGCTA 548
              |||||
Db        791 AGCTA 795


RESULT 23
AAF26097
ID   AAF26097 standard; DNA; 679 BP.
XX
AC   AAF26097;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline fil12p35a DNA.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS   Felis sp.
XX
PN   WO200104155-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002263.
XX
PR   08-JUL-1999;   99CH-00001259.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Lutz H,  Leutenegger C,  Pedersen N,  Schroff M,  Wittig B;
XX
DR   WPI; 2001-147178/15.
XX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs.
XX
PS   Disclosure; Fig 2; 35pp; German.
XX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
CC   following: (i) as immunostimulant, for preventative or therapeutic use;
CC   and (ii) treating tumors and autoimmune diseases, or diseases associated
CC   with a Th1 defect, especially pre-existing infections by feline immune
CC   deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ   Sequence 679 BP; 196 A; 180 C; 140 G; 163 T; 0 U; 0 Other;

  Query Match            60.2%;  Score 338;  DB 4;  Length 679;
  Best Local Similarity   99.5%;  Pred. No. 1.5e-162;
  Matches  438;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        169 AAGGCCAGACAAACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGGCTGGCCTCC 348

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528

Qy        424 AGTGTGACTGTGCCACAGAA 443
              ||||||||||||||||||||
Db        529 AGTGTGACTGTGCCACAGAA 548


RESULT 24
AAV56641
ID   AAV56641 standard; DNA; 689 BP.
XX
AC   AAV56641;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp35 DNA fragment.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ss.
XX
OS   Felis catus.
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP001824.
XX
PR   04-JUN-1996;   96JP-00165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
XX
PT   Novel feline cytokine protein - useful for treating feline auto:immune
PT   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS   Claim 24; Page 67; 94pp; Japanese.
XX
CC   This sequence encodes a fragment of a novel feline cytokine protein,
CC   FLAFp35. This protein can be used in the production of a FLAFp35/FLAFp40
CC   heterodimer which can potentiate the cytotoxic activity of feline
CC   cytotoxic T lymphocyte cells. Such proteins are used for treatment of
CC   feline autoimmune diseases e.g. as caused by feline herpes virus or
CC   feline calcivirus
XX
SQ   Sequence 689 BP; 192 A; 193 C; 145 G; 159 T; 0 U; 0 Other;

  Query Match             39.4%;  Score 221;  DB 2;  Length 689;
  Best Local Similarity   99.2%;  Pred. No. 1.4e-102;
  Matches  371;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        175 ACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGC 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 ACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGC 345

Qy        235 CTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGAC 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 CTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGAC 405

Qy        295 TTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAA 354
              |||||||||||||||||||||||||||||||||||||||||||||||| | ||||||||||||

Db        406 TTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAA 465

Qy        355 AGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTG 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 AGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTG 525

Qy        415 AATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAA 474
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        526 AATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAA 585

Qy        475 ACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAAT 534
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAAT 645

Qy        535 AGAATGATGAGCTA 548
              ||||||||||||||
Db        646 AGAATGATGAGCTA 659


RESULT 25
AAF26083
ID   AAF26083 standard; DNA; 669 BP.
XX
AC   AAF26083;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p35 encoding DNA SEQ ID 4.
XX
KW   Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW   interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS   Felis sp.
XX
PN   WO200104280-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002262.
XX
PR   08-JUL-1999;   99CH-00001258.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
XX
PI   Leutenegger C,  Schroff M,  Wittig B,  Lutz H;
XX
DR   WPI; 2001-147190/15.
XX
PT   Vaccine for treating or preventing lentivirus infection in cats, contains
PT   nucleic acid sequence encoding viral protein under control of eukaryotic
PT   promoter.
XX
PS   Claim 14; Page 37; 37pp; German.
XX
CC   This invention describes a novel vaccine (A) for prevention or treatment
CC   of lentivirus infection in felines which comprises an immunizing nucleic
CC   acid sequence (I) that contains, or comprises, at least part of a gene
CC   encoding a protein (II) of the virus, under control of a eukaryotic
CC   promoter functional in the relevant animal. (II) is especially the
CC   envelope (env) protein. The invention also describes (1) vaccine (A)
CC   containing an immunizing protein, or fragment, from a lentivirus plus at
CC   least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC   lentivirus protein, or fragment, especially derived from feline immune
CC   deficiency virus (FIV), by expressing the corresponding nucleic acid
CC   sequence in a host cell. The products of the invention have antiviral
CC   activity. The vaccine (A) and related protein-based vaccines, are
CC   particularly used to treat or prevent lentivirus infections in domestic
CC   cats, especially feline immune deficiency virus (FIV). Vaccination with
CC   (A) allows differentiation between vaccinated and infected animals, from
CC   the antibody status. The vaccines may be formulated with an adjuvant
CC   (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC   immune response, particularly a Th1 response
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XX
SQ   Sequence 669 BP; 189 A; 179 C; 140 G; 161 T; 0 U; 0 Other;

  Query Match            34.8%;  Score 195;  DB 4;  Length 669;
  Best Local Similarity   99.0%;  Pred. No. 3e-89;
  Matches  395;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        169 AAGGCCAGACAAACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAAT 288

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              |||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCC 348

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 402
              |||||||||||||||||||||||||||||||||||||||
Db        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 507


RESULT 26
AAF26086
ID   AAF26086 standard; DNA; 669 BP.
XX
AC   AAF26086;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p35 encoding DNA.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS   Felis sp.
XX
PN   WO200104155-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002263.
XX
PR   08-JUL-1999;   99CH-00001259.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Lutz H,  Leutenegger C,  Pedersen N,  Schroff M,  Wittig B;
XX
DR   WPI; 2001-147178/15.
XX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs.
XX
PS   Claim 3; Page 31; 35pp; German.
XX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
CC   following: (i) as immunostimulant, for preventative or therapeutic use;
CC   and (ii) treating tumors and autoimmune diseases, or diseases associated
CC   with a Th1 defect, especially pre-existing infections by feline immune
CC   deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ   Sequence 669 BP; 189 A; 179 C; 140 G; 161 T; 0 U; 0 Other;

  Query Match            34.8%;  Score 195;  DB 4;  Length 669;
  Best Local Similarity   99.0%;  Pred. No. 3e-89;
  Matches  395;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        169 AAGGCCAGACAAACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAAT 288

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              |||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCC 348

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 402
              |||||||||||||||||||||||||||||||||||||||
Db        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 507


RESULT 27
AAF26077
ID   AAF26077 standard; DNA; 4201 BP.
XX
AC   AAF26077;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p35 encoding DNA SEQ ID 3.
XX
KW   Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW   interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS   Felis sp.
XX
```

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PN   WO200104280-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002262.
XX
PR   08-JUL-1999;   99CH-00001258.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
XX
PI   Leutenegger C,  Schroff M,  Wittig B,  Lutz H;
XX
DR   WPI; 2001-147190/15.
XX
PT   Vaccine for treating or preventing lentivirus infection in cats, contains
PT   nucleic acid sequence encoding viral protein under control of eukaryotic
PT   promoter.
XX
PS   Disclosure; Page 31-33; 37pp; German.
XX
CC   This invention describes a novel vaccine (A) for prevention or treatment
CC   of lentivirus infection in felines which comprises an immunizing nucleic
CC   acid sequence (I) that contains, or comprises, at least part of a gene
CC   encoding a protein (II) of the virus, under control of a eukaryotic
CC   promoter functional in the relevant animal. (II) is especially the
CC   envelope (env) protein. The invention also describes (1) vaccine (A)
CC   containing an immunizing protein, or fragment, from a lentivirus plus at
CC   least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC   lentivirus protein, or fragment, especially derived from feline immune
CC   deficiency virus (FIV), by expressing the corresponding nucleic acid
CC   sequence in a host cell. The products of the invention have antiviral
CC   activity. The vaccine (A) and related protein-based vaccines, are
CC   particularly used to treat or prevent lentivirus infections in domestic
CC   cats, especially feline immune deficiency virus (FIV). Vaccination with
CC   (A) allows differentiation between vaccinated and infected animals, from
CC   the antibody status. The vaccines may be formulated with an adjuvant
CC   (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC   immune response, particularly a Th1 response
XX
SQ   Sequence 4201 BP; 1086 A; 1055 C; 999 G; 1061 T; 0 U; 0 Other;

  Query Match             34.8%;  Score 195;  DB 4;  Length 4201;
  Best Local Similarity   99.0%;  Pred. No. 3e-89;
  Matches  395;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3155 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 3214

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       3215 AAGGCCAGACAAACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGAT 3274

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db       3275 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAAT 3334

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              |||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db       3335 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCC 3394

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3395 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 3454

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3455 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 3514

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 402
              |||||||||||||||||||||||||||||||||||||||
Db       3515 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 3553
```

```
RESULT 28
AAD15214
ID   AAD15214 standard; DNA; 660 BP.
XX
AC   AAD15214;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 encoding DNA from clone R2-631.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p35; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "Modified p35 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .657
FT                   /*tag=  c
FT                   /product= "Mature modified p35 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08607.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 87; Page 139; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein encoding
CC   DNA
XX
SQ   Sequence 660 BP; 182 A; 178 C; 142 G; 158 T; 0 U; 0 Other;

  Query Match             31.7%;  Score 178;  DB 5;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-80;
  Matches  178;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        207 GATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGAC 266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 GATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGAC 362

Qy        267 CCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCAT 326
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 CCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCAT 422

Qy        327 GAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 384
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 GAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480


RESULT 29
AAF26098
ID   AAF26098 standard; DNA; 639 BP.
XX
AC   AAF26098;
XX
DT   24-APR-2001  (first entry)
XX
DE   Plasmid pMOL-fIL12 p35 DNA.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS   Synthetic.
XX
PN   WO200104155-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002263.
XX
PR   08-JUL-1999;   99CH-00001259.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Lutz H,  Leutenegger C,  Pedersen N,  Schroff M,  Wittig B;
XX
DR   WPI; 2001-147178/15.
XX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs.
XX
PS   Disclosure; Fig 2; 35pp; German.
XX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
CC   following: (i) as immunostimulant, for preventative or therapeutic use;
CC   and (ii) treating tumors and autoimmune diseases, or diseases associated
CC   with a Th1 defect, especially pre-existing infections by feline immune
CC   deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ   Sequence 639 BP; 189 A; 166 C; 133 G; 151 T; 0 U; 0 Other;

  Query Match             28.9%;  Score 162;  DB 4;  Length 639;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-72;
  Matches  162;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 352

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 412

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 402
                ||||||||||||||||||||||||||||||||||||||||||
Db        413 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 454


RESULT 30
AAD15215
ID   AAD15215 standard; DNA; 660 BP.
XX
AC   AAD15215;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 encoding DNA from clone R2-613.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p35; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "Modified p35 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .657
FT                   /*tag=  c
FT                   /product= "Mature modified p35 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08608.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 87; Page 139-140; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein encoding
CC   DNA
```

```
XX
SQ   Sequence 660 BP; 190 A; 171 C; 137 G; 162 T; 0 U; 0 Other;

  Query Match             21.4%;  Score 120;  DB 5;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 8.6e-51;
  Matches  120;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        265 ACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCC 324
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCC 420

Qy        325 ATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 384
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480


RESULT 31
AAD15213
ID   AAD15213 standard; DNA; 660 BP.
XX
AC   AAD15213;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 encoding DNA from clone R2-796.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p35; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "Modified p35 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .657
FT                   /*tag=  c
FT                   /product= "Mature modified p35 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08606.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 87; Page 139; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein encoding
CC   DNA
XX
SQ   Sequence 660 BP; 189 A; 172 C; 136 G; 163 T; 0 U; 0 Other;

  Query Match             20.5%;  Score 115;  DB 5;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-48;
  Matches  115;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 216

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAA 175
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        217 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAA 271


RESULT 32
AAD15220
ID   AAD15220 standard; DNA; 660 BP.
XX
AC   AAD15220;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 encoding DNA from clone R1-4-87.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p35; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "Modified p35 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .657
FT                   /*tag=  c
FT                   /product= "Mature modified p35 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08613.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 87; Page 140-141; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
```

```
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein encoding
CC   DNA
XX
SQ   Sequence 660 BP; 189 A; 172 C; 136 G; 163 T; 0 U; 0 Other;

  Query Match             20.5%;  Score 115;  DB 5;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-48;
  Matches  115;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 216

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAA 175
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        217 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAA 271


RESULT 33
AAD15218
ID   AAD15218 standard; DNA; 660 BP.
XX
AC   AAD15218;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 encoding DNA from clone R2-162.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p35; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "Modified p35 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .657
FT                   /*tag=  c
FT                   /product= "Mature modified p35 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08611.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 87; Page 140; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein encoding
CC   DNA
XX
SQ   Sequence 660 BP; 182 A; 180 C; 144 G; 154 T; 0 U; 0 Other;

  Query Match             18.2%;  Score 102;  DB 5;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-41;
  Matches  102;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        283 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 438

Qy        343 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 384
              |||||||||||||||||||||||||||||||||||||||||
Db        439 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480


RESULT 34
AAD15216
ID   AAD15216 standard; DNA; 660 BP.
XX
AC   AAD15216;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 encoding DNA from clone R2-571.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p35; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "Modified p35 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .657
FT                   /*tag=  c
FT                   /product= "Mature modified p35 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08609.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 87; Page 140; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
```

```
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein encoding
CC   DNA
XX
SQ   Sequence 660 BP; 184 A; 172 C; 141 G; 163 T; 0 U; 0 Other;

  Query Match             17.5%;  Score 98;  DB 5;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-39;
  Matches   98;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 216

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 158
              |||||||||||||||||||||||||||||||||||||
Db        217 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 254


RESULT 35
AAD15219
ID   AAD15219 standard; DNA; 660 BP.
XX
AC   AAD15219;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 encoding DNA from clone R2-157.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p35; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "Modified p35 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .657
FT                   /*tag=  c
FT                   /product= "Mature modified p35 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08612.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 87; Page 140; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein encoding
CC   DNA
XX
SQ   Sequence 660 BP; 181 A; 178 C; 144 G; 157 T; 0 U; 0 Other;

  Query Match             15.0%;  Score 84;  DB 5;  Length 660;
  Best Local Similarity   99.3%;  Pred. No. 2.4e-32;
  Matches  134;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        207 GATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGAC 266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 GATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGAC 362

Qy        267 CCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCAT 326
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        363 CCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCAT 422

Qy        327 GAATGCAAAGCTGTT 341
              |||||||||||||||
Db        423 GAATGCAAAGCTGTT 437


RESULT 36
AAX18179
ID   AAX18179 standard; cDNA; 591 BP.
XX
AC   AAX18179;
XX
DT   07-MAY-1999  (first entry)
XX
DE   Canine mature CLAF p35 subunit coding sequence.
XX
KW   CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW   viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW   canine infectious hepatitis; ds.
XX
OS   Canis sp.
XX
PN   WO9855511-A1.
XX
PD   10-DEC-1998.
XX
PF   26-MAY-1998;   98WO-JP002295.
XX
PR   03-JUN-1997;   97JP-00161936.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Tokiyoshi S,  Eda Y;
XX
DR   WPI; 1999-070260/06.
DR   P-PSDB; AAW74325.
XX
PT   Canine cytokine protein which activates canine cytotoxic T lymphocytes -
PT   is useful for treatment of viral and autoimmune diseases in dogs.
XX
PS   Claim 8; Page 34-35; 51pp; Japanese.
XX
CC   This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC   the invention. CLAF activates lymphocytes, especially canine cytotoxic T
CC   cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC   recognising it may be used in the treatment of viral diseases in dogs
CC   (such as canine distemper, canine parvovirus and canine infectious
CC   hepatitis). The antibodies may also be used in isolation of CLAF from
CC   culture of the transformant host cells by affinity chromatography. The
```

```
CC   p40 homodimer can be used for the treatment of autoimmune diseases in
CC   dogs
XX
SQ   Sequence 591 BP; 173 A; 146 C; 127 G; 145 T; 0 U; 0 Other;

  Query Match             14.4%;  Score 81;  DB 2;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        223 CTGGCTTCCAGAGAGATCTCT 243


RESULT 37
ABK98958/c
ID   ABK98958 standard; cDNA; 591 BP.
XX
AC   ABK98958;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p35-591 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Disclosure; Page 70; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 591 BP; 145 A; 127 C; 146 G; 173 T; 0 U; 0 Other;

  Query Match             14.4%;  Score 81;  DB 6;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 38
ABK98957
ID   ABK98957 standard; cDNA; 591 BP.
XX
AC   ABK98957;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p35-591 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69309.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 69; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 591 BP; 173 A; 146 C; 127 G; 145 T; 0 U; 0 Other;

  Query Match             14.4%;  Score 81;  DB 6;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
```

```
Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        223 CTGGCTTCCAGAGAGATCTCT 243


RESULT 39
ADV34701
ID   ADV34701 standard; cDNA; 591 BP.
XX
AC   ADV34701;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p35 protein cDNA, nCaIL-12p35 591.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .591
FT                   /*tag=  a
FT                   /product= "PCaIL-12P35 197 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34702.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 49; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p35 subunit protein
CC   encoding cDNA.
XX
SQ   Sequence 591 BP; 173 A; 146 C; 127 G; 145 T; 0 U; 0 Other;

  Query Match             14.4%;  Score 81;  DB 14;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        223 CTGGCTTCCAGAGAGATCTCT 243


RESULT 40
ADV34703/c
ID   ADV34703 standard; DNA; 591 BP.
XX
AC   ADV34703;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p35 complementary DNA, nCaIL-12p35 591.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 51; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p35 subunit
CC   complementary DNA.
XX
SQ   Sequence 591 BP; 145 A; 127 C; 146 G; 173 T; 0 U; 0 Other;

  Query Match             14.4%;  Score 81;  DB 14;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 41
ABK98955
ID   ABK98955 standard; cDNA; 666 BP.
XX
AC   ABK98955;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p35-666 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
```

KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69308.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 1; Page 67-68; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 666 BP; 182 A; 177 C; 145 G; 162 T; 0 U; 0 Other;

Query Match 14.4%; Score 81; DB 6; Length 666;
Best Local Similarity 100.0%; Pred. No. 8.4e-31;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy 193 CTGGCTTCCAGAGAGATCTCT 213
||||||||||||||||||||
Db 298 CTGGCTTCCAGAGAGATCTCT 318

RESULT 42
ABK98956/c
ID ABK98956 standard; cDNA; 666 BP.
XX
AC ABK98956;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12p35-66 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Disclosure; Page 68-69; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 666 BP; 162 A; 145 C; 177 G; 182 T; 0 U; 0 Other;

Query Match 14.4%; Score 81; DB 6; Length 666;
Best Local Similarity 100.0%; Pred. No. 8.4e-31;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy 193 CTGGCTTCCAGAGAGATCTCT 213
||||||||||||||||||||
Db 369 CTGGCTTCCAGAGAGATCTCT 349

RESULT 43
ADV34700/c
ID ADV34700 standard; DNA; 666 BP.
XX
AC ADV34700;
XX
DT 24-FEB-2005 (first entry)
XX
DE Canine single chain IL-12p35 complementary DNA, nCaIL-12p35 666.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Canis familiaris.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX

```
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 48; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p35 subunit full-length
CC   complementary DNA.
XX
SQ   Sequence 666 BP; 162 A; 145 C; 177 G; 182 T; 0 U; 0 Other;

  Query Match             14.4%;  Score 81;  DB 14;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 44
ADV34698
ID   ADV34698 standard; cDNA; 666 BP.
XX
AC   ADV34698;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p35 full-length cDNA, nCaIL-12p35 666.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .666
FT                   /*tag=  a
FT                   /product= "PCaIL-12p222 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34699.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 46; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p35 subunit protein
CC   encoding full-length cDNA.
XX
SQ   Sequence 666 BP; 182 A; 177 C; 145 G; 162 T; 0 U; 0 Other;

  Query Match             14.4%;  Score 81;  DB 14;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 45
AAV13818
ID   AAV13818 standard; cDNA to mRNA; 669 BP.
XX
AC   AAV13818;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P35 subunit cDNA.
XX
KW   Canine; interleukin-12 P35 subunit; IL-12 P35 subunit; antitumour;
KW   antiviral; vaccine adjuvant; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag=  a
FT                   /product= "interleukin-12_P35_subunit"
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-00296789.
XX
PR   08-NOV-1995;   95JP-00289729.
PR   23-MAY-1996;   96JP-00128104.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   P-PSDB; AAW41792.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected.
XX
PS   Claim 9; Page 9; 12pp; Japanese.
XX
```

```
CC   The present sequence encodes a canine interleukin-12 (IL-12) P35 subunit.
CC   A canine IL-12 comprising a P40 and P35 subunit is capable of inducing an
CC   antiviral activating factor and the expression of class II MHC molecules
CC   in canine tumour cells, stimulating proliferation of canine blastogenic
CC   lymphocytes and activating canine leukocytes to inhibit canine tumour
CC   cells. The canine IL-12 can be used in veterinary medicines, e.g.
CC   antitumour, antivirus and vaccine adjuvant activities are expected
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 U; 0 Other;

  Query Match             14.4%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 46
AAV13819
ID   AAV13819 standard; cDNA to mRNA; 669 BP.
XX
AC   AAV13819;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P35 subunit cDNA.
XX
KW   Canine; interleukin-12 P35 subunit; IL-12 P35 subunit; antitumour;
KW   antiviral; vaccine adjuvant; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag=  a
FT                   /product= "interleukin-12_P35_subunit"
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-00296789.
XX
PR   08-NOV-1995;   95JP-00289729.
PR   23-MAY-1996;   96JP-00128104.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   P-PSDB; AAW41793.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected.
XX
PS   Claim 11; Page 11-12; 12pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin-12 (IL-12) P35 subunit.
CC   A canine IL-12 comprising a P40 and P35 subunit is capable of inducing an
CC   antiviral activating factor and the expression of class II MHC molecules
CC   in canine tumour cells, stimulating proliferation of canine blastogenic
CC   lymphocytes and activating canine leukocytes to inhibit canine tumour
CC   cells. The canine IL-12 can be used in veterinary medicines, e.g.
CC   antitumour, antivirus and vaccine adjuvant activities are expected
XX
SQ   Sequence 669 BP; 185 A; 177 C; 144 G; 163 T; 0 U; 0 Other;

  Query Match             14.4%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 47
AAX03163
ID   AAX03163 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX03163;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Nucleic acid encoding canine interleukin 12.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag=  a
FT                   /product= "interleukin_12"
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP002031.
XX
PR   16-MAY-1997;   97JP-00127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   P-PSDB; AAW84374.
XX
PT   New therapeutic and prophylactic agents - comprise genetically-engineered
PT   canine interleukin 12, used to treat, e.g. canine and feline
PT   immunological diseases.
XX
PS   Claim 1; Page 33-34; 45pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin 12 (IL-12) protein. The
CC   IL-12 protein can be used in therapeutic or prophylactic agents. The
CC   agents can be used to prevent and treat canine and feline immunological
CC   diseases including dog and cat tumours, skin diseases, viral infections
CC   and allergic diseases, especially tumours, breast tumour, oesinophilic
CC   granuloma, epidermoid tumour, skin tumour, lipoma, othematoma,
CC   pneumonoedema, skin soft pedicled soft tumour and anal tumour; skin
CC   diseases, otitis externa, dermatitis, eczema, fungal diseases of the
CC   skin, pyoderma, allergic dermatitis, nettle rash, traumatic dermatitis
CC   and hair loss; infections; dog Parvovirus infection and distemper virus,
CC   cat plaque virus infection and feline leukaemia, and allergic diseases,
CC   e.g. pollinosis
XX
```

```
SQ   Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 U; 0 Other;

  Query Match            14.4%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity  100.0%;  Pred. No. 8.4e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 48
AAX03153
ID   AAX03153 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX03153;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Nucleic acid encoding canine interleukin 12.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag=  a
FT                   /product= "interleukin_12"
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP002031.
XX
PR   16-MAY-1997;   97JP-00127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   P-PSDB; AAW84372.
XX
PT   New therapeutic and prophylactic agents - comprise genetically-engineered
PT   canine interleukin 12, used to treat, e.g. canine and feline
PT   immunological diseases.
XX
PS   Claim 1; Page 26-27; 45pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin 12 (IL-12) protein. The
CC   IL-12 protein can be used in therapeutic or prophylactic agents. The
CC   agents can be used to prevent and treat canine and feline immunological
CC   diseases including dog and cat tumours, skin diseases, viral infections
CC   and allergic diseases, especially tumours, breast tumour, oesinophilic
CC   granuloma, epidermoid tumour, skin tumour, lipoma, othematoma,
CC   pneumonoedema, skin soft pedicled soft tumour and anal tumour; skin
CC   diseases, otitis externa, dermatitis, eczema, fungal diseases of the
CC   skin, pyoderma, allergic dermatitis, nettle rash, traumatic dermatitis
CC   and hair loss; infections; dog Parvovirus infection and distemper virus,
CC   cat plaque virus infection and feline leukaemia, and allergic diseases,
CC   e.g. pollinosis
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 U; 0 Other;

  Query Match            14.4%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity  100.0%;  Pred. No. 8.4e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 49
AAX35616
ID   AAX35616 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX35616;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag=  a
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-00133345.
XX
PR   16-MAY-1997;   97JP-00127690.
PR   07-AUG-1997;   97JP-00213755.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   P-PSDB; AAY02340.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) - for
PT   prevention and treatment of dog and cat immune diseases.
XX
PS   Claim 1; Page 13; 16pp; Japanese.
XX
CC   The present sequence encodes canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment of dog
CC   and cat immune diseases. The treatment used an agent comprising dog IL-12
CC   (CaIL12) proteins to form a heterodimer. The agent is useful for
CC   preventing and treating dog and cat immune diseases, including tumours,
CC   skin diseases, infectious diseases and allergic diseases
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 U; 0 Other;

  Query Match            14.4%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity  100.0%;  Pred. No. 8.4e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
```

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                    ||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 50
AAX35626
ID   AAX35626 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX35626;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag=  a
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-00133345.
XX
PR   16-MAY-1997;   97JP-00127690.
PR   07-AUG-1997;   97JP-00213755.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   P-PSDB; AAY02343.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) - for
PT   prevention and treatment of dog and cat immune diseases.
XX
PS   Claim 1; Page 15-16; 16pp; Japanese.
XX
CC   The present sequence encodes canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment of dog
CC   and cat immune diseases. The treatment used an agent comprising dog IL-12
CC   (CaIL12) proteins to form a heterodimer. The agent is useful for
CC   preventing and treating dog and cat immune diseases, including tumours,
CC   skin diseases, infectious diseases and allergic diseases
XX
SQ   Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 U; 0 Other;

  Query Match             14.4%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 51
AAI64389
ID   AAI64389 standard; DNA; 669 BP.
XX
AC   AAI64389;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine coding sequence #4.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag=  a
FT                   /product= "Canine protein #4"
FT   sig_peptide     1. .75
FT                   /*tag=  b
FT   mat_peptide     76. .666
FT                   /*tag=  c
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-00292946.
XX
PR   01-OCT-1999;   99JP-00281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   P-PSDB; AAG66483.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian.
XX
PS   Claim 6; Page 18; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention
XX
SQ   Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 U; 0 Other;

  Query Match             14.4%;  Score 81;  DB 4;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 52
AAI64379
ID   AAI64379 standard; DNA; 669 BP.
XX
AC   AAI64379;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine coding sequence #2.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag=  a
FT                   /product= "Canine protein #2"
```

```
FT   sig_peptide     1. .75
FT                   /*tag=  b
FT   mat_peptide     76. .666
FT                   /*tag=  c
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-00292946.
XX
PR   01-OCT-1999;   99JP-00281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   P-PSDB; AAG66481.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian.
XX
PS   Claim 6; Page 15; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 U; 0 Other;

  Query Match             14.4%;  Score 81;  DB 4;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 53
ADZ25701
ID   ADZ25701 standard; cDNA; 669 BP.
XX
AC   ADZ25701;
XX
DT   16-JUN-2005  (first entry)
XX
DE   Canine interleukin 12 P35 encoding cDNA SEQ ID NO:6.
XX
KW   interleukin-12; antiviral; gene; ss.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag=  b
FT                   /product= "interleukin-12 P40"
FT   sig_peptide     1. .75
FT                   /*tag=  a
FT   mat_peptide     76. .666
FT                   /*tag=  c
FT                   /product= "interleukin-12 P40"
XX
PN   JP2003284585-A.
XX
PD   07-OCT-2003.
XX
PF   28-MAR-2002; 2002JP-00090161.
XX
PR   28-MAR-2002; 2002JP-00090161.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2003-885430/82.
DR   P-PSDB; ADZ25703.
XX
PT   Large scale production of interleukin-12 for pharmaceutical applications,
PT   comprises infecting an insect cell with a recombinant virus containing
PT   gene encoding IL-12, and producing IL-12 by carrying out spinner culture
PT   of insect cell.
XX
PS   Example; SEQ ID NO 6; 8pp; Japanese.
XX
CC   The invention related to the large scale production of interleukin-12 (IL
CC   -12), which involves infecting an insect cell with a recombinant virus
CC   containing a gene encoding IL-12, and producing IL-12 by carrying out
CC   spinner culture of insect cell. The method is useful for producing IL-12,
CC   preferably canine IL-12. IL-12 has pharmaceutical applications. The
CC   present sequence encodes canine IL-12 P35, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 U; 0 Other;

  Query Match             14.4%;  Score 81;  DB 11;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 54
ADT04852
ID   ADT04852 standard; DNA; 669 BP.
XX
AC   ADT04852;
XX
DT   13-JAN-2005  (first entry)
XX
DE   Canine interleukin-12 (IL-12) p35 DNA.
XX
KW   gene expression; insect; ds; interleukin-12; IL-12.
XX
OS   Canis familiaris.
XX
PN   JP2004290182-A.
XX
PD   21-OCT-2004.
XX
PF   06-FEB-2004; 2004JP-00030183.
XX
PR   10-MAR-2003; 2003JP-00062907.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2004-740760/73.
XX
PT   Novel gene vector for expression in insect useful for expression of
PT   foreign gene such as dog interleukin 12 gene, comprises two promoters.
XX
PS   Claim 4; SEQ ID NO 8; 13pp; Japanese.
XX
CC   The invention relates to a novel gene vector for expression in an insect
CC   comprising at least two promoters, particularly the polyhedrin promoter
```

CC and p10 promoter. The vector contains at least two types of foreign
CC protein expression gene and the gene product of the vector is produced
CC using a gene recombinant baculovirus, particularly a recombinant silkworm
CC nuclear polyhedrosis virus. The baculovirus is proliferated in a
CC silkworm. The vector of the invention may be useful for expression of a
CC foreign gene, such as canine interleukin 12. Within the vector, two types
CC of foreign protein expression genes are integrated simultaneously for
CC their simultaneous expression. The current sequence is that of the canine
CC interleukin-12 (IL-12) p35 DNA of the invention.
XX
SQ Sequence 669 BP; 183 A; 177 C; 145 G; 164 T; 0 U; 0 Other;

Query Match 14.4%; Score 81; DB 13; Length 669;
Best Local Similarity 100.0%; Pred. No. 8.4e-31;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy 193 CTGGCTTCCAGAGAGATCTCT 213
||||||||||||||||||||
Db 298 CTGGCTTCCAGAGAGATCTCT 318

RESULT 55
AAX18178
ID AAX18178 standard; cDNA; 1282 BP.
XX
AC AAX18178;
XX
DT 07-MAY-1999 (first entry)
XX
DE Canine full length CLAF p35 subunit coding sequence.
XX
KW CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW canine infectious hepatitis; ds.
XX
OS Canis sp.
XX
PN WO9855511-A1.
XX
PD 10-DEC-1998.
XX
PF 26-MAY-1998; 98WO-JP002295.
XX
PR 03-JUN-1997; 97JP-00161936.
XX
PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI Imamura T, Maeda H, Tokiyoshi S, Eda Y;
XX
DR WPI; 1999-070260/06.
DR P-PSDB; AAW74324.
XX
PT Canine cytokine protein which activates canine cytotoxic T lymphocytes -
PT is useful for treatment of viral and autoimmune diseases in dogs.
XX
PS Claim 8; Page 33-34; 51pp; Japanese.
XX
CC This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC the invention. CLAF activates lymphocytes, especially canine cytotoxic T
CC cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC recognising it may be used in the treatment of viral diseases in dogs
CC (such as canine distemper, canine parvovirus and canine infectious
CC hepatitis). The antibodies may also be used in isolation of CLAF from
CC culture of the transformant host cells by affinity chromatography. The
CC p40 homodimer can be used for the treatment of autoimmune diseases in
CC dogs
XX
SQ Sequence 1282 BP; 391 A; 279 C; 257 G; 355 T; 0 U; 0 Other;

Query Match 14.4%; Score 81; DB 2; Length 1282;
Best Local Similarity 100.0%; Pred. No. 8.4e-31;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 303 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 362

Qy 193 CTGGCTTCCAGAGAGATCTCT 213
||||||||||||||||||||
Db 363 CTGGCTTCCAGAGAGATCTCT 383

RESULT 56
ABK99003
ID ABK99003 standard; cDNA; 1455 BP.
XX
AC ABK99003;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12p35-1455 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69316.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Example 4; Page 94-95; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1455 BP; 437 A; 341 C; 304 G; 373 T; 0 U; 0 Other;

Query Match 14.4%; Score 81; DB 6; Length 1455;
Best Local Similarity 100.0%; Pred. No. 8.4e-31;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```
Db        469 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 528

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        529 CTGGCTTCCAGAGAGATCTCT 549


RESULT 57
ABK99004/c
ID   ABK99004 standard; cDNA; 1455 BP.
XX
AC   ABK99004;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p35-1455 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 4; Page 96; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1455 BP; 373 A; 304 C; 341 G; 437 T; 0 U; 0 Other;

  Query Match             14.4%;  Score 81;  DB 6;  Length 1455;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 928

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        927 CTGGCTTCCAGAGAGATCTCT 907


RESULT 58
ADV34756/c
ID   ADV34756 standard; DNA; 1455 BP.
XX
AC   ADV34756;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p35 complementary DNA, nCaIL-12p35 1455.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 106; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p35 subunit
CC   complementary DNA.
XX
SQ   Sequence 1455 BP; 373 A; 304 C; 341 G; 437 T; 0 U; 0 Other;

  Query Match             14.4%;  Score 81;  DB 14;  Length 1455;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 928

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        927 CTGGCTTCCAGAGAGATCTCT 907


RESULT 59
ADV34754
ID   ADV34754 standard; cDNA; 1455 BP.
XX
AC   ADV34754;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p35 protein cDNA, nCaIL-12p35 1455.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
```

```
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             232. .900
FT                   /*tag= a
FT                   /product= "PCaIL-12p35 222 protein"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34755.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 104; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p35 subunit protein
CC   encoding cDNA.
XX
SQ   Sequence 1455 BP; 437 A; 341 C; 304 G; 373 T; 0 U; 0 Other;

  Query Match            14.4%;  Score 81;  DB 14;  Length 1455;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 528

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        529 CTGGCTTCCAGAGAGATCTCT 549


RESULT 60
ABK98967
ID   ABK98967 standard; cDNA; 1533 BP.
XX
AC   ABK98967;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1533 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69314.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 83-85; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 446 A; 368 C; 369 G; 350 T; 0 U; 0 Other;

  Query Match            14.4%;  Score 81;  DB 6;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1105 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1164

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db       1165 CTGGCTTCCAGAGAGATCTCT 1185


RESULT 61
ABK98968/c
ID   ABK98968 standard; cDNA; 1533 BP.
XX
AC   ABK98968;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1533 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
```

PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 86-87; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

Query Match 14.4%; Score 81; DB 6; Length 1533;
Best Local Similarity 100.0%; Pred. No. 8.4e-31;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy 193 CTGGCTTCCAGAGAGATCTCT 213
||||||||||||||||||||
Db 369 CTGGCTTCCAGAGAGATCTCT 349

RESULT 62
ADV34718/c
ID ADV34718 standard; DNA; 1533 BP.
XX
AC ADV34718;
XX
DT 24-FEB-2005 (first entry)
XX
DE Canine single chain IL-12 complementary DNA, nCaIL-12 1533.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Canis familiaris.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 4; SEQ ID NO 68; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the canine single chain IL-12 complementary DNA.
XX
SQ Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

Query Match 14.4%; Score 81; DB 14; Length 1533;
Best Local Similarity 100.0%; Pred. No. 8.4e-31;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy 193 CTGGCTTCCAGAGAGATCTCT 213
||||||||||||||||||||
Db 369 CTGGCTTCCAGAGAGATCTCT 349

RESULT 63
ADV34716
ID ADV34716 standard; cDNA; 1533 BP.
XX
AC ADV34716;
XX
DT 24-FEB-2005 (first entry)
XX
DE Canine single chain IL-12 protein cDNA, nCaIL-12 1533.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; gene; ss.
XX
OS Canis familiaris.
XX
FH Key Location/Qualifiers
FT CDS 1. .1533
FT /*tag= a
FT /product= "PCaIL-12 511 protein"
FT /partial
FT /note= "No start and stop codon"
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
DR P-PSDB; ADV34717.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 4; SEQ ID NO 66; 103pp; English.

XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the canine single chain IL-12 protein encoding cDNA.
XX
SQ Sequence 1533 BP; 446 A; 368 C; 369 G; 350 T; 0 U; 0 Other;

Query Match 14.4%; Score 81; DB 14; Length 1533;
Best Local Similarity 100.0%; Pred. No. 8.4e-31;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1105 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1164

Qy 193 CTGGCTTCCAGAGAGATCTCT 213
||||||||||||||||||||
Db 1165 CTGGCTTCCAGAGAGATCTCT 1185

RESULT 64
ABK98965
ID ABK98965 standard; cDNA; 1599 BP.
XX
AC ABK98965;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12-1599 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69313.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 79-80; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1599 BP; 452 A; 392 C; 383 G; 372 T; 0 U; 0 Other;

Query Match 14.4%; Score 81; DB 6; Length 1599;
Best Local Similarity 100.0%; Pred. No. 8.4e-31;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1171 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1230

Qy 193 CTGGCTTCCAGAGAGATCTCT 213
||||||||||||||||||||
Db 1231 CTGGCTTCCAGAGAGATCTCT 1251

RESULT 65
ABK98966/c
ID ABK98966 standard; cDNA; 1599 BP.
XX
AC ABK98966;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12-1599 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 82-83; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1599 BP; 372 A; 383 C; 392 G; 452 T; 0 U; 0 Other;

Query Match 14.4%; Score 81; DB 6; Length 1599;
Best Local Similarity 100.0%; Pred. No. 8.4e-31;

```
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 66
ADV34715/c
ID   ADV34715 standard; DNA; 1599 BP.
XX
AC   ADV34715;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12 complementary DNA, nCaIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 63; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 complementary DNA.
XX
SQ   Sequence 1599 BP; 372 A; 383 C; 392 G; 452 T; 0 U; 0 Other;

  Query Match             14.4%;  Score 81;  DB 14;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 67
ADV34713
ID   ADV34713 standard; cDNA; 1599 BP.
XX
AC   ADV34713;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12 protein cDNA, nCaIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1599
FT                   /*tag=  a
FT                   /product= "PCaIL-12 533 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34714.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 61; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1599 BP; 452 A; 392 C; 383 G; 372 T; 0 U; 0 Other;

  Query Match             14.4%;  Score 81;  DB 14;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1230

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db       1231 CTGGCTTCCAGAGAGATCTCT 1251


RESULT 68
AAF26092
ID   AAF26092 standard; DNA; 71 BP.
XX
AC   AAF26092;
XX
DT   24-APR-2001  (first entry)
```

XX
DE Feline IL-12p35 PCR primer SEQ ID 8.
XX
KW Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW Th1 defect; autoimmune disease; IL-12p40; IL-12p35; PCR primer; ss.
XX
OS Felis sp.
XX
PN WO200104155-A2.
XX
PD 18-JAN-2001.
XX
PF 08-JUL-2000; 2000WO-DE002263.
XX
PR 08-JUL-1999; 99CH-00001259.
XX
PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA (UYZU-) UNIV ZUERICH.
PA (REGC) UNIV CALIFORNIA.
XX
PI Lutz H, Leutenegger C, Pedersen N, Schroff M, Wittig B;
XX
DR WPI; 2001-147178/15.
XX
PT Recombinant feline interleukin-12, useful as immunostimulant and for
PT treating e.g. viral infections in cats, and related nucleic acid
PT constructs.
XX
PS Example 1b; Page 33; 35pp; German.
XX
CC This invention describes a novel feline interleukin-12 (fIL-12)
CC polypeptide (I) that is expressed, by recombinant gene expression in
CC eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC of subunits p35 and p40. These proteins are formed so that, in equimolar
CC concentrations and in presence of an immunizing antigen, they can be
CC administered to carnivores, particularly domestic cats. The invention
CC also describes a nucleic acid construct (II) encoding fIL-12 containing
CC sequences at least 95% identical with the p40- and p35-encoding sequences
CC (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC as immunostimulants for immunization against infectious diseases and/or
CC for treating infections or tumors in felines, especially domestic cats.
CC The products of the invention have immunostimulatory, antiviral and
CC antitumor activity. Nucleic acid constructs that encode (II) are useful
CC as adjuvants for prophylactic immunization against viral diseases and for
CC treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC is useful for carnivores, and particularly domestic cats in the
CC following: (i) as immunostimulant, for preventative or therapeutic use;
CC and (ii) treating tumors and autoimmune diseases, or diseases associated
CC with a Th1 defect, especially pre-existing infections by feline immune
CC deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ Sequence 71 BP; 17 A; 19 C; 17 G; 18 T; 0 U; 0 Other;

```
  Query Match             12.7%;  Score 71;  DB 4;  Length 71;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-25;
  Matches   71;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        380 TGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCAC 439
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCAC 60

Qy        440 AGAACTCCTCC 450
              ||||||||||||
Db         61 AGAACTCCTCC 71
```

RESULT 69
AAF26099
ID AAF26099 standard; DNA; 71 BP.
XX
AC AAF26099;
XX
DT 24-APR-2001 (first entry)
XX
DE Feline Il-12 associated DNA #1.
XX
KW Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS Unidentified.
XX
PN WO200104155-A2.
XX
PD 18-JAN-2001.
XX
PF 08-JUL-2000; 2000WO-DE002263.
XX
PR 08-JUL-1999; 99CH-00001259.
XX
PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA (UYZU-) UNIV ZUERICH.
PA (REGC) UNIV CALIFORNIA.
XX
PI Lutz H, Leutenegger C, Pedersen N, Schroff M, Wittig B;
XX
DR WPI; 2001-147178/15.
XX
PT Recombinant feline interleukin-12, useful as immunostimulant and for
PT treating e.g. viral infections in cats, and related nucleic acid
PT constructs.
XX
PS Disclosure; Fig 2; 35pp; German.
XX
CC This invention describes a novel feline interleukin-12 (fIL-12)
CC polypeptide (I) that is expressed, by recombinant gene expression in
CC eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC of subunits p35 and p40. These proteins are formed so that, in equimolar
CC concentrations and in presence of an immunizing antigen, they can be
CC administered to carnivores, particularly domestic cats. The invention
CC also describes a nucleic acid construct (II) encoding fIL-12 containing
CC sequences at least 95% identical with the p40- and p35-encoding sequences
CC (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC as immunostimulants for immunization against infectious diseases and/or
CC for treating infections or tumors in felines, especially domestic cats.
CC The products of the invention have immunostimulatory, antiviral and
CC antitumor activity. Nucleic acid constructs that encode (II) are useful
CC as adjuvants for prophylactic immunization against viral diseases and for
CC treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC is useful for carnivores, and particularly domestic cats in the
CC following: (i) as immunostimulant, for preventative or therapeutic use;
CC and (ii) treating tumors and autoimmune diseases, or diseases associated
CC with a Th1 defect, especially pre-existing infections by feline immune
CC deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ Sequence 71 BP; 17 A; 19 C; 17 G; 18 T; 0 U; 0 Other;

```
  Query Match             12.7%;  Score 71;  DB 4;  Length 71;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-25;
  Matches   71;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        380 TGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCAC 439
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCAC 60

Qy        440 AGAACTCCTCC 450
              ||||||||||||
Db         61 AGAACTCCTCC 71
```

RESULT 70
ADQ41825
ID ADQ41825 standard; DNA; 201 BP.

XX
AC ADQ41825;
XX
DT 18-NOV-2004 (first entry)
XX
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 3488.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human; ds.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JJ, Iakoubova O;
XX
DR WPI; 2004-533949/51.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 7; SEQ ID NO 3488; 145pp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a transcript-based context sequence
CC which flanks an SNP found in a human myocardial infarction-associated
CC gene of the invention. Note: This sequence was not shown in the
CC specification. The sequence has come from an electronic sequence listing
CC downloaded from the WIPO website.
XX
SQ Sequence 201 BP; 64 A; 39 C; 37 G; 60 T; 0 U; 1 Other;

Query Match 11.6%; Score 65; DB 13; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 21 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 80

Qy 514 ATTCG 518
|||||
Db 81 ATTCG 85

RESULT 71
ADQ41824
ID ADQ41824 standard; DNA; 201 BP.
XX
AC ADQ41824;
XX
DT 18-NOV-2004 (first entry)
XX
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 3487.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human; ds.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JJ, Iakoubova O;
XX
DR WPI; 2004-533949/51.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 7; SEQ ID NO 3487; 145pp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a transcript-based context sequence
CC which flanks an SNP found in a human myocardial infarction-associated
CC gene of the invention. Note: This sequence was not shown in the
CC specification. The sequence has come from an electronic sequence listing
CC downloaded from the WIPO website.
XX

```
SQ   Sequence 201 BP; 65 A; 36 C; 38 G; 61 T; 0 U; 1 Other;

  Query Match             11.6%;  Score 65;  DB 13;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 72

Qy        514 ATTCG 518
              |||||
Db         73 ATTCG 77


RESULT 72
ADQ41835
ID   ADQ41835 standard; DNA; 201 BP.
XX
AC   ADQ41835;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Myocardial infarction-associated SNP flanking transcript, SEQ ID 3498.
XX
KW   Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW   cardiant; gene therapy; human; ds.
XX
OS   Homo sapiens.
XX
PN   WO2004058052-A2.
XX
PD   15-JUL-2004.
XX
PF   22-DEC-2003; 2003WO-US040978.
XX
PR   20-DEC-2002; 2002US-0434778P.
PR   10-MAR-2003; 2003US-0453135P.
PR   30-APR-2003; 2003US-0466412P.
PR   23-SEP-2003; 2003US-0504955P.
XX
PA   (APPL-) APPLERA CORP.
XX
PI   Cargill M,  Devlin JJ,  Iakoubova O;
XX
DR   WPI; 2004-533949/51.
XX
PT   Identifying an individual who has an altered risk for developing
PT   myocardial infarction by detecting a single nucleotide polymorphism in
PT   the individual's nucleic acids.
XX
PS   Claim 7; SEQ ID NO 3498; 145pp; English.
XX
CC   The invention relates to a novel method for identifying an individual who
CC   has an altered risk for developing myocardial infarction. The method
CC   comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC   the nucleotide sequences given in the specification in the individual's
CC   nucleic acids, where the presence of the SNP is correlated with an
CC   altered risk for myocardial infarction in the individual. The invention
CC   further comprises: an isolated nucleic acid molecule comprising at least
CC   8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC   the specification or its complement and encoding any one of the amino
CC   acid sequences given in the specification; an isolated polypeptide
CC   comprising an amino acid sequence given in the specification; an antibody
CC   that specifically binds to the polypeptide or its antigen-binding
CC   fragment; an amplified polynucleotide containing an SNP given in the
CC   specification and which is between about 16 and 1000 nucleotides in
CC   length; a kit for detecting an SNP in a nucleic acid, comprising the
CC   polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC   nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC   method for identifying an agent useful in treating or preventing
CC   myocardial infarction. The novel detection method has cardiant activity.
CC   The nucleic acids of the invention may be used in gene therapy. The
CC   method is useful in identifying an individual who has an increased or
CC   decreased risk for developing myocardial infarction and for preparing a
CC   composition for treating or preventing myocardial infarction. This
CC   polynucleotide sequence represents a transcript-based context sequence
CC   which flanks an SNP found in a human myocardial infarction-associated
CC   gene of the invention. Note: This sequence was not shown in the
CC   specification. The sequence has come from an electronic sequence listing
CC   downloaded from the WIPO website.
XX
SQ   Sequence 201 BP; 64 A; 39 C; 37 G; 60 T; 0 U; 1 Other;

  Query Match             11.6%;  Score 65;  DB 13;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 80

Qy        514 ATTCG 518
              |||||
Db         81 ATTCG 85


RESULT 73
ADQ41829
ID   ADQ41829 standard; DNA; 201 BP.
XX
AC   ADQ41829;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Myocardial infarction-associated SNP flanking transcript, SEQ ID 3492.
XX
KW   Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW   cardiant; gene therapy; human; ds.
XX
OS   Homo sapiens.
XX
PN   WO2004058052-A2.
XX
PD   15-JUL-2004.
XX
PF   22-DEC-2003; 2003WO-US040978.
XX
PR   20-DEC-2002; 2002US-0434778P.
PR   10-MAR-2003; 2003US-0453135P.
PR   30-APR-2003; 2003US-0466412P.
PR   23-SEP-2003; 2003US-0504955P.
XX
PA   (APPL-) APPLERA CORP.
XX
PI   Cargill M,  Devlin JJ,  Iakoubova O;
XX
DR   WPI; 2004-533949/51.
XX
PT   Identifying an individual who has an altered risk for developing
PT   myocardial infarction by detecting a single nucleotide polymorphism in
PT   the individual's nucleic acids.
XX
PS   Claim 7; SEQ ID NO 3492; 145pp; English.
XX
CC   The invention relates to a novel method for identifying an individual who
CC   has an altered risk for developing myocardial infarction. The method
CC   comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC   the nucleotide sequences given in the specification in the individual's
CC   nucleic acids, where the presence of the SNP is correlated with an
CC   altered risk for myocardial infarction in the individual. The invention
CC   further comprises: an isolated nucleic acid molecule comprising at least
CC   8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC   the specification or its complement and encoding any one of the amino
CC   acid sequences given in the specification; an isolated polypeptide
CC   comprising an amino acid sequence given in the specification; an antibody
```

CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a transcript-based context sequence
CC which flanks an SNP found in a human myocardial infarction-associated
CC gene of the invention. Note: This sequence was not shown in the
CC specification. The sequence has come from an electronic sequence listing
CC downloaded from the WIPO website.
XX
SQ Sequence 201 BP; 62 A; 42 C; 39 G; 57 T; 0 U; 1 Other;

Query Match 11.6%; Score 65; DB 13; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 122 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 181

Qy 514 ATTCG 518
|||||
Db 182 ATTCG 186

RESULT 74
ADQ41838
ID ADQ41838 standard; DNA; 201 BP.
XX
AC ADQ41838;
XX
DT 18-NOV-2004 (first entry)
XX
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 3501.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human; ds.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JJ, Iakoubova O;
XX
DR WPI; 2004-533949/51.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 7; SEQ ID NO 3501; 145pp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a transcript-based context sequence
CC which flanks an SNP found in a human myocardial infarction-associated
CC gene of the invention. Note: This sequence was not shown in the
CC specification. The sequence has come from an electronic sequence listing
CC downloaded from the WIPO website.
XX
SQ Sequence 201 BP; 62 A; 42 C; 39 G; 57 T; 0 U; 1 Other;

Query Match 11.6%; Score 65; DB 13; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 122 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 181

Qy 514 ATTCG 518
|||||
Db 182 ATTCG 186

RESULT 75
ADQ41833
ID ADQ41833 standard; DNA; 201 BP.
XX
AC ADQ41833;
XX
DT 18-NOV-2004 (first entry)
XX
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 3496.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human; ds.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JJ, Iakoubova O;
XX
DR WPI; 2004-533949/51.

```
XX
PT   Identifying an individual who has an altered risk for developing
PT   myocardial infarction by detecting a single nucleotide polymorphism in
PT   the individual's nucleic acids.
XX
PS   Claim 7; SEQ ID NO 3496; 145pp; English.
XX
CC   The invention relates to a novel method for identifying an individual who
CC   has an altered risk for developing myocardial infarction. The method
CC   comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC   the nucleotide sequences given in the specification in the individual's
CC   nucleic acids, where the presence of the SNP is correlated with an
CC   altered risk for myocardial infarction in the individual. The invention
CC   further comprises: an isolated nucleic acid molecule comprising at least
CC   8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC   the specification or its complement and encoding any one of the amino
CC   acid sequences given in the specification; an isolated polypeptide
CC   comprising an amino acid sequence given in the specification; an antibody
CC   that specifically binds to the polypeptide or its antigen-binding
CC   fragment; an amplified polynucleotide containing an SNP given in the
CC   specification and which is between about 16 and 1000 nucleotides in
CC   length; a kit for detecting an SNP in a nucleic acid, comprising the
CC   polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC   nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC   method for identifying an agent useful in treating or preventing
CC   myocardial infarction. The novel detection method has cardiant activity.
CC   The nucleic acids of the invention may be used in gene therapy. The
CC   method is useful in identifying an individual who has an increased or
CC   decreased risk for developing myocardial infarction and for preparing a
CC   composition for treating or preventing myocardial infarction. This
CC   polynucleotide sequence represents a transcript-based context sequence
CC   which flanks an SNP found in a human myocardial infarction-associated
CC   gene of the invention. Note: This sequence was not shown in the
CC   specification. The sequence has come from an electronic sequence listing
CC   downloaded from the WIPO website.
XX
SQ   Sequence 201 BP; 65 A; 36 C; 38 G; 61 T; 0 U; 1 Other;

  Query Match             11.6%;  Score 65;  DB 13;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 72

Qy        514 ATTCG 518
              |||||
Db         73 ATTCG 77


RESULT 76
ADG39431
ID   ADG39431 standard; DNA; 657 BP.
XX
AC   ADG39431;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human CLMF 35 kDa subunit DNA.
XX
KW   human; cytotoxic lymphocyte maturation factor; CLMF;
KW   activated T-cell stimulator; natural killer cell stimulator;
KW   immunoenhancer; antitumour; tumour; cancer; ds; gene.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             67. .657
FT                   /*tag=  a
FT                   /partial
FT                   /product= "CLMF 35 kDa subunit"
FT                   /note= "No start or stop codon given"
XX
PN   US2003204059-A1.
XX
PD   30-OCT-2003.
XX
PF   08-OCT-2002; 2002US-00267565.
XX
PR   22-DEC-1989;   89US-00455708.
PR   09-MAY-1990;   90US-00520935.
PR   27-AUG-1990;   90US-00572284.
PR   24-MAR-1992;   92US-00857023.
PR   02-MAR-1994;   94US-00205011.
PR   02-JUN-1995;   95US-00459151.
PR   22-SEP-1999;   99US-00401839.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CIE SA F.
XX
PI   Gately MK,  Gubler UA,  Hulmes JD,  Podlaski FJ,  Stern AS;
PI   Chizzonite RA,  Pan YE;
XX
DR   WPI; 2004-010534/01.
DR   P-PSDB; ADG39428.
XX
PT   Novel protein comprising cytotoxic lymphocyte maturation factor in
PT   substantially pure form or protein which exhibits cytotoxic lymphocyte
PT   maturation factor activity, useful as antitumor and immunoenhancing
PT   agent.
XX
PS   Claim 20; Page 29; 74pp; English.
XX
CC   The invention relates to a protein which comprises a cytotoxic lymphocyte
CC   maturation factor (CLMF). The protein is useful for stimulating activated
CC   T-cells which involves treating T-cells with the protein. The method
CC   further involves treating the activated T-cells with IL2 or its
CC   biologically active fragment. The protein is useful for stimulating
CC   natural killer cells which involves treating the natural killer cells
CC   with the protein. The protein has immunoenhancing and antitumour effects
CC   when used as single therapeutic agent in vivo. The present sequence is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 657 BP; 186 A; 166 C; 139 G; 166 T; 0 U; 0 Other;

  Query Match             11.6%;  Score 65;  DB 12;  Length 657;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        514 ATTCG 518
              |||||
Db        610 ATTCG 614


RESULT 77
AAQ97485
ID   AAQ97485 standard; cDNA; 660 BP.
XX
AC   AAQ97485;
XX
DT   25-MAR-2003  (revised)
DT   22-DEC-1995  (first entry)
XX
DE   Human interleukin-12 35 kD subunit.
XX
KW   Interleukin-12; IL-12; cytokine; gamma-interferon; T cell;
KW   natural killer cell; graft vs. host disease; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
```

```
FT                   /*tag=  a
XX
PN   WO9519786-A1.
XX
PD   27-JUL-1995.
XX
PF   20-JAN-1995;   95WO-US000879.
XX
PR   21-JAN-1994;   94US-00186529.
XX
PA   (GEMY ) GENETICS INST INC.
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Wolf SF,  Sykes M;
XX
DR   WPI; 1995-269273/35.
DR   P-PSDB; AAR79187.
XX
PT   Control of graft versus host disease using interleukin 12 - partic.
PT   admin. at the time of bone marrow transplant.
XX
PS   Disclosure; Page 23-24; 32pp; English.
XX
CC   AAQ97484 and AAQ97485 are from human lymphoblast cell line RMPI 8866. IL-
CC   12 is a heterodimeric cytokine which was originally identified as a
CC   factor which induces gamma-interferon from T cells and natural killer
CC   cells as set forth in PCT/US91/06332, published April 2 1992, and
CC   incorporated by reference. EP 433827, published June 26 1991, disclosed
CC   IL-12 as a cytotoxin lymphocyte maturation factor. In the patent, IL-12
CC   is defined as a heterodimeric glycoprotein comprised of two covalently
CC   linked subunits having mol. wts of about 40 kD and 35 kD. The two
CC   subunits may be disulfide-bonded. IL-12 is administered to prevent or
CC   ameliorate GVHD. Dosage is 1 ng-0.1 mg (esp. 1.0 ng-1 microg)/kg daily
CC   for 3 days, the first dose given 1 hr. after transplant. IL-12 can be
CC   used as the native heterodimer or as subunits. (Updated on 25-MAR-2003 to
CC   correct PN field.)
XX
SQ   Sequence 660 BP; 188 A; 164 C; 139 G; 169 T; 0 U; 0 Other;

  Query Match             11.6%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        514 ATTCG 518
              |||||
Db        610 ATTCG 614


RESULT 78
AAV07274
ID   AAV07274 standard; cDNA; 660 BP.
XX
AC   AAV07274;
XX
DT   25-SEP-1998  (first entry)
XX
DE   Human Interleukin-12 p35 gene.
XX
KW   IL-12 subunit; expression construct; treatment; asthma;
KW   microbial infection; viral infection; cancer; Human; Interleukin; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "IL-12 p35"
FT                   /transl_except= (pos:58. .60,aa:Ser)
XX
PN   WO9817689-A2.
XX
PD   30-APR-1998.
XX
PF   10-OCT-1997;   97WO-US018779.
XX
PR   18-OCT-1996;   96US-0028676P.
XX
PA   (GENE-) GENEMEDICINE INC.
XX
PI   Nordstrom J,  Freimark B,  Deshpande D;
XX
DR   WPI; 1998-261428/23.
DR   P-PSDB; AAV07274.
XX
PT   Constructs for expression of interleukin-12 sub-units - are used for
PT   delivery of IL-12 sub-units for treating e.g. asthma, microbial or viral
PT   infections and certain cancers.
XX
PS   Claim 1; Page 34-35; 80pp; English.
XX
CC   The IL-12 subunits AAV07273 and AAV07274 can be expressed using an
CC   appropriate expression construct engineered into a plasmid. The plasmids
CC   can provide for efficient expression of IL-12 subunits. The products can
CC   be used for the treatment of asthma, microbial and viral infections and
CC   certain cancers
XX
SQ   Sequence 660 BP; 188 A; 167 C; 138 G; 167 T; 0 U; 0 Other;

  Query Match             11.6%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        514 ATTCG 518
              |||||
Db        610 ATTCG 614


RESULT 79
AAV07218
ID   AAV07218 standard; DNA; 660 BP.
XX
AC   AAV07218;
XX
DT   12-AUG-1998  (first entry)
XX
DE   DNA encoding human interleukin-12 35kDa subunit.
XX
KW   Interleukin-12; IL-12; graft-versus-host disease;
KW   GVHD. bone marrow transplantation; graft-versus-leukemia; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "Interleukin-12_35kDa_subunit"
XX
PN   US5756085-A.
XX
PD   26-MAY-1998.
XX
PF   30-APR-1996;   96US-00640386.
XX
PR   21-JAN-1994;   94US-00186529.
XX
PA   (GEMY ) GENETICS INST INC.
PA   (GEHO ) GEN HOSPITAL CORP.
XX
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PI Sykes M, Wolf SF;
XX
DR WPI; 1998-321459/28.
DR P-PSDB; AAW51222.
XX
PT Therapy of graft-versus-host disease - by administration of interleukin-
PT 12 to maintain and/or promote graft-versus-leukaemia effects.
XX
PS Disclosure; Col 23-24; 20pp; English.
XX
CC The invention relates to a method for the treatment or prevention of
CC graft-versus-host disease (GVHD) which comprises the administration of
CC interleukin-12 (IL-12) at the time of bone-marrow transplantation to
CC maintain or promote graft-versus-leukaemia effects. Preferably, dosage is
CC 0.001-100 (preferably 1-100) mu g/kg for 3 days starting on the day of
CC the bone marrow transplant. IL-12 is administered daily until there is an
CC improvement in the condition. Administration is oral, cutaneous,
CC subcutaneous, intravenous or by inhalation preferably subcutaneous, or
CC intravenous. The present sequence encodes the human interleukin-12 35kDa
CC subunit
XX
SQ Sequence 660 BP; 188 A; 164 C; 139 G; 169 T; 0 U; 0 Other;

Query Match 11.6%; Score 65; DB 2; Length 660;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy 514 ATTCG 518
|||||
Db 610 ATTCG 614

RESULT 80
AAZ40407
ID AAZ40407 standard; DNA; 660 BP.
XX
AC AAZ40407;
XX
DT 15-FEB-2000 (first entry)
XX
DE Human interleukin 12 p35 subunit wild type coding sequence.
XX
KW Wild type; human; interferon-alpha; plasmid; cytomegalovirus; CMV;
KW promoter; growth hormone; untranslated region; UTR; mammal; disease;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO9947678-A2.
XX
PD 23-SEP-1999.
XX
PF 12-MAR-1999; 99WO-US005394.
XX
PR 19-MAR-1998; 98US-0078654P.
XX
PA (GENE-) GENEMEDICINE INC.
XX
PI Nordstrom J, Pericle F, Rolland A, Ralston R;
XX
DR WPI; 1999-562116/47.
DR P-PSDB; AAY42488.
XX
PT New plasmids containing an interferon-alpha coding sequence, used for the
PT treatment of a mammalian condition or disease, particularly cancer.
XX
PS Claim 11; Page 38-39; 137pp; English.
XX
CC This sequence represents the wild type coding region for the human
CC interleukin 12 p35 subunit. The invention relates to a novel plasmid
CC comprising a cytomegalovirus (CMV) promoter transcriptionally linked with
CC an interferon alpha (IFN-alpha) coding sequence, and a growth hormone 3'-
CC untranslated region (UTR). The plasmids can be used for treating a
CC mammalian condition or disease, particularly cancer
XX
SQ Sequence 660 BP; 188 A; 167 C; 138 G; 167 T; 0 U; 0 Other;

Query Match 11.6%; Score 65; DB 2; Length 660;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy 514 ATTCG 518
|||||
Db 610 ATTCG 614

RESULT 81
AAD15217
ID AAD15217 standard; DNA; 660 BP.
XX
AC AAD15217;
XX
DT 01-NOV-2001 (first entry)
XX
DE Modified human cytokine p35 encoding DNA from clone R2-555.
XX
KW Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW p35; mutant; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1. .660
FT /*tag= a
FT /product= "Modified p35 protein precursor"
FT sig_peptide 1. .66
FT /*tag= b
FT mat_peptide 67. .657
FT /*tag= c
FT /product= "Mature modified p35 protein"
XX
PN WO200140257-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000WO-US032664.
XX
PR 02-DEC-1999; 99US-0169035P.
PR 28-NOV-2000; 2000US-00725324.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Leong SR, Punnonen J;
XX
DR WPI; 2001-502381/55.
DR P-PSDB; AAE08610.
XX
PT Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT retinopathy and cancer.
XX
PS Claim 87; Page 140; 223pp; English.
XX
CC The invention relates to nucleic acids encoding modified cytokine
CC polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC cytokine polypeptides have T-cell proliferative and interferon (IFN)-

```
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein encoding
CC   DNA
XX
SQ   Sequence 660 BP; 189 A; 173 C; 136 G; 162 T; 0 U; 0 Other;

  Query Match            11.6%;  Score 65;  DB 5;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        111 TGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGA 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 TGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGA 266

Qy        171 ATTAA 175
              |||||
Db        267 ATTAA 271


RESULT 82
AAD15221
ID   AAD15221 standard; DNA; 660 BP.
XX
AC   AAD15221;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Human cytokine p35 DNA.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p35; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "p35 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .657
FT                   /*tag=  c
FT                   /product= "Mature p35 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08614.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 91; Page 142; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is human p35 protein encoding DNA
XX
SQ   Sequence 660 BP; 188 A; 166 C; 139 G; 167 T; 0 U; 0 Other;

  Query Match            11.6%;  Score 65;  DB 5;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        514 ATTCG 518
              |||||
Db        610 ATTCG 614


RESULT 83
AAL44226
ID   AAL44226 standard; DNA; 660 BP.
XX
AC   AAL44226;
XX
DT   08-NOV-2002  (first entry)
XX
DE   Human interleukin 12A (IL-12A) coding sequence.
XX
KW   Human; gene; ds; interleukin 12A; IL-12A; drug screening; AIDS; malaria;
KW   tuberculosis; cancer; haplotyping; genotyping; transgenic animal.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "Human interleukin 12A (IL-12A)"
FT   variation       replace(142, A)
FT                   /*tag=  b
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   WO200229115-A1.
XX
PD   11-APR-2002.
XX
PF   05-OCT-2001; 2001WO-US031656.
XX
PR   06-OCT-2000; 2000US-0238693P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Armstrong B,  Cappola G,  Choi JY,  Gilson CR,  Kliem SE,  Koshy B;
PI   Parks KE;
XX
DR   WPI; 2002-315865/35.
DR   P-PSDB; AAO15506.
XX
PT   New interleukin 12A (IL-12A) gene polymorphic variants, for studying the
PT   expression and function of IL-12A and screening candidate drugs for
PT   treating AIDS and cancer.
XX
PS   Claim 28; Fig 2; 72pp; English.
XX
CC   The invention comprises the amino acid and coding sequence of the human
CC   interleukin 12A (IL-12A) protein. Specifically the invention relates to
CC   the identification of polymorphisms within the human (IL-12A) gene
CC   sequence. The polymorphisms identified in the human IL-12A gene sequence
CC   are useful in studying the expression and function of IL-12A, and in
```

```
CC   screening drugs for the treatment of disorders such as AIDS, malaria,
CC   tuberculosis and cancer. The IL-12A polymorphisms may be used to
CC   haplotype and genotype the IL-12A gene of an individual. The IL-12A DNA
CC   sequences of the invention can be used to create transgenic animals for
CC   studying expression of the IL-12A isogenes in vivo. The present DNA
CC   sequence represents the coding sequence of the human interleukin 12A (IL-
CC   12A) gene
XX
SQ   Sequence 660 BP; 188 A; 166 C; 139 G; 167 T; 0 U; 0 Other;

  Query Match             11.6%;  Score 65;  DB 6;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        514 ATTCG 518
              |||||
Db        610 ATTCG 614


RESULT 84
ACC47589
ID   ACC47589 standard; DNA; 660 BP.
XX
AC   ACC47589;
XX
DT   12-JUN-2003  (first entry)
XX
DE   Human interleukin 12 (hIL-12) P35 subunit gene.
XX
KW   Human; interleukin 12; hIL-12; baculovirus vector;
KW   recombinant production; AcNPV-hIL12;
KW   Autographa california nuclear polyhedrosis virus; tumour; cancer;
KW   infection; bacterial; viral; cytostatic; P35 subunit; gene; ds.
XX
OS   Homo sapiens.
XX
PN   CN1357622-A.
XX
PD   10-JUL-2002.
XX
PF   02-NOV-2001; 2001CN-00133631.
XX
PR   02-NOV-2001; 2001CN-00133631.
XX
PA   (UYWU-) UNIV WUHAN.
XX
PI   Meng X,  Xu J,  Yu Z;
XX
DR   WPI; 2002-741792/81.
XX
PT   Human interleukin-12 recombinant insect virus strain and its preparation.
XX
PS   Claim 4; Fig 6; 17pp; Chinese.
XX
CC   The invention relates to a recombinant baculovirus comprising DNA
CC   encoding human interleukin 12 (hIL-12) and methods for its preparation.
CC   The recombinant baculovirus strain is designated Autographa california
CC   nuclear polyhedrosis virus AcNPV-hIL12 (CCTCC No. 2 V200108). This strain
CC   contains two human IL-12 subunit genes, the IL-12 P35 subunit gene
CC   (ACC47589) and the IL-12 P40 subunit gene (ACC47592) which are
CC   respectively under the control of the viral polyhedrin and P10 promoters.
CC   The baculovirus can be used in the recombinant production of human IL-12
CC   which is suitable for treating tumours and bacterial, viral and other
CC   infections. The present sequence represents the human IL-12 P35 subunit
CC   gene used in construction of the baculovirus vector of the invention
XX
SQ   Sequence 660 BP; 188 A; 166 C; 139 G; 167 T; 0 U; 0 Other;

  Query Match             11.6%;  Score 65;  DB 6;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        514 ATTCG 518
              |||||
Db        610 ATTCG 614


RESULT 85
ADF77244
ID   ADF77244 standard; DNA; 660 BP.
XX
AC   ADF77244;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human IL-12 p35 subunit DNA.
XX
KW   ds; human; interferon alpha expression plasmid; tumour; IL-12.
XX
OS   Homo sapiens.
XX
PN   US2003181405-A1.
XX
PD   25-SEP-2003.
XX
PF   29-APR-2002; 2002US-00136837.
XX
PR   12-MAR-1999;   99US-00268135.
XX
PA   (NORD/) NORDSTROM J L.
PA   (PERI/) PERICLE F.
PA   (ROLL/) ROLLAND A.
PA   (RALS/) RALSTON R O.
XX
PI   Nordstrom JL,  Pericle F,  Rolland A,  Ralston RO;
XX
DR   WPI; 2004-020834/02.
XX
PT   A mammalian interferon alpha expression plasmid is useful in gene therapy
PT   to deliver interferon alpha to cells to modulate tumor activity in the
PT   treatment of cancer.
XX
PS   Disclosure; SEQ ID NO 6; 65pp; English.
XX
CC   The invention relates to a mammalian interferon alpha expression plasmid,
CC   comprising a promoter and a synthetic 5' intron transcriptionally linked
CC   with an interferon alpha coding sequence and a 3' untranslated region.
CC   The mammalian interferon alpha expression plasmid is useful for treating
CC   tumour growth. The present sequence is used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 660 BP; 188 A; 167 C; 138 G; 167 T; 0 U; 0 Other;

  Query Match             11.6%;  Score 65;  DB 12;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        514 ATTCG 518
              |||||
Db        610 ATTCG 614


RESULT 86
ADP88401
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```
ID   ADP88401 standard; cDNA; 702 BP.
XX
AC   ADP88401;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human interleukin-12 alpha chain coding sequence.
XX
KW   antiinflammatory; antiasthmatic; antiallergic; immunosuppressive;
KW   antibacterial; protozoacide; gene therapy; expression vector;
KW   interleukin; ecdysone-inducible promoter; ss; gene; interleukin-12;
KW   human.
XX
OS   Homo sapiens.
XX
PN   WO2004052929-A2.
XX
PD   24-JUN-2004.
XX
PF   08-DEC-2003; 2003WO-IB006404.
XX
PR   06-DEC-2002; 2002GB-00028465.
XX
PA   (UYBE-) UNIV QUEENS BELFAST.
XX
PI   Vandenbroeck K,  Alloza I;
XX
DR   WPI; 2004-487887/46.
XX
PT   New expression vector comprising DNA encoding a subunit of a dimeric form
PT   of interleukin under transcriptional control of an ecdysone-inducible
PT   promoter, useful in preparing a composition for treating e.g.,
PT   inflammatory disease.
XX
PS   Disclosure; Page 85-86; 87pp; English.
XX
CC   The present invention relates to an expression vector comprising DNA
CC   encoding a subunit of a dimeric form of interleukin under transcriptional
CC   control of an ecdysone-inducible promoter. The expression vector is
CC   useful in preparing a composition for treating a disease having a
CC   pathogenesis which includes endogenous production of cytokine IL-12, IL-
CC   23 or IL-27, e.g., infectious diseases, bacterial, protozoal or virus-
CC   induced inflammation, epithelial airway inflammation such as asthma,
CC   allergic disease, or autoimmune disease such as multiple sclerosis or
CC   inflammatory bowel disease. The present sequence is the coding sequence
CC   of the human interleukin-12 alpha chain used in the exemplification of
CC   the invention.
XX
SQ   Sequence 702 BP; 199 A; 184 C; 147 G; 172 T; 0 U; 0 Other;

  Query Match             11.6%;  Score 65;  DB 12;  Length 702;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 624

Qy        514 ATTCG 518
              |||||
Db        625 ATTCG 629


RESULT 87
AAQ67880
ID   AAQ67880 standard; DNA; 721 BP.
XX
AC   AAQ67880;
XX
DT   25-MAR-2003  (revised)
DT   23-MAR-1995  (first entry)
XX
DE   EPV 42 kD promoter/Human IL-12 p35 subunit expression cassette.
XX
KW   Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant;
KW   murine; interleukin-2; IL-2; pRW825; pmut-1; pBS-SK; pMM151; TK vector;
KW   plasmid; vaccinia; H6 promoter; amplify; primer; antigenic response;
KW   polymerase chain reaction; poxvirus; pSD542; immunological response;
KW   pathogen; human; interferon; IFN; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   promoter        1. .61
FT                   /*tag=  a
FT                   /note= "Vaccinia E3L promoter"
FT   CDS             32. .1018
FT                   /*tag=  b
FT                   /product= "Human IL-12 p35"
XX
PN   WO9416716-A1.
XX
PD   04-AUG-1994.
XX
PF   21-JAN-1994;   94WO-US000888.
XX
PR   21-JAN-1993;   93US-00007115.
PR   19-JAN-1994;   94US-00184009.
XX
PA   (VIRO-) VIROGENETICS CORP.
XX
PI   Paoletti E,  Tartaglia J,  Cox WI;
XX
DR   WPI; 1994-263767/32.
XX
PT   Attenuated recombinant virus used for cancer therapy - comprises DNA
PT   encoding cytokine and/or tumour associated antigen.
XX
PS   Example 27; Fig 34; 232pp; English.
XX
CC   The sequences given in AAQ67879-80 are expression cassettes which contain
CC   the p40 and p35 subunits of human interleukin-12 (IL-12) under the
CC   control of the entomopox virus (EPV) promoter and the vaccinia E3L
CC   promoter, respectively. These sequences were used in the construction of
CC   an ALVAC-based recombinant virus containing the genes for the two
CC   subunits of human IL-12. The p40 subunit was amplified using primers
CC   JP202 and JP189 and placed under the control of the entomopox virus (EPV)
CC   42 kD promoter in plasmid PBSHIL12p40II. The p35 subunit was amplified
CC   using primers JP186 and JP201 and placed under the control of the
CC   vaccinia E3L promoter using primers JP218 and JP220. The expression
CC   cassette was isolated and ligated with pBSSK+ generating plasmid
CC   PBSHIL12p35II. The p35 and p40 expression cassettes were excised and
CC   assembled in pBSSK+ to give PBSHIL12 in which the two expression
CC   cassettes are orientated head-to-head relative to each other. The
CC   combination casette containing the poxvirus promoted genes for both IL-12
CC   subunits was excised from PBSHIL12 and cloned in to ALVAC C6 vector
CC   plasmid pC6L to give pC6HIL12. Recombination between this donor plasmid
CC   and ALVAC rescuing virus produced recombinant virus ALVAC+IL12, which
CC   contains both the human IL-12 genes in the C6 locus. The resulting virus
CC   may be used in a composition for inducing an antigenic or immunological
CC   response, ie. for immunisation against pathogens. (Updated on 25-MAR-2003
CC   to correct PN field.)
XX
SQ   Sequence 721 BP; 209 A; 171 C; 151 G; 190 T; 0 U; 0 Other;

  Query Match             11.6%;  Score 65;  DB 2;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy        514 ATTCG 518
              |||||
Db        671 ATTCG 675
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```
RESULT 88
AAZ08515
ID   AAZ08515 standard; DNA; 721 BP.
XX
AC   AAZ08515;
XX
DT   19-OCT-1999  (first entry)
XX
DE   Vaccinia E3L/human IL-12 P35 expression cassette.
XX
KW   Attenuated recombinant virus; cytokine; tumour associated antigen;
KW   NYVAC recombinant virus; ALVAC recombinant virus; gene therapy; rabies;
KW   cancer; tumour necrosis factor; nuclear phosphoprotein; p53; IL-2; GMCSF;
KW   interleukin; interferon; IFN-gamma; IL-4; melanoma associated antigen;
KW   carcinoembryonic antigen; immunisation; antigenic; poxvirus; influenza;
KW   immunological response; immunotherapy; vaccine; Newcastle Disease; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
OS   Vaccinia virus.
XX
PN   US5942235-A.
XX
PD   24-AUG-1999.
XX
PF   02-JUN-1995;   95US-00458356.
XX
PR   24-DEC-1981;   81US-00334456.
PR   08-DEC-1982;   82US-00446824.
PR   19-JUN-1984;   84US-00622135.
PR   27-AUG-1987;   87US-00090209.
PR   28-AUG-1987;   87US-00090711.
PR   20-OCT-1987;   87US-00110335.
PR   25-APR-1988;   88US-00186054.
PR   23-AUG-1988;   88US-00234390.
PR   14-JUN-1990;   90US-00537882.
PR   14-JUN-1990;   90US-00537890.
PR   16-DEC-1991;   91US-00805567.
PR   03-MAR-1992;   92US-00847977.
PR   06-MAR-1992;   92US-00847951.
PR   04-MAY-1992;   92US-00881995.
PR   22-JUL-1992;   92US-00918278.
PR   20-JAN-1993;   93US-00007115.
PR   19-JAN-1994;   94US-00184009.
PR   14-APR-1994;   94US-00228926.
PR   13-SEP-1994;   94US-00306259.
XX
PA   (HEAL-) HEALTH RES INC.
XX
PI   Paoletti E;
XX
DR   WPI; 1999-493494/41.
XX
PT   Recombinant poxviruses comprising exogenous DNA encoding antigenic
PT   determinants useful in immunotherapy to immunize against cancers and
PT   other diseases such as influenza, Newcastle Disease and rabies.
XX
PS   Example 27; Fig 34; 163pp; English.
XX
CC   The present invention describes a recombinant poxvirus (I), comprising
CC   exogenous DNA encoding an antigenic determinant of a pathogen which is
CC   then expressed in vivo in infected host cells after administration to a
CC   patient and therefore induces an immunological response. (I) may be used
CC   to vaccinate patients against a wide range of diseases and disorders
CC   depending on the type of antigen encoded by the exogenous DNA. (I) may be
CC   used to vaccinate against diseases such as rabies, influenza and
CC   Newcastle Disease. It is particularly useful for immunising against
CC   cancers. The poxvirus (I) also provides a means of manipulating
CC   lymphocytes and tumour cells for use in cell-based immunotherapeutic
CC   modalities for cancer. (I) also have enhanced safety compared to
CC   unattenuated viruses (attenuation reduces the virulence of the viruses)
CC   and known recombinant poxvirus vaccines. This increased level of safety
CC   reduces the possibility of a 'runaway' infection in the host and reduces
CC   the chance of transmission from vaccinated to unvaccinated individuals
CC   and contamination of the environment. The present sequence represents a
CC   Vaccinia E3L/human IL-12 P35 expression cassette used in the
CC   exemplification of the present invention
XX
SQ   Sequence 721 BP; 209 A; 171 C; 151 G; 190 T; 0 U; 0 Other;

  Query Match            11.6%;  Score 65;  DB 2;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy        514 ATTCG 518
              |||||
Db        671 ATTCG 675


RESULT 89
ADR21891
ID   ADR21891 standard; DNA; 721 BP.
XX
AC   ADR21891;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Vaccinia E3L/human IL-12 expression cassette.
XX
KW   Cytostatic; Vaccine; recombinant poxvirus; nonessential region;
KW   attenuated avipox Virus; carcinoembryonic antigen; B7 protein;
KW   cancer therapy; ds; human; IL-12; interleukin-12; E3L;
KW   expression cassette.
XX
OS   Vaccinia virus.
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US6780407-B1.
XX
PD   24-AUG-2004.
XX
PF   15-SEP-2000; 2000US-00663667.
XX
PR   08-MAR-1989;   89US-00320471.
PR   14-FEB-1990;   90US-00478179.
PR   07-JAN-1991;   91US-00638080.
PR   07-MAR-1991;   91US-00666056.
PR   11-JUN-1991;   91US-00713967.
PR   16-DEC-1991;   91US-00805567.
PR   03-MAR-1992;   92US-00847977.
PR   06-MAR-1992;   92US-00847951.
PR   21-JAN-1993;   93US-00007115.
PR   19-JAN-1994;   94US-00184009.
PR   30-AUG-1995;   95US-00521016.
XX
PA   (AVET ) AVENTIS PASTEUR.
XX
PI   Paoletti E,  Tartaglia J,  Cox WI;
XX
DR   WPI; 2004-601998/58.
XX
PT   New recombinant poxvirus which is an attenuated avipox Virus that
PT   expresses an exogenous DNA encoding carcinoembryonic antigen and an
PT   exogenous DNA encoding B7 protein, useful for cancer therapy.
XX
PS   Example 27; SEQ ID NO 199; 181pp; English.
XX
CC   The invention describes a recombinant poxvirus containing exogenous DNA
CC   in a nonessential region of the poxvirus, where the poxvirus is an
```

```
CC   attenuated avipox Virus that expresses an exogenous DNA encoding
CC   carcinoembryonic antigen and an exogenous DNA encoding B7 protein. Also
CC   described are: a composition comprising a poxvirus above in admixture
CC   with a carrier; and expressing carcinoembryonic antigen and B7 protein in
CC   vivo comprising administering to a mammal the composition above.
CC   Disclosed are: making recombinant poxvirus defined above; recombinant
CC   poxvirus vaccine having an increased level of safety compared to known
CC   recombinant poxvirus vaccines; and a modified vector for expressing a
CC   gene product in a host. The recombinant poxvirus is useful for providing
CC   a recombinant poxvirus vaccine having an increased level of safety
CC   compared to known recombinant poxvirus vaccines. The recombinant poxvirus
CC   is useful for cancer therapy. This sequence represents a human IL-12
CC   expression cassette used in the creation of NYVAC rescue virus and
CC   canarypox virus vector ALVAC comprising the human IL-12 gene.
XX
SQ   Sequence 721 BP; 209 A; 171 C; 151 G; 190 T; 0 U; 0 Other;

  Query Match             11.6%;  Score 65;  DB 13;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy        514 ATTCG 518
              |||||
Db        671 ATTCG 675


RESULT 90
ADK98708
ID   ADK98708 standard; DNA; 761 BP.
XX
AC   ADK98708;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human interleukin-12 (IL-12) P35 subunit DNA seqid 3.
XX
KW   human; recombinant interleukin-12; IL-12; P35 subunit; P40 subunit; ds.
XX
OS   Homo sapiens.
XX
PN   CN1408727-A.
XX
PD   09-APR-2003.
XX
PF   29-SEP-2001; 2001CN-00126923.
XX
PR   29-SEP-2001; 2001CN-00126923.
XX
PA   (ZHON-) ZHONGXIN GUOJIAN PHARM CO LTD SHANGHAI.
XX
PI   Wan G,  Li C;
XX
DR   WPI; 2003-664076/63.
XX
PT   Method for efficiently expressing recombinant human interleukin 12 in
PT   eukaryotic cell.
XX
PS   Claim 6; SEQ ID NO 3; 14pp; Chinese.
XX
CC   The invention describes the process of producing human recombinant
CC   interleukin-12 (IL-12) includes: providing a nucleotide sequence
CC   corresponding to the P35 subunit with the first signal peptide and a
CC   nucleotide sequence corresponding to the P40 subunit; inserting the
CC   nucleotide sequences into an expression vector; converting the eukaryotic
CC   cell with the expression vector; and culturing the transfected eukaryotic
CC   cell in condition suitable for recombinant human IL-12 expression. The
CC   process balances the expression amount of both P35 and P40 subunits and
CC   thus raises the expression amount of IL-12 with bioactivity via raising
CC   the expression strength of P35 subunit. This sequence represents the
CC   human interleukin-12 (IL-12) P35 subunit polynucleotide.
XX
SQ   Sequence 761 BP; 205 A; 204 C; 164 G; 187 T; 0 U; 1 Other;

  Query Match             11.6%;  Score 65;  DB 10;  Length 761;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        651 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 710

Qy        514 ATTCG 518
              |||||
Db        711 ATTCG 715


RESULT 91
ADK98706
ID   ADK98706 standard; DNA; 761 BP.
XX
AC   ADK98706;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human interleukin-12 (IL-12) P35 subunit DNA seqid 1.
XX
KW   human; recombinant interleukin-12; IL-12; P35 subunit; P40 subunit; ds.
XX
OS   Homo sapiens.
XX
PN   CN1408727-A.
XX
PD   09-APR-2003.
XX
PF   29-SEP-2001; 2001CN-00126923.
XX
PR   29-SEP-2001; 2001CN-00126923.
XX
PA   (ZHON-) ZHONGXIN GUOJIAN PHARM CO LTD SHANGHAI.
XX
PI   Wan G,  Li C;
XX
DR   WPI; 2003-664076/63.
XX
PT   Method for efficiently expressing recombinant human interleukin 12 in
PT   eukaryotic cell.
XX
PS   Claim 4; SEQ ID NO 1; 14pp; Chinese.
XX
CC   The invention describes the process of producing human recombinant
CC   interleukin-12 (IL-12) includes: providing a nucleotide sequence
CC   corresponding to the P35 subunit with the first signal peptide and a
CC   nucleotide sequence corresponding to the P40 subunit; inserting the
CC   nucleotide sequences into an expression vector; converting the eukaryotic
CC   cell with the expression vector; and culturing the transfected eukaryotic
CC   cell in condition suitable for recombinant human IL-12 expression. The
CC   process balances the expression amount of both P35 and P40 subunits and
CC   thus raises the expression amount of IL-12 with bioactivity via raising
CC   the expression strength of P35 subunit. This sequence represents the
CC   human interleukin-12 (IL-12) P35 subunit polynucleotide.
XX
SQ   Sequence 761 BP; 199 A; 209 C; 167 G; 185 T; 0 U; 1 Other;

  Query Match             11.6%;  Score 65;  DB 10;  Length 761;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        651 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 710

Qy        514 ATTCG 518
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              |||||
Db        711 ATTCG 715


RESULT 92
AAV83207
ID   AAV83207 standard; cDNA; 762 BP.
XX
AC   AAV83207;
XX
DT   02-MAR-1999  (first entry)
XX
DE   Interleukin (IL)-12A cDNA.
XX
KW   Mouse; immunodeficient; pathogen; tumour; lymphocyte; antigen;
KW   immunomodulator; vector; vaccine; cancer; HIV; Leishmania; Mycobacterium;
KW   Listeria; Plasmodium; retrovirus; evaluation;
KW   human immunodeficiency virus; ds.
XX
OS   Homo sapiens.
XX
PN   WO9844788-A2.
XX
PD   15-OCT-1998.
XX
PF   09-APR-1998;   98WO-US006944.
XX
PR   09-APR-1997;   97US-00838702.
PR   01-MAY-1997;   97US-00848760.
PR   09-DEC-1997;   97US-0069163P.
XX
PA   (CHAN/) CHANG L.
XX
PI   Chang L;
XX
DR   WPI; 1999-024005/02.
XX
PT   Use of immunodeficient mice comprising human cells - particularly
PT   SCTD/beige mice comprising human immune cells for evaluating vaccines
PT   against cancers or human pathogens, e.g. HIV.
XX
PS   Example 10(c)(i); Page 108-109; 154pp; English.
XX
CC   Immunodeficient mice comprising human cells can be used for exposure to
CC   human pathogens and/or their components or human tumour cells and human
CC   peripheral blood lymphocytes. Also claimed is a vaccine comprising a cell
CC   modified to express an antigen and an immune-modulating protein, this is
CC   preferably an expression vector comprising a polynucleotide sequence that
CC   encodes the antigen and immune-modulating protein. Such vectors can be
CC   used to treat a subject having a tumour by transferring the expression
CC   vector into the tumour so that the antigen and the immune-modulator are
CC   expressed by at least the tumour. The methods can be used for producing
CC   and evaluating vaccines including cancer vaccines and vaccines directed
CC   against human pathogens, e.g. HIV, Leishmania, Mycobacterium, Listeria or
CC   Plasmodium. Two primers (AAV83197, AAV83198) were used to amplify the IL-
CC   12B for insertion into expression vectors of the invention
XX
SQ   Sequence 762 BP; 199 A; 211 C; 166 G; 186 T; 0 U; 0 Other;

  Query Match             11.6%;  Score 65;  DB 2;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        514 ATTCG 518
              |||||
Db        712 ATTCG 716


RESULT 93
AAA35201
ID   AAA35201 standard; DNA; 762 BP.
XX
AC   AAA35201;
XX
DT   28-JUL-2000  (first entry)
XX
DE   Human adenosine receptor related polynucleotide 2nd SEQ ID NO:75.
XX
KW   Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW   phosphorothioate; impaired respiration; inflammation; allergy;
KW   allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW   antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW   lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW   respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW   pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW   cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200009525-A2.
XX
PD   24-FEB-2000.
XX
PF   03-AUG-1999;   99WO-US017712.
XX
PR   03-AUG-1998;   98US-0095212P.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-205971/18.
XX
PT   New antisense oligonucleotides useful for treating e.g. pulmonary
PT   vasoconstruction, inflammation, allergies, asthma, hypertension,
PT   bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT   cancers.
XX
PS   Disclosure; Page 1242; 1343pp; English.
XX
CC   The present invention describes a new composition comprising an antisense
CC   oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC   nucleic acids involved in bronchoconstriction, allergies, and/or
CC   inflammation. The ON can have antiinflammatory, antiallergic,
CC   antiasthmatic, cytostatic and analgesic activities. The compositions are
CC   useful for the treatment of diseases associated with inflammation,
CC   impaired airways, including lung disease and diseases whose secondary
CC   effects afflict the lungs of a subject. They can be used for treating
CC   e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC   impeded respiration, respiratory distress syndrome, pain, cystic
CC   fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC   carcinomas, and cancers which may metastasise to the lungs, including
CC   breast and prostate cancer. The reduction of the adenosine content of the
CC   ONs reduces side effects. The A-containing ONs break down with the
CC   release of deoxyadenosine which activates adenosine receptors causing
CC   bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC   nucleotide sequences given in the sequence listing from the present
CC   invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC   sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC   from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC   AAA33992) are specifically claimed ONs from the present invention. N.B.
CC   Sequences given in the disclosure of the present invention do not match
CC   up with their corresponding SEQ ID NO: sequences given in the sequence
CC   listing
XX
SQ   Sequence 762 BP; 199 A; 210 C; 167 G; 186 T; 0 U; 0 Other;

  Query Match             11.6%;  Score 65;  DB 3;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        514 ATTCG 518
              |||||
Db        712 ATTCG 716
```

RESULT 94
AAF21323
ID AAF21323 standard; DNA; 762 BP.
XX
AC AAF21323;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human low adenosine antisense oligonucleotide related sequence #2890.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US008020.
XX
PR 06-APR-1999; 99US-0127958P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.
XX
PS Disclosure; Page 1326; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention
XX
SQ Sequence 762 BP; 199 A; 210 C; 167 G; 186 T; 0 U; 0 Other;

Query Match 11.6%; Score 65; DB 3; Length 762;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        514 ATTCG 518
              |||||
Db        712 ATTCG 716
```

RESULT 95
ABZ97017
ID ABZ97017 standard; DNA; 762 BP.
XX
AC ABZ97017;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human nucleic acid sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 12259; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention

CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 762 BP; 199 A; 210 C; 167 G; 186 T; 0 U; 0 Other;

Query Match 11.6%; Score 65; DB 10; Length 762;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy 514 ATTCG 518
|||||
Db 712 ATTCG 716

RESULT 96
ABD20866
ID ABD20866 standard; DNA; 762 BP.
XX
AC ABD20866;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human pulmonary and inflammatory target DNA #477.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ds.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 12259; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 762 BP; 199 A; 210 C; 167 G; 186 T; 0 U; 0 Other;

Query Match 11.6%; Score 65; DB 11; Length 762;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy 514 ATTCG 518
|||||
Db 712 ATTCG 716

RESULT 97
ADO07654
ID ADO07654 standard; DNA; 762 BP.
XX
AC ADO07654;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human interleukin-12 35kDa coding sequence.
XX
KW cytostatic; virucide; anti-HIV; hepatotropic; neuroprotective;
KW immunostimulant; expression cassette; viral vector; interleukin-12;
KW co-stimulatory protein; cancer; infection; ds; gene; human.
XX
OS Homo sapiens.
XX
PN WO2004035799-A2.
XX
PD 29-APR-2004.
XX
PF 10-OCT-2003; 2003WO-EP011252.
XX
PR 11-OCT-2002; 2002DE-01048141.
XX
PA (UYHA-) UNIV HAMBURG-EPPENDORF KLINIKUM.
XX
PI Waehler R, Schnieders F;
XX

DR WPI; 2004-357221/33.
XX
PT Viral vector that expresses single-chain interleukin-12 and costimulator,
PT useful for treatment of tumors, viral infections, e.g. human
PT immunodeficiency virus, and prion diseases.
XX
PS Claim 4; Fig 20; 129pp; German.
XX
CC The present invention relates to a viral vector that includes a nucleic
CC acid encoding a single-chain interleukin-12 (IL-12) and a co-stimulatory
CC protein. Viral vectors and virus particles derived from them are useful
CC for treatment of tumours, infectious diseases (e.g. HIV, hepatitis A, B
CC or C, cytomegalovirus or human papilloma virus), or prion diseases. The
CC present sequence is a human interleukin-12 coding sequence used in the
CC exemplification of the invention.
XX
SQ Sequence 762 BP; 199 A; 210 C; 167 G; 186 T; 0 U; 0 Other;

Query Match 11.6%; Score 65; DB 12; Length 762;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy 514 ATTCG 518
|||||
Db 712 ATTCG 716

RESULT 98
ADS88021
ID ADS88021 standard; DNA; 762 BP.
XX
AC ADS88021;
XX
DT 18-NOV-2004 (first entry)
XX
DE Tumour treatment-related human gene sequence SeqID57.
XX
KW tumour inhibition; tumour treatment; metastasis; infectious lesion;
KW antigen presenting cell; immunostimulatory cytokine; cytostatic;
KW vulnerary; immunomodulator; melanoma; hepatoma; adenocarcinoma;
KW colorectal cancer; basal cell cancer; oral cancer; nasopharyngeal cancer;
KW laryngeal cancer; bladder cancer; head cancer; neck cancer;
KW renal cell cancer; pancreatic cancer; pulmonary cancer; cervical cancer;
KW ovarian cancer; oesophageal cancer; gastric cancer; prostrate cancer;
KW testicular cancer; breast cancer; gene; ds; human.
XX
OS Homo sapiens.
XX
PN WO2004034995-A2.
XX
PD 29-APR-2004.
XX
PF 15-OCT-2003; 2003WO-US032827.
XX
PR 15-OCT-2002; 2002US-0418865P.
XX
PA (UYPI-) UNIV PITTSBURGH.
XX
PI Lotze MT, Tahara H;
XX
DR WPI; 2004-365083/34.
DR P-PSDB; ADS88022.
XX
PT Inhibiting or treating a tumor, metastasis or infectious lesion comprises
PT administering into or near site of a tumor or infectious lesion an
PT antigen presenting cell and an immunostimulatory cytokine or a nucleic
PT acid encoding the cytokine.
XX
PS Disclosure; SEQ ID NO 57; 169pp; English.
XX
CC This invention relates to a novel method of inhibiting or treating a
CC tumour, metastasis or infectious lesion in a subject which comprises
CC administering into or near a site of a tumour or infectious lesion in a
CC subject an antigen presenting cell and an immunostimulatory cytokine or a
CC nucleic acid encoding the cytokine. The invention may be useful for the
CC production of compounds with a cytostatic or vulnerary activity acting as
CC immunomodulators. The method is useful in inhibiting or treating a
CC tumour, metastasis or infectious lesion in a subject, where the size of
CC the tumour, metastasis (where number is also decreased) or infectious
CC lesion is decreased. The tumour is selected from melanoma, hepatoma,
CC adenocarcinoma, colorectal cancer, basal cell cancer, oral cancer,
CC nasopharyngeal cancer, laryngeal cancer, bladder cancer, head and neck
CC cancer, renal cell cancer, pancreatic cancer, pulmonary cancer, cervical
CC cancer, ovarian cancer, oesophageal cancer, gastric cancer, prostrate
CC cancer, testicular cancer and breast cancer. The present sequence is that
CC of a gene which is related to the invention.
XX
SQ Sequence 762 BP; 199 A; 210 C; 167 G; 186 T; 0 U; 0 Other;

Query Match 11.6%; Score 65; DB 13; Length 762;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy 514 ATTCG 518
|||||
Db 712 ATTCG 716

RESULT 99
ADV42511
ID ADV42511 standard; cDNA; 762 BP.
XX
AC ADV42511;
XX
DT 10-MAR-2005 (first entry)
XX
DE Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 139.
XX
KW microarray; psychoneuroendocrinimmune; chronic fatigue;
KW non-insulin dependent diabetes; allergy; immune disorder; inflammation;
KW cancer; neoplasm; infection; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO2004108899-A2.
XX
PD 16-DEC-2004.
XX
PF 04-JUN-2004; 2004WO-US017686.
XX
PR 04-JUN-2003; 2003US-0475915P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Nicholson A, Vernon SD;
XX
DR WPI; 2005-031682/03.
XX
PT New microarray comprising probes for genes involved in
PT psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a
PT condition associated with PNI activity, e.g., inflammatory or infectious
PT diseases.
XX
PS Claim 1; SEQ ID NO 139; 254pp; English.
XX
CC The invention relates to a new microarray which comprises probes for
CC genes involved in psychoneuroendocrinimmune (PNI) activity. The
CC microarray is useful in diagnosing a condition associated with PNI

```
CC   activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
CC   cancer and infection. The present sequence represents a
CC   psychoneuroendocrinimmune gene expressed sequence tag. Note the
CC   specificatio mentions SEQ ID NO of up to 3314 but only sequences up to
CC   SEQ ID NO 1829 are provided.
XX
SQ   Sequence 762 BP; 199 A; 210 C; 167 G; 186 T; 0 U; 0 Other;

  Query Match             11.6%;  Score 65;  DB 14;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        514 ATTCG 518
              |||||
Db        712 ATTCG 716


RESULT 100
ACD26420
ID   ACD26420 standard; cDNA; 823 BP.
XX
AC   ACD26420;
XX
DT   15-SEP-2003  (first entry)
XX
DE   cDNA encoding interleukin-12 (IL-12) P35 subunit.
XX
KW   Interleukin-12; IL-12; P35 subunit; tumour; virus infection;
KW   fungal infection; parasite infection; gene; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   CDS             60. .821
FT                   /*tag=  a
FT                   /product= "Interleukin-12 P35 subunit"
XX
PN   CN1373221-A.
XX
PD   09-OCT-2002.
XX
PF   04-FEB-2002; 2002CN-00100866.
XX
PR   04-FEB-2002; 2002CN-00100866.
XX
PA   (VIRO-) INST VIROLOGY CHINESE ACAD PREVENTIVE ME.
XX
PI   Jiao H,  Zhan M;
XX
DR   WPI; 2003-141476/14.
DR   P-PSDB; ABU62768.
XX
PT   Recombinant Chinese interleukin-12 with bio-activity and its preparation
PT   process.
XX
PS   Claim 1; Page 1-2; 20pp; Chinese.
XX
CC   The invention describes a recombinant Chinese interleukin (IL)-12 with
CC   bioactivity for resisting tumour, virus, fungus and parasites. This
CC   sequence encodes the interleukin-12 (IL-12) P35 subunit
XX
SQ   Sequence 823 BP; 222 A; 225 C; 183 G; 193 T; 0 U; 0 Other;

  Query Match             11.6%;  Score 65;  DB 10;  Length 823;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        711 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 770

Qy        514 ATTCG 518
              |||||
Db        771 ATTCG 775


Search completed: June  9, 2006, 23:30:46
Job time : 436.296 secs
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2006, 22:34:58 ; Search time 3436.62 Seconds
(without alignments)
9128.382 Million cell updates/sec

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Scoring table: OLIGO_NUC
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Maximum DB seq length: 2000000000

Post-processing: Listing first 200 summaries

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2: gb_est3:*
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4: gb_est5:*
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6: gb_htc:*
7: gb_est2:*
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12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	65	11.6	762	14	DQ033872	DQ033872 Homo sapi
	2	65	11.6	863	4	CD013916	CD013916 90138296
	3	65	11.6	935	4	CD013914	CD013914 90138124
	4	65	11.6	1136	4	CD013915	CD013915 90138132
	5	65	11.6	1938	6	BC035571	BC035571 Homo sapi
	6	57	10.2	762	14	DQ033873	DQ033873 Pan trogl
	7	56	10.0	581	3	BP260963	BP260963 BP260963
	8	56	10.0	832	2	BI523569	BI523569 603175938
	9	48	8.6	592	12	CE159257	CE159257 tigr-gss-
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	12	41	7.3	447	2	BI824638	BI824638 603033580
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	14	29	5.2	539	14	CR813130	CR813130 GR0AAA37C
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	17	27	4.8	427	10	DT930939	DT930939 S13.1784
	18	27	4.8	456	10	DT913216	DT913216 S13.1426
	19	27	4.8	561	3	BU699383	BU699383 LL2in1157
	20	27	4.8	563	3	BU698113	BU698113 LL2in1206
	21	27	4.8	589	1	AI050362	AI050362 ub30a07.r
	22	27	4.8	692	5	CJ137697	CJ137697 CJ137697
	23	27	4.8	1299	6	AK153729	AK153729 Mus muscu
	24	24	4.3	777	14	CT080894	CT080894 Sus scrof
	25	23	4.1	354	4	BY230958	BY230958 BY230958
c	26	23	4.1	528	1	AI332701	AI332701 qq19a07.x
	27	23	4.1	840	11	BZ261813	BZ261813 CH230-420
c	28	22	3.9	588	12	CE841948	CE841948 tigr-gss-
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	30	21	3.7	380	11	AQ100596	AQ100596 HS_3064_B
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c	34	20	3.6	241	11	AZ891891	AZ891891 RPCI-24-2
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	36	20	3.6	452	4	BW935403	BW935403 BW935403
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c	38	20	3.6	574	11	AZ855572	AZ855572 2M0159K08
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c	40	20	3.6	604	10	W63576	W63576 zc55h09.r1
c	41	20	3.6	691	11	BH373165	BH373165 AG-ND-159
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	48	20	3.6	959	13	CL465003	CL465003 SAIL_1232
	49	20	3.6	1035	14	CNS01GIY	AL143195 Anopheles
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	52	19	3.4	196	10	DY151937	DY151937 000923BEM
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	74	19	3.4	350	9	CX358439	CX358439 JGI_XZT28
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c	78	19	3.4	365	10	DR612001	DR612001 EST100212
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c	80	19	3.4	379	8	CR437136	CR437136 CR437136
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	82	19	3.4	410	8	CR437137	CR437137 CR437137
	83	19	3.4	421	3	BQ394236	BQ394236 NISC_ng08
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	97	19	3.4	472	2	BG371292 BG371292 dac43b03.
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	106	19	3.4	485	10	DR855772 DR855772 JGI_CABG2
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c	114	19	3.4	502	10	DR855771 DR855771 JGI_CABG2
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	122	19	3.4	529	3	BQ525812 BQ525812 NISC_no12
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	124	19	3.4	531	2	BM363212 BM363212 BS320054A
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	129	19	3.4	548	1	AL634301 AL634301 AL634301
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	162	19	3.4	597	4	BX683918 BX683918 BX683918
	163	19	3.4	597	9	CX746186 CX746186 JGI_ANBT3
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	167	19	3.4	605	10	DT407799 DT407799 JGI_CABI8
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c	173	19	3.4	611	1	AL803606 AL803606 AL803606
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	187	19	3.4	617	3	BQ390030 BQ390030 NISC_mq10
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	196	19	3.4	630	10	DR893080 DR893080 JGI_XZT26
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ALIGNMENTS

RESULT 1
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DEFINITION Homo sapiens IL12A gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION DQ033872
VERSION DQ033872.1 GI:66885081
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 762)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 762)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.
FEATURES Location/Qualifiers
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DEFINITION  90138296 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD013916
VERSION     CD013916.1  GI:37777446
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 863)
  AUTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
            Au-Young,J. and Stuve,L.L.
  TITLE     PCR isolation and cloning of novel splice variant mRNAs from known
            drug target genes
  JOURNAL   Genomics 83 (4), 566-571 (2004)
   PUBMED   15028279
COMMENT     Contact: Jin, P.
            Incyte Corporation
            3160 Porter Drive, Palo Alto, CA 94304, USA
            Tel: 650 621 8639
            Fax: 650 621 8965
            Email: pjin@incyte.com.
FEATURES             Location/Qualifiers
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                     reverse primers. Sequencing gaps were closed by
                     re-sequencig using primers flanking the gapped areas."
ORIGIN

  Query Match             11.6%;  Score 65;  DB 4;  Length 863;
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LOCUS       CD013914                935 bp    mRNA    linear   EST 21-OCT-2003
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KEYWORDS    EST.
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 935)
  AUTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
            Au-Young,J. and Stuve,L.L.
  TITLE     PCR isolation and cloning of novel splice variant mRNAs from known
            drug target genes
  JOURNAL   Genomics 83 (4), 566-571 (2004)
   PUBMED   15028279
COMMENT     Contact: Jin, P.
            Incyte Corporation
            3160 Porter Drive, Palo Alto, CA 94304, USA
            Tel: 650 621 8639
            Fax: 650 621 8965
            Email: pjin@incyte.com.
FEATURES             Location/Qualifiers
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                     using gene-specific primers flanking the open-reading
                     frame. PCR products were subcloned into pDrive Cloning
                     Vector and sequenced completely using M13 forward and
                     reverse primers. Sequencing gaps were closed by
                     re-sequencig using primers flanking the gapped areas."
ORIGIN

  Query Match             11.6%;  Score 65;  DB 4;  Length 935;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-24;
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Qy        514 ATTCG 518
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Db        773 ATTCG 777


RESULT 4
CD013915
LOCUS       CD013915               1136 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION  90138132 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD013915
VERSION     CD013915.1  GI:37777445
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1136)
  AUTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
            Au-Young,J. and Stuve,L.L.
  TITLE     PCR isolation and cloning of novel splice variant mRNAs from known
            drug target genes
  JOURNAL   Genomics 83 (4), 566-571 (2004)
   PUBMED   15028279
COMMENT     Contact: Jin, P.
```

```
            Incyte Corporation
            3160 Porter Drive, Palo Alto, CA 94304, USA
            Tel: 650 621 8639
            Fax: 650 621 8965
            Email: pjin@incyte.com.
FEATURES              Location/Qualifiers
     source           1. .1136
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone_lib="Single gene library"
                      /note="Vector: pDrive Cloning Vector; RT-PCR was performed
                      using gene-specific primers flanking the open-reading
                      frame. PCR products were subcloned into pDrive Cloning
                      Vector and sequenced completely using M13 forward and
                      reverse primers. Sequencing gaps were closed by
                      re-sequencig using primers flanking the gapped areas."
ORIGIN

  Query Match             11.6%;  Score 65;  DB 4;  Length 1136;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        914 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 973

Qy        514 ATTCG 518
              |||||
Db        974 ATTCG 978


RESULT 5
BC035571
LOCUS       BC035571               1938 bp    mRNA    linear   HTC 04-MAR-2003
DEFINITION  Homo sapiens, clone IMAGE:5240216, mRNA.
ACCESSION   BC035571
VERSION     BC035571.1  GI:23958681
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1938)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 69 Row: b Column: 15
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 4504638
            This clone has the following problem: retained intron.
FEATURES              Location/Qualifiers
     source           1. .1938
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:5240216"
                      /tissue_type="Brain, fetal, whole pooled"
                      /clone_lib="NIH_MGC_121"
                      /lab_host="DH10B"
                      /note="Vector: pCMV-SPORT6"
ORIGIN

  Query Match             11.6%;  Score 65;  DB 6;  Length 1938;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1335 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1394

Qy        514 ATTCG 518
              |||||
Db       1395 ATTCG 1399


RESULT 6
DQ033873
LOCUS       DQ033873               762 bp    DNA     linear   GSS 02-JUN-2005
DEFINITION  Pan troglodytes IL12A gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   DQ033873
VERSION     DQ033873.1  GI:66885082
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     A Scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
  JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
   PUBMED   15869325
REFERENCE   2  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.  Translation starts at the beginning of
            alignment.
FEATURES              Location/Qualifiers
     source           1. .762
                      /organism="Pan troglodytes"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9598"
     gene             <1. .>762
                      /gene="IL12A"
                      /locus_tag="HC3464"
ORIGIN

  Query Match             10.2%;  Score 57;  DB 14;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 2e-19;
  Matches   57;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy        462 GGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 518
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 GGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 716
```

```
RESULT 7
BP260963
LOCUS       BP260963                581 bp    mRNA    linear   EST 16-SEP-2004
DEFINITION  BP260963 Sugano cDNA library, small intestine Homo sapiens cDNA
            clone HSI02082, mRNA sequence.
ACCESSION   BP260963
VERSION     BP260963.1  GI:52176194
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 581)
  AUTHORS   Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
            Mizushima-Sugano,J., Nakai,K. and Sugano,S.
  TITLE     Sequence comparison of human and mouse genes reveals a homologous
            block structure in the promoter regions
  JOURNAL   Genome Res. 14 (9), 1711-1718 (2004)
   PUBMED   15342556
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Tel: 81-3-5449-5343
            Fax: 81-3-5449-5416
            Email: ysuzuki@hgc.jp.
FEATURES             Location/Qualifiers
     source          1. .581
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HSI02082"
                     /tissue_type="small intestine"
                     /clone_lib="Sugano cDNA library, small intestine"
ORIGIN

  Query Match             10.0%;  Score 56;  DB 3;  Length 581;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-19;
  Matches   56;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        103 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 158
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        517 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 572
```

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RESULT 8
BI523569
LOCUS       BI523569                832 bp    mRNA    linear   EST 29-AUG-2001
DEFINITION  603175938F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 5',
            mRNA sequence.
ACCESSION   BI523569
VERSION     BI523569.1  GI:15348361
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 832)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11605  row: l  column: 09
            High quality sequence start: 23
            High quality sequence stop: 821.
FEATURES             Location/Qualifiers
     source          1. .832
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240216"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_121"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 017. Note:
                     this is a NIH_MGC Library."
ORIGIN

  Query Match             10.0%;  Score 56;  DB 2;  Length 832;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-19;
  Matches   56;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        103 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 158
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        520 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 575
```

```
RESULT 9
CE159257
LOCUS       CE159257                592 bp    DNA     linear   GSS 25-SEP-2003
DEFINITION  tigr-gss-dog-17000371408491 Dog Library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION   CE159257
VERSION     CE159257.1  GI:35287296
KEYWORDS    GSS.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 592)
  AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
            Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
            Venter,J.C.
  TITLE     The dog genome: survey sequencing and comparative analysis
  JOURNAL   Science 301 (5641), 1898-1903 (2003)
   PUBMED   14512627
COMMENT     Contact: Kirkness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirknes@tigr.org
            Class: shotgun.
FEATURES             Location/Qualifiers
     source          1. .592
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /strain="Standard Poodle"
                     /db_xref="taxon:9615"
                     /clone_lib="Dog Library"
                     /note="Site_1: BstXI; Libraries were prepared from
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peripheral blood"
ORIGIN

Query Match 8.6%; Score 48; DB 12; Length 592;
Best Local Similarity 100.0%; Pred. No. 1.8e-14;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
||||||||||||||||||||||||||||||||||||||||||||||||
Db 66 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 113

RESULT 10
BG702253
LOCUS BG702253 812 bp mRNA linear EST 07-MAY-2001
DEFINITION 602683459F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4816118 5',
mRNA sequence.
ACCESSION BG702253
VERSION BG702253.1 GI:13973409
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 812)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10714 row: e column: 15
High quality sequence stop: 804.
FEATURES Location/Qualifiers
source 1. .812
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4816118"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_95"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
(gtcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.5 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: this
is a NIH_MGC Library."
ORIGIN

Query Match 8.4%; Score 47; DB 2; Length 812;
Best Local Similarity 100.0%; Pred. No. 6.9e-14;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 112 GATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 158
|||||||||||||||||||||||||||||||||||||||||||||||
Db 624 GATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 670

RESULT 11
BM257856
LOCUS BM257856 342 bp mRNA linear EST 17-DEC-2001
DEFINITION 521721 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BM257856
VERSION BM257856.1 GI:17893455
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 342)
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F.,
Quackenbush,J. and Keele,J.W.
TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
JOURNAL Genome Res. 11 (4), 626-630 (2001)
PUBMED 11282978
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR PRimers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 125 row: E column: 18
Seq primer: ATTTAGGTGACACTATAG.
FEATURES Location/Qualifiers
source 1. .342
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 3BOV"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendonosus muscle, and fetal
longissimus muscle."
ORIGIN

Query Match 7.3%; Score 41; DB 2; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTC 101
|||||||||||||||||||||||||||||||||||||||||
Db 294 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTC 334

RESULT 12
BI824638
LOCUS BI824638 447 bp mRNA linear EST 04-OCT-2001
DEFINITION 603033580F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175018 5',
mRNA sequence.
ACCESSION BI824638
VERSION BI824638.1 GI:15936188
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 447)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

```
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11435  row: o  column: 19
            High quality sequence start: 3
            High quality sequence stop: 445.
FEATURES             Location/Qualifiers
     source          1. .447
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5175018"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_115"
                     /note="Organ: pooled brain, lung, testis; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of 6 male brains, age range 23-27; 1
                     male lung, age 27; and 1 male testis, age 69.  Library is
                     oligo-dT primed and directionally cloned (EcoRV site is
                     destroyed upon  cloning).  Average insert size 1.8 kb,
                     insert size range 1-3 kb. Library is normalized and
                     enriched for full-length clones and was  constructed by C.
                     Gruber (Invitrogen).  Research Genetics tracking  code
                     021. Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             7.3%;  Score 41;  DB 2;  Length 447;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-10;
  Matches   41;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        478 AAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 518
              |||||||||||||||||||||||||||||||||||||||||
Db          1 AAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 41


RESULT 13
BI523344/c
LOCUS       BI523344                1099 bp    mRNA    linear   EST 29-AUG-2001
DEFINITION  603175938T1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 3',
            mRNA sequence.
ACCESSION   BI523344
VERSION     BI523344.1  GI:15348136
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1099)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11605  row: l  column: 09
            High quality sequence start: 40
            High quality sequence stop: 727.
FEATURES             Location/Qualifiers
     source          1. .1099
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240216"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_121"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 017. Note:
                     this is a NIH_MGC Library."
ORIGIN

  Query Match             7.1%;  Score 40;  DB 2;  Length 1099;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-10;
  Matches   40;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        479 AAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 518
              ||||||||||||||||||||||||||||||||||||||||
Db        524 AAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 485


RESULT 14
CR813130
LOCUS       CR813130                539 bp    DNA     linear   GSS 27-SEP-2004
DEFINITION  GR0AAA37CD06RM1 INRA BAC Bos taurus genomic clone INRAb_622G01, DNA
            sequence, genomic survey sequence.
ACCESSION   CR813130
VERSION     CR813130.1  GI:52749218
KEYWORDS    GSS.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 539)
  AUTHORS   Eggen,A., Schibler,L. and Roy,A.
  TITLE     Bovine BAC End Sequences from the INRA bovine BAC library
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 539)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-SEP-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Contact: Andre Eggen
            Department of Animal Genetics - LGbC
            INRA
            78350 Jouy-en-Josas, France
            Tel: 33 1 34 65 24 24
            Fax: 33 1 34 65 24 78
            Email: eggen@jouy.inra.fr
            Clones are derived from the INRA bovine BAC library
            (http://locus.jouy.inra.fr/fpc/cattle_bac_map.htm). For BAC library
            availability, please contact Andre Eggen (eggen@jouy.inra.fr). This
            work  was undertaken as part of the International Bovine BAC
            Mapping Consortium (IBBMC) by INRA (Jouy-en-Josas) and Genoscope
            (Evry) Plate: 622 row: G column: 01
            Seq primer: M13 Reverse
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .539
                     /organism="Bos taurus"
                     /mol_type="genomic DNA"
                     /strain="breed: Holstein"
                     /db_xref="taxon:9913"
                     /clone="INRAb_622G01"
                     /sex="Male"
```

```
                     /cell_type="fibroblast"
                     /clone_lib="INRA bovine BAC"
                     /note="Vector: pBeloBAC11; Site_1: HindIII; Holstein bull;
                     INRA Bovine BAC library (Male) produced by Andre Eggen
                     Genoscope sequence ID : GR0AAA37CD06RM1"
ORIGIN

  Query Match             5.2%;  Score 29;  DB 14;  Length 539;
  Best Local Similarity   100.0%;  Pred. No. 0.00059;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        180 GAATGAGAGTTGCCTGGCTTCCAGAGAGA 208
              |||||||||||||||||||||||||||||
Db        330 GAATGAGAGTTGCCTGGCTTCCAGAGAGA 358


RESULT 15
CR795312
LOCUS       CR795312                568 bp    DNA     linear   GSS 24-SEP-2004
DEFINITION  GR0AAA12DG09RM1 INRA BAC Bos taurus genomic clone INRAb_238E06, DNA
            sequence, genomic survey sequence.
ACCESSION   CR795312
VERSION     CR795312.1  GI:52676311
KEYWORDS    GSS.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 568)
  AUTHORS   Eggen,A., Schibler,L. and Roy,A.
  TITLE     Bovine BAC End Sequences from the INRA bovine BAC library
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 568)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-SEP-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Contact: Andre Eggen
            Department of Animal Genetics - LGbC
            INRA
            78350 Jouy-en-Josas, France
            Tel: 33 1 34 65 24 24
            Fax: 33 1 34 65 24 78
            Email: eggen@jouy.inra.fr
            Clones are derived from the INRA bovine BAC library
            (http://locus.jouy.inra.fr/fpc/cattle_bac_map.htm). For BAC library
            availability, please contact Andre Eggen (eggen@jouy.inra.fr). This
            work  was undertaken as part of the International Bovine BAC
            Mapping Consortium (IBBMC) by INRA (Jouy-en-Josas) and Genoscope
            (Evry) Plate: 238 row: E column: 06
            Seq primer: M13 Reverse
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .568
                     /organism="Bos taurus"
                     /mol_type="genomic DNA"
                     /strain="breed: Holstein"
                     /db_xref="taxon:9913"
                     /clone="INRAb_238E06"
                     /sex="Male"
                     /cell_type="fibroblast"
                     /clone_lib="INRA bovine BAC"
                     /note="Vector: pBeloBAC11; Site_1: HindIII; Holstein bull;
                     INRA Bovine BAC library (Male) produced by Andre Eggen
                     Genoscope sequence ID : GR0AAA12DG09RM1"
ORIGIN

  Query Match             5.2%;  Score 29;  DB 14;  Length 568;
  Best Local Similarity   100.0%;  Pred. No. 0.00059;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        180 GAATGAGAGTTGCCTGGCTTCCAGAGAGA 208
              |||||||||||||||||||||||||||||
Db        329 GAATGAGAGTTGCCTGGCTTCCAGAGAGA 357


RESULT 16
BF552757
LOCUS       BF552757                373 bp    mRNA    linear   EST 12-DEC-2000
DEFINITION  UI-R-C0-iz-d-02-0-UI.r1 UI-R-C0 Rattus norvegicus cDNA clone
            UI-R-C0-iz-d-02-0-UI 5', mRNA sequence.
ACCESSION   BF552757
VERSION     BF552757.1  GI:11662487
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 373)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  PUBMED    8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156  MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            cDNA Library Preparation: M.B. Soares Lab Clone distribution:
            clones will be available through Research Genetics (www.resgen.com)
            This clone is also available through the I.M.A.G.E. Consortium at
            LLNL (info@image.llnl.gov). IMAGE ID= 1782759
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .373
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="UI-R-C0-iz-d-02-0-UI"
                     /dev_stage="adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="UI-R-C0"
                     /note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI;
                     The UI-R-C0 library is a subtracted library derived from
                     the UI-R-A1 and UI-R-E1 libraries. The UI-R-A1 library
                     consisted of a mixture of individually tagged normalized
                     libraries constructed from rat  placenta, adult lung,
                     brain, liver, kidney, heart, spleen, ovary,  and muscle.
                     The UI-R-E1 library  consisted of a mixture of
                     individually tagged normalized libraries constructed from
                     8, 12 and 18-day embryo. The tag is a string of 3-5
                     nucleotides present between the Not I  site and the
                     oligo-dT track which allows identification of the library
                     of origin of a clone within the mixture. The subtracted
                     library (UI-R-C0) was constructed as follows: PCR
                     amplified cDNA inserts from a pool of UI-R-A1 and UI-R-E1
                     clones from which 3' ESTs had been derived was used as a
                     driver in a hybridization with the pooled UI-R-A1 and
                     UI-R-E1 library in the form of single-stranded circles.
                     The remaining single-stranded circles (subtracted library)
                     was purified by hydroxyapatite column chromatography,
                     converted to double-stranded circles and electroporated
                     into DH10B bacteria (Life Technologies) to generate the
                     UI-R-C0 library. This procedure has been previously
                     described (Bonaldo, Lennon and Soares, Genome Research 6:
                     791-806, 1996)"
ORIGIN

  Query Match             4.8%;  Score 27;  DB 7;  Length 373;
```

```
  Best Local Similarity   100.0%;  Pred. No. 0.007;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        283 ATCTATGAGGACTTGAAGATGTACCAG 309
              |||||||||||||||||||||||||||
Db        101 ATCTATGAGGACTTGAAGATGTACCAG 127


RESULT 17
DT930939
LOCUS       DT930939                427 bp    mRNA    linear   EST 20-SEP-2005
DEFINITION  S13.1784 Hematopoietic stem cells Mus musculus cDNA, mRNA sequence.
ACCESSION   DT930939
VERSION     DT930939.1  GI:75963455
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 427)
  AUTHORS   Pritsker,M., Doniger,T.T., Kramer,L.C., Westcot,S.E. and
            Lemischka,I.R.
  TITLE     Diversification of Stem Cell Molecular Repertoire by Alternative
            Splicing
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. (2005) In press
COMMENT     Contact: Pritsker M
            Lab of Ihor Lemischka, Department of Molecular Biology
            Princeton University
            Princeton, NJ 08544, USA
            Tel: 609 258 5657
            Fax: 609 258 1704
            Email: pritsker@molbio.princeton.edu.
FEATURES             Location/Qualifiers
     source          1. .427
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /tissue_type="Hematopoietic stem cells"
                     /cell_type="Hematopoietic stem cells"
                     /clone_lib="Hematopoietic stem cells"
                     /note="cDNA library was made from FACS-purified
                     hematopoietic stem cells"
ORIGIN

  Query Match             4.8%;  Score 27;  DB 10;  Length 427;
  Best Local Similarity   100.0%;  Pred. No. 0.0072;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        283 ATCTATGAGGACTTGAAGATGTACCAG 309
              |||||||||||||||||||||||||||
Db        385 ATCTATGAGGACTTGAAGATGTACCAG 411


RESULT 18
DT913216
LOCUS       DT913216                456 bp    mRNA    linear   EST 19-SEP-2005
DEFINITION  S13.1426 Hematopoietic stem cells Mus musculus cDNA, mRNA sequence.
ACCESSION   DT913216
VERSION     DT913216.1  GI:75893697
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   Pritsker,M., Doniger,T.T., Kramer,L.C., Westcot,S.E. and
            Lemischka,I.R.
  TITLE     Diversification of Stem Cell Molecular Repertoire by Alternative
            Splicing
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. (2005) In press
COMMENT     Contact: Pritsker M
            Lab of Ihor Lemischka, Department of Molecular Biology
            Princeton University
            Princeton, NJ 08544, USA
            Tel: 609 258 5657
            Fax: 609 258 1704
            Email: pritsker@molbio.princeton.edu.
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /tissue_type="Hematopoietic stem cells"
                     /cell_type="Hematopoietic stem cells"
                     /clone_lib="Hematopoietic stem cells"
                     /note="cDNA library was made from FACS-purified
                     hematopoietic stem cells"
ORIGIN

  Query Match             4.8%;  Score 27;  DB 10;  Length 456;
  Best Local Similarity   100.0%;  Pred. No. 0.0072;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        283 ATCTATGAGGACTTGAAGATGTACCAG 309
              |||||||||||||||||||||||||||
Db        385 ATCTATGAGGACTTGAAGATGTACCAG 411


RESULT 19
BU699383
LOCUS       BU699383                561 bp    mRNA    linear   EST 09-OCT-2002
DEFINITION  LL2in11573T7 Hematopoietic Stem Cell Subtracted Library Mus
            musculus cDNA 5' similar to interleukin 12 p35 subunit, mRNA
            sequence.
ACCESSION   BU699383
VERSION     BU699383.1  GI:23615967
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 561)
  AUTHORS   Phillips,R.L., Ernst,R.E., Brunk,B.P., Ivanova,N., Mahan,M.A.,
            Deanehan,J.K., Moore,K.A., Overton,G.C. and Lemischka,I.R.
  TITLE     The genetic program of hematopoietic stem cells
  JOURNAL   Science 288 (5471), 1635-1640 (2000)
   PUBMED   10834841
COMMENT     Contact: Lemischka, Ihor R.
            Department of Molecular Biology
            Princeton University
            Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544, USA
            Tel: 609 258 2838
            Fax: 609 258 2759
            Email: ilemischka@molbio.princeton.edu
            These ESTs are derived from a subtracted cDNA library enriched for
            gene products expressed in day 14-14.5 fetal liver hematopoietic
            stem cells defined as Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E
            (Sca-1)pos
            Seq primer: M13Reverse or T7.
FEATURES             Location/Qualifiers
     source          1. .561
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /tissue_type="Hematopoietic"
                     /cell_type="Stem Cells; Lineageneg/lo, AA4.1pos, cKitpos,
                     Ly6A/E (Sca-1)pos"
                     /dev_stage="Embryonic day 14-14.5"
                     /lab_host="DH10B"
                     /clone_lib="Hematopoietic Stem Cell Subtracted Library"
                     /note="Organ: Fetal Liver; Vector: Sport 1; Site_1: Sal I;
                     Site_2: Not I; Two directionally cloned cDNA libraries
```

were made from fetal liver hematopoietic stem cells enriched to be Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E (Sca-1)pos called Scapos and from AA4.1neg fetal liver cells. Subtractive hybridization was performed by hybridization of the target, Scapos, single stranded cDNA library in pSport1 to biotinylated RNA transcribed from the driver, AA4.1neg cDNA library in pSport2 with inserts cloned in the complementary orientation. For detailed protocols and additional information please see our website at http://stemcell.princeton.edu."

ORIGIN

```
  Query Match             4.8%;  Score 27;  DB 3;  Length 561;
  Best Local Similarity   100.0%;  Pred. No. 0.0076;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        283 ATCTATGAGGACTTGAAGATGTACCAG 309
              |||||||||||||||||||||||||||
Db        302 ATCTATGAGGACTTGAAGATGTACCAG 328
```

RESULT 20
BU698113
LOCUS BU698113 563 bp mRNA linear EST 09-OCT-2002
DEFINITION LL2in12067T7 Hematopoietic Stem Cell Subtracted Library Mus musculus cDNA 5' similar to interleukin 12 p35 subunit, mRNA sequence.
ACCESSION BU698113
VERSION BU698113.1 GI:23610620
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 563)
AUTHORS Phillips,R.L., Ernst,R.E., Brunk,B.P., Ivanova,N., Mahan,M.A., Deanehan,J.K., Moore,K.A., Overton,G.C. and Lemischka,I.R.
TITLE The genetic program of hematopoietic stem cells
JOURNAL Science 288 (5471), 1635-1640 (2000)
PUBMED 10834841
COMMENT Contact: Lemischka, Ihor R.
Department of Molecular Biology
Princeton University
Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544, USA
Tel: 609 258 2838
Fax: 609 258 2759
Email: ilemischka@molbio.princeton.edu
These ESTs are derived from a subtracted cDNA library enriched for gene products expressed in day 14-14.5 fetal liver hematopoietic stem cells defined as Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E (Sca-1)pos
Seq primer: M13Reverse or T7.
FEATURES Location/Qualifiers
source 1. .563
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/tissue_type="Hematopoietic"
/cell_type="Stem Cells; Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E (Sca-1)pos"
/dev_stage="Embryonic day 14-14.5"
/lab_host="DH10B"
/clone_lib="Hematopoietic Stem Cell Subtracted Library"
/note="Organ: Fetal Liver; Vector: Sport 1; Site_1: Sal I; Site_2: Not I; Two directionally cloned cDNA libraries were made from fetal liver hematopoietic stem cells enriched to be Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E (Sca-1)pos called Scapos and from AA4.1neg fetal liver cells. Subtractive hybridization was performed by hybridization of the target, Scapos, single stranded cDNA library in pSport1 to biotinylated RNA transcribed from the driver, AA4.1neg cDNA library in pSport2 with inserts cloned in the complementary orientation. For detailed protocols and additional information please see our website at http://stemcell.princeton.edu."
ORIGIN

```
  Query Match             4.8%;  Score 27;  DB 3;  Length 563;
  Best Local Similarity   100.0%;  Pred. No. 0.0076;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        283 ATCTATGAGGACTTGAAGATGTACCAG 309
              |||||||||||||||||||||||||||
Db        318 ATCTATGAGGACTTGAAGATGTACCAG 344
```

RESULT 21
AI050362
LOCUS AI050362 589 bp mRNA linear EST 09-JUL-1998
DEFINITION ub30a07.r1 Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:1379220 5' similar to gb:M65291 INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (HUMAN); gb:M86672 Mus musculus interleukin 12 p35 subunit, complete cds (MOUSE);, mRNA sequence.
ACCESSION AI050362
VERSION AI050362.1 GI:3299479
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 589)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:901688
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 60.
FEATURES Location/Qualifiers
source 1. .589
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1379220"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares_thymus_2NbMT"
/note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCGTTTTTTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
ORIGIN

```
  Query Match             4.8%;  Score 27;  DB 1;  Length 589;
  Best Local Similarity   100.0%;  Pred. No. 0.0076;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        283 ATCTATGAGGACTTGAAGATGTACCAG 309
              |||||||||||||||||||||||||||
Db        327 ATCTATGAGGACTTGAAGATGTACCAG 353


RESULT 22
CJ137697
LOCUS       CJ137697                692 bp    mRNA    linear   EST 23-SEP-2005
DEFINITION  CJ137697 RIKEN full-length enriched mouse cDNA library, C57BL/6J
            thymus 3 days neonate Mus musculus cDNA clone A630064E02 5', mRNA
            sequence.
ACCESSION   CJ137697
VERSION     CJ137697.1  GI:76238025
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 692)
  AUTHORS   The FANTOM Consortium and RIKEN Genome Exploration Research Group
            and Genome Science Group (Genome Network Project Core Group).
  TITLE     The transcriptional landscape of the mammalian genome
  JOURNAL   Science 309 (5740), 1559-1563 (2005)
   PUBMED   16141072
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. Tissues were provided by Dr. John Todd (
            Dept. of Medical Genetics Wellcome Trust Centre for Molecular
            Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes
            Hospital Cambridge ) whose assistance we gratefully acknowledge.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/.
FEATURES             Location/Qualifiers
     source          1. .692
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="A630064E02"
                     /tissue_type="thymus"
                     /dev_stage="3 days neonate"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library,
                     C57BL/6J thymus 3 days neonate"
ORIGIN

  Query Match             4.8%;  Score 27;  DB 5;  Length 692;
  Best Local Similarity   100.0%;  Pred. No. 0.0079;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        283 ATCTATGAGGACTTGAAGATGTACCAG 309
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Db        521 ATCTATGAGGACTTGAAGATGTACCAG 547


RESULT 23
AK153729
LOCUS       AK153729                1299 bp    mRNA    linear   HTC 21-SEP-2005
DEFINITION  Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
            library, clone:A630064E02 product:interleukin 12a, full insert
            sequence.
ACCESSION   AK153729
VERSION     AK153729.1  GI:74148962
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
            Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
            Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
            Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
            Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
            Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
            Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
            Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
            Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  CONSRTM   RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
   PUBMED   11217851
REFERENCE   5
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
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Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420 (6915), 563-573 (2002)

PUBMED 12466851

REFERENCE 6

AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE The transcriptional landscape of the mammalian genome

JOURNAL Science 309 (5740), 1559-1563 (2005)

PUBMED 16141072

REFERENCE 7

AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.

CONSRTM RIKEN Genome Exploration Research Group

TITLE Antisense transcription in the mammalian transcriptome

JOURNAL Science 309 (5740), 1564-1566 (2005)

PUBMED 16141073

REFERENCE 8 (bases 1 to 1299)

AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="3 days neonate"

misc_feature 1. .1299
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putative"

ORIGIN

Query Match 4.8%; Score 27; DB 6; Length 1299;
Best Local Similarity 100.0%; Pred. No. 0.0089;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        283 ATCTATGAGGACTTGAAGATGTACCAG 309
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Db        521 ATCTATGAGGACTTGAAGATGTACCAG 547
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RESULT 24
CT080894
LOCUS CT080894 777 bp DNA linear GSS 01-NOV-2005
DEFINITION Sus scrofa genomic clone PigE-253A7, genomic survey sequence.
ACCESSION CT080894
VERSION CT080894.1 GI:78647963
KEYWORDS GSS.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 777)
AUTHORS Humphray,S.J., Plumb,R.W. and Durham,J.L.
TITLE Direct Submission
JOURNAL Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished
COMMENT This sequence was generated from the SP6 end of BAC 253A7. 253A7 is part of the PigEBAC BAC Library created by Roslin Institute/RFCGR. Further details: http://www.sanger.ac.uk/Projects/S_scrofa/.
FEATURES Location/Qualifiers
source 1. .777

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                     sex male"
ORIGIN

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  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        264 GACCCTGTGCCTTAGCAGTATCTA 287
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Db        551 GACCCTGTGCCTTAGCAGTATCTA 574


RESULT 25
BY230958
LOCUS       BY230958                354 bp    mRNA    linear   EST 10-DEC-2002
DEFINITION  BY230958 RIKEN full-length enriched, adult inner ear Mus musculus
            cDNA clone F930017D02 5', mRNA sequence.
ACCESSION   BY230958
VERSION     BY230958.1  GI:26412068
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 354)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
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            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
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            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
            Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
            Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
            Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
            Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
            Hayashizaki,Y. Direct Submission
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
             cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
             Tissues were provided by Kirk W. Beisel ( Boys Town National
            Research Hospital 555 North 30th Street Omaha,NE 68131 USA ) whose
            assistance we gratefully acknowledge. Please visit our web site
            (http://genome.gsc.riken.go.jp) for further details.
FEATURES             Location/Qualifiers
     source          1. .354
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                     /mol_type="mRNA"
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                     /db_xref="taxon:10090"
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                     /tissue_type="inner ear"
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ORIGIN

  Query Match             4.1%;  Score 23;  DB 4;  Length 354;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        283 ATCTATGAGGACTTGAAGATGTA 305
              |||||||||||||||||||||||
Db        332 ATCTATGAGGACTTGAAGATGTA 354


RESULT 26
AI332701/c
LOCUS       AI332701                528 bp    mRNA    linear   EST 13-FEB-1999
DEFINITION  qq19a07.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1932948
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            (HUMAN);, mRNA sequence.
ACCESSION   AI332701
VERSION     AI332701.1  GI:4069260
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 528)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1469   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 451.
FEATURES             Location/Qualifiers
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/lab_host="DH10B"
/clone_lib="Soares_NhHMPu_S1"
/note="Organ: mixed (see below); Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
ORIGIN

Query Match 4.1%; Score 23; DB 1; Length 528;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 539 TGATGAGCTATCTGAATGCTTCC 561
||||||||||||||||||||||
Db 482 TGATGAGCTATCTGAATGCTTCC 460

RESULT 27
BZ261813
LOCUS BZ261813 840 bp DNA linear GSS 15-OCT-2002
DEFINITION CH230-420O11.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone CH230-420O11, genomic survey sequence.
ACCESSION BZ261813
VERSION BZ261813.1 GI:23972184
KEYWORDS GSS.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 840)
AUTHORS Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de Jong,P. and Fraser,C.M.
TITLE Rat BAC End Sequences from Library CHORI-230 MboI segment
JOURNAL Unpublished (1999)
COMMENT Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 420 row: O column: 11
Seq primer: T7
Class: BAC ends.
FEATURES Location/Qualifiers
source 1. .840
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-420O11"
/sex="Female"
/cell_type="Brain"
/clone_lib="CHORI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI; CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by Pieter de Jong"
ORIGIN

Query Match 4.1%; Score 23; DB 11; Length 840;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 149 TGGAGGCCTGCTTACCACTGGAA 171
|||||||||||||||||||||||
Db 377 TGGAGGCCTGCTTACCACTGGAA 399

RESULT 28
CE841948/c
LOCUS CE841948 588 bp DNA linear GSS 01-OCT-2003
DEFINITION tigr-gss-dog-17000332674172 Dog Library Canis familiaris genomic, genomic survey sequence.
ACCESSION CE841948
VERSION CE841948.1 GI:37204217
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 588)
AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K., Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and Venter,J.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
FEATURES Location/Qualifiers
source 1. .588
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site_1: BstXI; Libraries were prepared from peripheral blood"
ORIGIN

Query Match 3.9%; Score 22; DB 12; Length 588;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 464 ATTTTTATAAAACTAAAATCAA 485
||||||||||||||||||||||
Db 166 ATTTTTATAAAACTAAAATCAA 145

RESULT 29
CT100632
LOCUS CT100632 758 bp DNA linear GSS 01-NOV-2005
DEFINITION Sus scrofa genomic clone CH242-93N13, genomic survey sequence.
ACCESSION CT100632
VERSION CT100632.1 GI:78654237
KEYWORDS GSS.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 758)
  AUTHORS   Humphray,S.J., Plumb,R.W. and Durham,J.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Unpublished
COMMENT     This sequence was generated from the SP6 end of BAC 93N13. 93N13 is
            part of the CHORI-242 BAC Library created by P. de Jong. Further
            details: http://www.sanger.ac.uk/Projects/S_scrofa/.
FEATURES             Location/Qualifiers
     source          1. .758
                     /organism="Sus scrofa"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9823"
                     /clone="CH242-93N13"
                     /tissue_type="White blood cells"
                     /note="vector pTARBAC1.3_BamHI
                     sex female"
ORIGIN

  Query Match             3.9%;  Score 22;  DB 14;  Length 758;
  Best Local Similarity   100.0%;  Pred. No. 4.7;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        386 CAGCTATTGATGAGCTGTTACA 407
              ||||||||||||||||||||||
Db        351 CAGCTATTGATGAGCTGTTACA 372


RESULT 30
AQ100596
LOCUS       AQ100596                380 bp    DNA     linear   GSS 27-AUG-1998
DEFINITION  HS_3064_B1_F08_MR CIT Approved Human Genomic Sperm Library D Homo
            sapiens genomic clone Plate=3064 Col=15 Row=L, genomic survey
            sequence.
ACCESSION   AQ100596
VERSION     AQ100596.1  GI:3471625
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 380)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
   PUBMED   10449764
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Sequence Tagged Connector
            Plate: 3064  row: L  column: 15
            Class: BAC ends
            High quality sequence stop: 380.
FEATURES             Location/Qualifiers
     source          1. .380
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="Plate=3064 Col=15 Row=L"
                     /sex="male"
                     /clone_lib="CIT Approved Human Genomic Sperm Library D"
                     /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                     E-Coli DH10B"
ORIGIN

  Query Match             3.7%;  Score 21;  DB 11;  Length 380;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        220 ACTAATGGGAGTTGCCTGGCC 240
              |||||||||||||||||||||
Db         42 ACTAATGGGAGTTGCCTGGCC 62


RESULT 31
AQ393691/c
LOCUS       AQ393691                489 bp    DNA     linear   GSS 06-MAR-1999
DEFINITION  CITBI-E1-2544N3.TF CITBI-E1 Homo sapiens genomic clone 2544N3,
            genomic survey sequence.
ACCESSION   AQ393691
VERSION     AQ393691.1  GI:4364714
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 489)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
            Venter,J.C.
  TITLE     Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Other_GSSs: CITBI-E1-2544N3.TR
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are available from Research Genetics (info@resgen.com). BAC
            end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: M13-21
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .489
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="2544N3"
                     /sex="male"
                     /cell_type="sperm"
                     /clone_lib="CITBI-E1"
                     /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
                     CalTech Human BAC Library D"
ORIGIN

  Query Match             3.7%;  Score 21;  DB 11;  Length 489;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        182 ATGAGAGTTGCCTGGCTTCCA 202
              |||||||||||||||||||||
Db        441 ATGAGAGTTGCCTGGCTTCCA 421


RESULT 32
BU002107
LOCUS       BU002107                679 bp    mRNA    linear   EST 03-OCT-2005
DEFINITION  QGG30D21.yg.ab1 QG_EFGHJ lettuce serriola Lactuca serriola cDNA
            clone QGG30D21, mRNA sequence.
ACCESSION   BU002107
VERSION     BU002107.1  GI:22436502
```

```
KEYWORDS    EST.
SOURCE      Lactuca serriola
  ORGANISM  Lactuca serriola
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
            Cichorieae; Lactuca.
REFERENCE   1  (bases 1 to 679)
  AUTHORS   Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
            Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J.,
            Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,
            Lai,Z., Church,S., Jackson,L. and Bradford,K.
  TITLE     Lettuce and Sunflower ESTs from the Compositae Genome Project
            http://compgenomics.ucdavis.edu/
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Alexander Kozik [R.W.Michelmore]
            Department of Vegetable Crops, R.W.Michelmore Lab
            University of California at Davis (UCD)
            Asmundson Hall, UCD, Davis, CA 95616, USA
            Tel: 1-(530)-742-1742
            Fax: 1-(530)-752-9659
            Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
            singleton, see http://cgpdb.ucdavis.edu/ for details.
            Plate: QGG30  row: D  column: 21.
FEATURES             Location/Qualifiers
     source          1. .679
                     /organism="Lactuca serriola"
                     /mol_type="mRNA"
                     /db_xref="taxon:75943"
                     /clone="QGG30D21"
                     /lab_host="E.coli"
                     /clone_lib="QG_EFGHJ lettuce serriola"
                     /note="Vector: pBRcDNASfiAB; The library was constructed
                     from 10 different sources of RNA from a single genotype.
                     Separate cDNAs were generated using primers that
                     incorporated unique 5' and 3' tags to distinguish each
                     source of RNA. cDNAs were then pooled, size-fractionated,
                     directionally cloned into a custom medium-copy vector and
                     transformations made with four size classes to minimize
                     size bias. Details of each source of RNA and library
                     construction can be obtained at http://cgpdb.ucdavis.edu/
                     TAG_TISSUE=flowers pre-fertilized
                     TAG_LIB=QG_EFGHJ lettuce serriola
                     TAG_SEQ=GCTTGACGGG"
ORIGIN

  Query Match             3.7%;  Score 21;  DB 3;  Length 679;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        168 GGAATTAACCATGAATGAGAG 188
              ||||||||||||||||||||
Db          8 GGAATTAACCATGAATGAGAG 28


RESULT 33
AQ631366/c
LOCUS       AQ631366                733 bp    DNA     linear   GSS 17-JUN-1999
DEFINITION  RPCI-11-482B16.TV RPCI-11 Homo sapiens genomic clone
            RPCI-11-482B16, genomic survey sequence.
ACCESSION   AQ631366
VERSION     AQ631366.1  GI:5094001
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 733)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
            Venter,J.C.
  TITLE     Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genet cs (info@resgen.com). BAC end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .733
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="GDB:7684743"
                     /db_xref="taxon:9606"
                     /clone="RPCI-11-482B16"
                     /sex="Male"
                     /cell_type="Lymphocytes"
                     /clone_lib="RPCI-11"
                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     RPCI11 Human Male BAC Library"
ORIGIN

  Query Match             3.7%;  Score 21;  DB 11;  Length 733;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        464 ATTTTTATAAAACTAAAATCA 484
              |||||||||||||||||||||
Db        145 ATTTTTATAAAACTAAAATCA 125


RESULT 34
AZ891891/c
LOCUS       AZ891891                241 bp    DNA     linear   GSS 05-MAR-2001
DEFINITION  RPCI-24-201J11.TV RPCI-24 Mus musculus genomic clone
            RPCI-24-201J11, genomic survey sequence.
ACCESSION   AZ891891
VERSION     AZ891891.1  GI:13210836
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 241)
  AUTHORS   Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
            Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
            Russell,D., de Jong,P. and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-24
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-24. For BAC
            library availability, please contact Pieter de Jong
            (pdejong@mail.cho.org). Clones may be purchased from BACPAC
            Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
            page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 201  row: J  column: 11
            Seq primer: T7
            Class: BAC ends.
```

```
FEATURES             Location/Qualifiers
     source          1. .241
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="RPCI-24-201J11"
                     /sex="Male"
                     /cell_type="Spleen/Brain"
                     /clone_lib="RPCI-24"
                     /note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
                     RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
                     library was  cloned in the pTARBAC1 cloning vector at the
                     BamH1 sites using MboI  partially digested male C57BL/6J
                     DNA."
ORIGIN

  Query Match             3.6%;  Score 20;  DB 11;  Length 241;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        464 ATTTTTATAAAACTAAAATC 483
              ||||||||||||||||||||
Db         20 ATTTTTATAAAACTAAAATC 1


RESULT 35
BX537236
LOCUS       BX537236                344 bp    DNA     linear   GSS 05-JUN-2003
DEFINITION  INRA porcine BAC library, clone 0849A01 BAC end sequence (Uni M13),
            genomic survey sequence.
ACCESSION   BX537236
VERSION     BX537236.1  GI:31455351
KEYWORDS    GSS; genome survey sequence.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1
  AUTHORS   Rogel-Gaillard,C., Bourgeaux,N., Billault,A., Vaiman,M. and
            Chardon,P.
  TITLE     Construction of a swine BAC library: application to the
            characterization and mapping of porcine type C endoviral elements
  JOURNAL   Cytogenet. Cell Genet. 85 (3-4), 205-211 (1999)
   PUBMED   10449899
REFERENCE   2  (bases 1 to 344)
  AUTHORS   Robic,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JUN-2003) Robic A., INRA, Laboratoire de Genetique
            Cellulaire, chemin de Borde rouge, BP27, Auzeville, 31626, FRANCE
            Phone : 05 61 28 51 15 Fax : 05 61 28 53 08 Email :
            arobic@toulouse.inra.fr
FEATURES             Location/Qualifiers
     source          1. .344
                     /organism="Sus scrofa"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9823"
                     /clone="0849A01"
                     /note="library Rogel gaillard et al 1999, clone 0849A01
                     Clone distribution : AGENAE Resource center. Francois
                     PIUMI, Francois.Piumi@jouy.inra.fr, INRA, CEA
                     Radiobiologie et Etude du genome (LREG), Domaine de
                     Vilvert, 78352, Jouy-en-Josas cedex, FRANCE"
ORIGIN

  Query Match             3.6%;  Score 20;  DB 14;  Length 344;
  Best Local Similarity   100.0%;  Pred. No. 51;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        355 AGGCAGATCTTTCTGGATCA 374
              ||||||||||||||||||||
Db         22 AGGCAGATCTTTCTGGATCA 41


RESULT 36
BW935403
LOCUS       BW935403                452 bp    mRNA    linear   EST 24-DEC-2005
DEFINITION  BW935403 Amphioxus Branchiostoma floridae unpublished cDNA library,
            neurula whole animal Branchiostoma floridae cDNA clone bfne121g22
            3', mRNA sequence.
ACCESSION   BW935403
VERSION     BW935403.1  GI:66569299
KEYWORDS    EST.
SOURCE      Branchiostoma floridae (Florida lancelet)
  ORGANISM  Branchiostoma floridae
            Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
            Branchiostoma.
REFERENCE   1  (bases 1 to 452)
  AUTHORS   Yu,J., Holland,L.Z., Shin-i,T., Kohara,Y., Satou,Y. and Satoh,N.
  TITLE     Expressed genes in Branchiostoma floridae
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp
            If you want to have a cDNA clone for this EST or if you have any
            questions, please send an e-mail to Nori Satoh
            (satoh@ascidian.zool.kyoto-u.ac.jp) and its cc to Yutaka Satou
            (yutaka@ascidian.zool.kyoto-u.ac.jp).
FEATURES             Location/Qualifiers
     source          1. .452
                     /organism="Branchiostoma floridae"
                     /mol_type="mRNA"
                     /db_xref="taxon:7739"
                     /clone="bfne121g22"
                     /tissue_type="whole animal"
                     /dev_stage="neurula"
                     /clone_lib="Amphioxus Branchiostoma floridae unpublished
                     cDNA library, neurula whole animal"
ORIGIN

  Query Match             3.6%;  Score 20;  DB 4;  Length 452;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        113 ATCATGAAGATATCACAAAA 132
              ||||||||||||||||||||
Db        375 ATCATGAAGATATCACAAAA 394


RESULT 37
AQ478437/c
LOCUS       AQ478437                516 bp    DNA     linear   GSS 23-APR-1999
DEFINITION  RPCI-11-248M18.TJ RPCI-11 Homo sapiens genomic clone
            RPCI-11-248M18, genomic survey sequence.
ACCESSION   AQ478437
VERSION     AQ478437.1  GI:4660556
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 516)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
            Venter,J.C.
  TITLE     Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
```

```
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genet cs (info@resgen.com). BAC end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: SP6
            Class: BAC ends.
FEATURES              Location/Qualifiers
     source           1. .516
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="GDB:7595153"
                      /db_xref="taxon:9606"
                      /clone="RPCI-11-248M18"
                      /sex="Male"
                      /cell_type="Lymphocytes"
                      /clone_lib="RPCI-11"
                      /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                      RPCI11 Human Male BAC Library"
ORIGIN

  Query Match             3.6%;  Score 20;  DB 11;  Length 516;
  Best Local Similarity   100.0%;  Pred. No. 56;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         55 ACGCTTCAGAAGGCCAGACA 74
              ||||||||||||||||||||
Db         57 ACGCTTCAGAAGGCCAGACA 38


RESULT 38
AZ855572/c
LOCUS       AZ855572                 574 bp    DNA     linear   GSS 21-FEB-2001
DEFINITION  2M0159K08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0159K08 R, genomic survey sequence.
ACCESSION   AZ855572
VERSION     AZ855572.1  GI:13045870
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 574)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0159  row: K  column: 08
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 574.
FEATURES              Location/Qualifiers
     source           1. .574
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC2M0159K08"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
ORIGIN

  Query Match             3.6%;  Score 20;  DB 11;  Length 574;
  Best Local Similarity   100.0%;  Pred. No. 57;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        323 CCATGAATGCAAAGCTGTTA 342
              ||||||||||||||||||||
Db        232 CCATGAATGCAAAGCTGTTA 213


RESULT 39
CNS01PJI
LOCUS       CNS01PJI                 603 bp    DNA     linear   GSS 14-JUN-2001
DEFINITION  Anopheles gambiae GSS SP6 end of clone 28L22 of NotreDame1 library
            from strain PEST of Anopheles gambiae (African malaria mosquito),
            genomic survey sequence.
ACCESSION   AL154894
VERSION     AL154894.1  GI:7015813
KEYWORDS    GSS.
SOURCE      Anopheles gambiae (African malaria mosquito)
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Culicidae; Anophelinae; Anopheles.
REFERENCE   1  (bases 1 to 603)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
REFERENCE   2  (bases 1 to 603)
  AUTHORS   Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.
            Roux, Paris 75015, France
COMMENT     This clone is from an A. gambiae BAC library provided by F.H.
            Collins and sequenced by Genoscope in collaboration with the
            Laboratory of Biochem. and Biol. Molec. of Insects, Institut
            Pasteur.
FEATURES              Location/Qualifiers
     source           1. .603
                      /organism="Anopheles gambiae"
                      /mol_type="genomic DNA"
                      /strain="PEST"
                      /db_xref="taxon:7165"
                      /clone="28L22"
                      /clone_lib="NotreDame1"
```

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                     /note="end : SP6"
ORIGIN

  Query Match             3.6%;  Score 20;  DB 14;  Length 603;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        196 GCTTCCAGAGAGATCTCTCT 215
              ||||||||||||||||||||
Db        496 GCTTCCAGAGAGATCTCTCT 515


RESULT 40
W63576/c
LOCUS       W63576                   604 bp    mRNA    linear   EST 11-OCT-1996
DEFINITION  zc55h09.r1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA
            clone IMAGE:326273 5', mRNA sequence.
ACCESSION   W63576
VERSION     W63576.1  GI:1371149
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 604)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 566   Std Error: 0.00
            Seq primer: ETPrimer
            High quality sequence stop: 400.
FEATURES             Location/Qualifiers
     source          1. .604
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:1257786"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:326273"
                     /tissue_type="senescent fibroblast"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares_senescent_fibroblasts_NbHSF"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco
                     RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                     primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo."
ORIGIN

  Query Match             3.6%;  Score 20;  DB 10;  Length 604;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        371 ATCAAAACATGCTGACAGCT 390
              ||||||||||||||||||||
Db        357 ATCAAAACATGCTGACAGCT 338


RESULT 41
BH373165/c
LOCUS       BH373165                 691 bp    DNA     linear   GSS 10-DEC-2001
DEFINITION  AG-ND-159L10.TR ND-TAM Anopheles gambiae genomic clone
            AG-ND-159L10, genomic survey sequence.
ACCESSION   BH373165
VERSION     BH373165.1  GI:17319307
KEYWORDS    GSS.
SOURCE      Anopheles gambiae (African malaria mosquito)
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Culicidae; Anophelinae; Anopheles.
REFERENCE   1  (bases 1 to 691)
  AUTHORS   Hong,Y.S., Hogan,J.R., Wang,X., Sarkar,A., Sim,C., Loftus,B.J.,
            Ren,C., Huff,E.R., Carlile,J.L., Black,K., Zhang,H.-B.,
            Gardner,M.J. and Collins,F.H.
  TITLE     Construction of a BAC library and generation of BAC end
            sequence-tagged connectors for genome sequencing of the African
            malaria mosquito Anopheles gambiae
  JOURNAL   Mol. Genet. Genomics 268 (6), 720-728 (2003)
   PUBMED   12655398
COMMENT     Other_GSSs: AG-ND-159L10.TF
            Contact: Brendan J Loftus
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0208
            Fax: 301 838 3543
            Email: bjloftus@tigr.org
            This clone is from an A. gambiae BAC library (ND-TAM) provided by
            F.H. Collins and sequenced by The Institute for Genomic Research
            (TIGR). The BAC library was generated from A. gambiae PEST strain
            DNA. All DNA was extracted from newly hatched first instar larvae
            to minimize the inclusion of DNA from microorganisms that inhabit
            the gut. The DNA is derived from mixed sexes of larvae. The BAC
            library was constructed at Texas A&M Universty BAC Center
            University, College Station, Texas 77843-2123, USA using a HindIII
            partial digest.
            Seq primer: M13 Rev
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .691
                     /organism="Anopheles gambiae"
                     /mol_type="genomic DNA"
                     /strain="PEST"
                     /db_xref="taxon:7165"
                     /clone="AG-ND-159L10"
                     /clone_lib="ND-TAM"
                     /note="Vector: pECBAC1; Site_1: HindIII"
ORIGIN

  Query Match             3.6%;  Score 20;  DB 11;  Length 691;
  Best Local Similarity   100.0%;  Pred. No. 59;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        330 TGCAAAGCTGTTAATGGATC 349
              ||||||||||||||||||||
Db        384 TGCAAAGCTGTTAATGGATC 365


RESULT 42
BW754129
LOCUS       BW754129                 724 bp    mRNA    linear   EST 22-OCT-2005
DEFINITION  BW754129 Amphioxus Branchiostoma floridae unpublished cDNA library,
            egg whole animal Branchiostoma floridae cDNA clone bfeg020c16 3',
            mRNA sequence.
ACCESSION   BW754129
VERSION     BW754129.1  GI:66340777
KEYWORDS    EST.
```

```
SOURCE      Branchiostoma floridae (Florida lancelet)
  ORGANISM  Branchiostoma floridae
            Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
            Branchiostoma.
REFERENCE   1  (bases 1 to 724)
  AUTHORS   Yu,J., Holland,L.Z., Shin-i,T., Kohara,Y., Satou,Y. and Satoh,N.
  TITLE     Expressed genes in Branchiostoma floridae
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp
            If you want to have a cDNA clone for this EST or if you have any
            questions, please send an e-mail to Nori Satoh
            (satoh@ascidian.zool.kyoto-u.ac.jp) and its cc to Yutaka Satou
            (yutaka@ascidian.zool.kyoto-u.ac.jp).
FEATURES             Location/Qualifiers
     source          1. .724
                     /organism="Branchiostoma floridae"
                     /mol_type="mRNA"
                     /db_xref="taxon:7739"
                     /clone="bfeg020c16"
                     /tissue_type="whole animal"
                     /dev_stage="egg"
                     /clone_lib="Amphioxus Branchiostoma floridae unpublished
                     cDNA library, egg whole animal"
ORIGIN

  Query Match             3.6%;  Score 20;  DB 4;  Length 724;
  Best Local Similarity   100.0%;  Pred. No. 60;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        113 ATCATGAAGATATCACAAAA 132
              ||||||||||||||||||||
Db        366 ATCATGAAGATATCACAAAA 385


RESULT 43
BZ028162/c
LOCUS       BZ028162                734 bp    DNA     linear   GSS 08-OCT-2002
DEFINITION  oeg78e09.g1 B.oleracea002 Brassica oleracea genomic, genomic survey
            sequence.
ACCESSION   BZ028162
VERSION     BZ028162.1  GI:23591436
KEYWORDS    GSS.
SOURCE      Brassica oleracea
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 734)
  AUTHORS   Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
            Nash,W., Rabinowicz,P.D. and Wilson,R.K.
  TITLE     Whole genome shotgun reads from Brassica oleracea
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Richard K. Wilson
            Genome Sequencing Center
            Washington University School of Medicine
            Email: submissions@watson.wustl.edu
            Plate: oeg78  row: e  column: 09
            Seq primer: -28RPpOT reverse
            Class: shotgun
            High quality sequence start: 8
            High quality sequence stop: 551.
FEATURES             Location/Qualifiers
     source          1. .734
                     /organism="Brassica oleracea"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:3712"
                     /clone_lib="B.oleracea002"
                     /note="Vector: pOTw13; Whole genome shotgun library from
                     flowering buds. DNA was purified  from a crude nuclear
                     prep using Brassica oleracea TO1000DH3 buds  provided by
                     Thosmas Osborn at the University of Wisconsin. Genomic
                     DNA was provided by Pablo Rabinowicz (CSHL) and the
                     shotgun library  prepared at Washington University Genome
                     Sequencing Center."
ORIGIN

  Query Match             3.6%;  Score 20;  DB 11;  Length 734;
  Best Local Similarity   100.0%;  Pred. No. 60;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        464 ATTTTTATAAAACTAAAATC 483
              ||||||||||||||||||||
Db        722 ATTTTTATAAAACTAAAATC 703


RESULT 44
CD357085/c
LOCUS       CD357085                822 bp    mRNA    linear   EST 29-MAY-2003
DEFINITION  AGENCOURT_14284510 NIH_MGC_187 Homo sapiens cDNA clone
            IMAGE:30402141 5', mRNA sequence.
ACCESSION   CD357085
VERSION     CD357085.1  GI:31128496
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 822)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDCM183  row: p  column: 22
            High quality sequence stop: 252.
FEATURES             Location/Qualifiers
     source          1. .822
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:30402141"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_187"
                     /note="Organ: Blood vessels - aorta, basilar and artery;
                     Vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc); Site_2:
                     SfiI (ggccgcctcggcc); 5' and 3' adaptors were used in
                     cloning as follows: 5' adaptor sequence:
                     5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C, G, or T). Average insert size 1.4 kb
                     (range 0.5-4.0 kb). 14/15 colonies contained inserts by
                     PCR. This library was enriched for full-length clones and
                     was constructed by Clontech Laboratories (Palo Alto, CA).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             3.6%;  Score 20;  DB 5;  Length 822;
  Best Local Similarity   100.0%;  Pred. No. 61;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy        132 AGATAAAACCAGCACAGTGG 151
              ||||||||||||||||||||
Db        130 AGATAAAACCAGCACAGTGG 111


RESULT 45
AQ574005
LOCUS       AQ574005                855 bp    DNA     linear   GSS 02-JUN-1999
DEFINITION  nbxb0083O17f CUGI Rice BAC Library Oryza sativa (japonica
            cultivar-group) genomic clone nbxb0083O17f, genomic survey
            sequence.
ACCESSION   AQ574005
VERSION     AQ574005.1  GI:4973806
KEYWORDS    GSS.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 855)
  AUTHORS   Wing,R.A. and Dean,R.A.
  TITLE     A BAC End Sequencing Framework to Sequence the Rice Genome
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Seq primer: TAATACGACTCACTATAGGG
            Class: BAC ends
            High quality sequence stop: 408.
FEATURES             Location/Qualifiers
     source          1. .855
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="genomic DNA"
                     /cultivar="japonica"
                     /cultivar="Nipponbare"
                     /db_xref="taxon:39947"
                     /clone="nbxb0083O17f"
                     /tissue_type="Leaf"
                     /lab_host="E. coli DH10B"
                     /clone_lib="CUGI Rice BAC Library"
                     /note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                     HindIII; Rice is one of two most popular grains in the
                     world. Half of the world  population especially those
                     inhabiting highly populated areas of the  humid tropics
                     and subtropics, rely on rice as their primary source of
                     carbohydrate. Monocotyledonous rice is a diploid plant
                     (2n=24) with a  haploid genome equivalent of 431 Mbp
                     (Arumuganathan and Earle, 1991).  The relatively small
                     genome of rice, three times larger than that of
                     Arabidopsis, makes it suitable for genomic studies. In
                     order to  facilitate positional cloning, physical mapping
                     and genome sequencing  of rice, we have constructed a BAC
                     library from Oryza sativa, Nipponbare  variety. The
                     library contains 36,864 clones with an average insert size
                     of 128.5 Kb providing 10.9 haploid genome equivalents. The
                     deep  coverage allows the isolation a particular sequence
                     with a probability  of 99.9 %. Two high density filters,
                     each containing 18,432 clones  (doubly spotted), represent
                     the whole library for colony screening."
ORIGIN

  Query Match             3.6%;  Score 20;  DB 11;  Length 855;
  Best Local Similarity   100.0%;  Pred. No. 62;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        458 AACCGGATTTTTATAAAACT 477
              ||||||||||||||||||||
Db        760 AACCGGATTTTTATAAAACT 779


RESULT 46
CL868149/c
LOCUS       CL868149                875 bp    DNA     linear   GSS 26-AUG-2004
DEFINITION  Gma_01_C05_T3 Soybean Genome Shotgun Sequences Glycine max genomic,
            genomic survey sequence.
ACCESSION   CL868149
VERSION     CL868149.1  GI:51562374
KEYWORDS    GSS.
SOURCE      Glycine max (soybean)
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 875)
  AUTHORS   Jackson,S.A., Walling,J.G. and SanMiguel,P.M.
  TITLE     Molecular and cytogenetic characterization of the heterochromatic,
            gene-poor centric regions of chromosomes of Glycine max L. Merr
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Scott A. Jackson
            Jackson Laboratory
            Purdue University
            915 W. State St., West Lafayette, IN 47907, USA
            Tel: 7654963621
            Fax: 7654967255
            Email: sjackson@purdue.edu
            Plate: 01  row: C  column: 05
            Seq primer: T3
            Class: shotgun
            High quality sequence stop: 875.
FEATURES             Location/Qualifiers
     source          1. .875
                     /organism="Glycine max"
                     /mol_type="genomic DNA"
                     /cultivar="Williams 82"
                     /db_xref="taxon:3847"
                     /sex="hermaphrodite"
                     /tissue_type="Leaf"
                     /dev_stage="seedling"
                     /clone_lib="Soybean Genome Shotgun Sequences"
                     /note="Organ: Leaf; Vector: Invitrogen ToPo vector;
                     Approximately 3-kb randomly sheared inserts"
ORIGIN

  Query Match             3.6%;  Score 20;  DB 13;  Length 875;
  Best Local Similarity   100.0%;  Pred. No. 62;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        465 TTTTTATAAAACTAAAATCA 484
              ||||||||||||||||||||
Db        770 TTTTTATAAAACTAAAATCA 751


RESULT 47
BF530961/c
LOCUS       BF530961                920 bp    mRNA    linear   EST 11-DEC-2000
DEFINITION  602072472F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4215425
            5', mRNA sequence.
ACCESSION   BF530961
VERSION     BF530961.1  GI:11618324
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 920)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
```

```
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9790  row: p  column: 18
            High quality sequence stop: 652.
FEATURES              Location/Qualifiers
     source           1. .920
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:4215425"
                      /tissue_type="anaplastic oligodendroglioma with 1p/19q
                      loss"
                      /lab_host="DH10B (T1 phage-resistant)"
                      /clone_lib="NCI_CGAP_Brn67"
                      /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                      Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                      Average insert size 2.3 kb. Constructed by Life
                      Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match             3.6%;  Score 20;  DB 7;  Length 920;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        428 TGACTGTGCCACAGAACTCC 447
              ||||||||||||||||||||
Db        308 TGACTGTGCCACAGAACTCC 289


RESULT 48
CL465003
LOCUS       CL465003                959 bp    DNA     linear   GSS 31-MAR-2004
DEFINITION  SAIL_1232_C07.v1 SAIL Collection Arabidopsis thaliana genomic clone
            SAIL_1232_C07.v1, genomic survey sequence.
ACCESSION   CL465003
VERSION     CL465003.1  GI:45867908
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 959)
  AUTHORS   Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D.,
            Dietrich,B., Ho,P., Bacwaden,J., Ko,C., Clarke,J.D., Cotton,D.,
            Bullis,D., Snell,J., Miguel,T., Hutchison,D., Kimmerly,B.,
            Mitzel,T., Katagiri,F., Glazebrook,J., Law,M. and Goff,S.A.
  TITLE     A high-throughput Arabidopsis reverse genetics system
  JOURNAL   Plant Cell 14 (12), 2985-2994 (2002)
   PUBMED   12468722
COMMENT     Contact: Sessions A
            Applied Trait Genetics
            Syngenta Biotechnology Inc.
            3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
            Email: allen.sessions@syngenta.com
            ABRC Stock Number CS845125; T-DNA left border flanking sequences of
            Syngenta Arabidopsis Insertion Library (SAIL) lines are available
            through the Arabidopsis Biological Resource Center (ABRC).
            Sequences represent a pool of amplified genomic regions and not
            single contiguous sequences.
            Class: TDNA tagged.
FEATURES              Location/Qualifiers
     source           1. .959
                      /organism="Arabidopsis thaliana"
                      /mol_type="genomic DNA"
                      /ecotype="Columbia"
                      /db_xref="taxon:3702"
                      /clone="SAIL_1232_C07.v1"
                      /clone_lib="SAIL Collection"
                      /note="T-DNA left border sequences were isolated using a
                      modified TAIL-PCR strategy"
ORIGIN

  Query Match             3.6%;  Score 20;  DB 13;  Length 959;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 CCTCAACCACTCCCAAACCC 34
              ||||||||||||||||||||
Db        590 CCTCAACCACTCCCAAACCC 609


RESULT 49
CNS01GIY
LOCUS       CNS01GIY                1035 bp    DNA     linear   GSS 01-JUN-2001
DEFINITION  Anopheles gambiae GSS T7 end of clone 06N18 of NotreDame1 library
            from strain PEST of Anopheles gambiae (African malaria mosquito),
            genomic survey sequence.
ACCESSION   AL143195
VERSION     AL143195.1  GI:7001313
KEYWORDS    GSS.
SOURCE      Anopheles gambiae (African malaria mosquito)
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Culicidae; Anophelinae; Anopheles.
REFERENCE   1  (bases 1 to 1035)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
REFERENCE   2  (bases 1 to 1035)
  AUTHORS   Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.
            Roux, Paris 75015, France
COMMENT     This clone is from an A. gambiae BAC library provided by F.H.
            Collins and sequenced by Genoscope in collaboration with the
            Laboratory of Biochem. and Biol. Molec. of Insects, Institut
            Pasteur.
FEATURES              Location/Qualifiers
     source           1. .1035
                      /organism="Anopheles gambiae"
                      /mol_type="genomic DNA"
                      /strain="PEST"
                      /db_xref="taxon:7165"
                      /clone="06N18"
                      /clone_lib="NotreDame1"
                      /note="end : T7"
ORIGIN

  Query Match             3.6%;  Score 20;  DB 14;  Length 1035;
  Best Local Similarity   100.0%;  Pred. No. 64;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        330 TGCAAAGCTGTTAATGGATC 349
              ||||||||||||||||||||
Db        308 TGCAAAGCTGTTAATGGATC 327


RESULT 50
DT990937
LOCUS       DT990937                1321 bp    mRNA    linear   EST 22-SEP-2005
DEFINITION  CNB152-F06.x1d-t SHGC-CNB Gasterosteus aculeatus cDNA clone
            CNB152-F06 3', mRNA sequence.
ACCESSION   DT990937
VERSION     DT990937.1  GI:76114747
KEYWORDS    EST.
SOURCE      Gasterosteus aculeatus (three spined stickleback)
```

```
  ORGANISM  Gasterosteus aculeatus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
            Gasterosteidae; Gasterosteus.
REFERENCE   1  (bases 1 to 1321)
  AUTHORS   Kingsley,D.M., Peichel,C., Balabahdra,S., Grimwood,J., Dickson,M.,
            Schmutz,J. and Myers,R.M.
  TITLE     Expressed sequence tags from Gasterosteus aculeatus
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Grimwood, Jane
            Stanford Human Genome Center
            Stanford University School of Medicine
            975 S California Ave, Palo Alto, CA 94304, USA
            Tel: 650 320 5917
            Fax: 650 320 5801
            Email: jane@shgc.stanford.edu
            Plate: 152
            High quality sequence start: 18
            High quality sequence stop: 787.
FEATURES             Location/Qualifiers
     source          1. .1321
                     /organism="Gasterosteus aculeatus"
                     /mol_type="mRNA"
                     /strain="Conner Creek sticklebacks, WA USA"
                     /db_xref="taxon:69293"
                     /clone="CNB152-F06"
                     /sex="mixed male and female"
                     /tissue_type="brain"
                     /dev_stage="adult"
                     /lab_host="DH10B (T1 phage resistant)"
                     /clone_lib="SHGC-CNB"
                     /note="Vector: Express 1; Total and poly A+ RNA was
                     isolated from the indicated stickleback tissue, and a cDNA
                     library was constructed in the Express 1 plasmid vector by
                     Open Biosystems. First strand cDNA synthesis was primed
                     with an 54 bp linker primer containing an oligodT sequence
                     preceeded by a synthetic NotI site (first strand primer:
                     5'-GACTAGTTCTAGATCGCGAGCGGCCGCCC(T)25-3'). Following
                     second strand synthesis, cDNAs were made blunt at the end
                     corresponding to the original 5 prime end of mRNA, and
                     cloned directionally into the NotI and EcoRV sites of
                     Express 1. Note that the EcoRV site is typically destroyed
                     in the blunt end cloning, leaving a junction of the form
                     'xxxATC'(where is ATC is the second half of the EcoRV
                     site, and xxx is derived from the cDNA sequence). A map of
                     the Express 1 vector is available at:
                     http://www.openbiosystems.com/cdna_library_construction_fa
                     q.php#8 The primary library was transformed and amplified
                     in DH10B (T1 phage resistant) bacteria. Clones available
                     from Open Biosystems:
                     http://www.openbiosystems.com/stickleback"
ORIGIN

  Query Match             3.6%;  Score 20;  DB 10;  Length 1321;
  Best Local Similarity   100.0%;  Pred. No. 67;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        100 TCCGAAGAGATTGATCATGA 119
              ||||||||||||||||||||
Db        941 TCCGAAGAGATTGATCATGA 960


RESULT 51
CN094503
LOCUS       CN094503                167 bp    mRNA    linear   EST 31-MAR-2004
DEFINITION  EC2BBA9DE06.b1 Xenopus tropicalis xtbs plasmid library Xenopus
            tropicalis cDNA clone xtbs09J12 3', mRNA sequence.
ACCESSION   CN094503
VERSION     CN094503.1  GI:45887199
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 167)
  AUTHORS   Thuret,R., Fierro,A.C., Coen,L., Perron,M., Demeneix,B., Wegnez,M.,
            Gyapay,G., Weissenbach,J., Wincker,P., Mazabraud,A. and Pollet,N.
  TITLE     Exploring the nervous system transcriptome in the model Xenopus
            tropicalis using EST analysis
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Pollet N
            Transgenese et Genetique des Amphibiens
            CNRS UMR 8080
            IBAIC bat 447, Universite Paris Sud, Orsay, F-91405, France
            Tel: +33 169157272
            Fax: +33 169156816
            Email: Nicolas.Pollet@ibaic.u-psud.fr.
FEATURES             Location/Qualifiers
     source          1. .167
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /strain="Ivory Coast"
                     /db_xref="taxon:8364"
                     /clone="xtbs09J12"
                     /tissue_type="pool of brains and spinal cords from
                     tadpoles at stages 51-52 and 61-62"
                     /dev_stage="stage 51-52 and 61-62"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Xenopus tropicalis xtbs plasmid library"
                     /note="Vector: pCMVSPORT6_xtbs; Site_1: SfiI; Site_2:
                     SfiI; Xenopus tropicalis polyA+ RNA was obtained from
                     brain and spinal cord of tadpoles at stages 51-52 and
                     61-62. cDNAs were synthesized using the SMART system of
                     CLONTECH and directionally cloned into pCMVSPORT6_xtbs, a
                     modified version of pCMVSPORT6 allowing directional
                     cloning using asymetric SfiI sites. For antisense RNA
                     synthesis, use T7 promoter and for sense RNA use SP6
                     promoter. Library constructed by Dr. L. Coen and Prof. B.
                     Demeneix (Museum National d'Histoire Naturelle and CNRS
                     UMR 5166, Paris, France)."
ORIGIN

  Query Match             3.4%;  Score 19;  DB 8;  Length 167;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        465 TTTTTATAAAACTAAAATC 483
              |||||||||||||||||||
Db         89 TTTTTATAAAACTAAAATC 107


RESULT 52
DY151937
LOCUS       DY151937                196 bp    mRNA    linear   EST 01-FEB-2006
DEFINITION  000923BEMN018313HT BEMN Bos taurus cDNA, mRNA sequence.
ACCESSION   DY151937
VERSION     DY151937.1  GI:86346112
KEYWORDS    EST.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 196)
  AUTHORS   McCulloch,A., Wilson,T., Molenaar,A., Grigor,M., Davis,S.,
            Glenn,M., Havukkala,I., Watson,J., Crawford,A., Wheeler,T.,
            Hagemann,L., Lee,R., Hein,W., Johnstone,P., Maqbool,N., McMahon,C.,
            McCracken,J., Stelwagen,K., Farr,V., Singh,K., Whitley,J.,
            Nicholas,K., Savin,K., Mather,A., McPartlan,H., Whitley,J.,
            Wells,M., Bowman,P., Goddard,M., Langford,C., McEwan,J. and
            Atkinson,P.
  TITLE     AgResearch, Genesis and Primary Industry Victoria Bovine EST
            project
  JOURNAL   Unpublished (2006)
```

```
COMMENT     Contact: Maqbool N
            AgResearch Ltd.
            Invermay Agricultural Centre, Puddle Alley, Private Bag 50034,
            Mosgiel, New Zealand
            Email: nauman.maqbool@agresearch.co.nz.
FEATURES             Location/Qualifiers
     source          1. .196
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="Life Tech Normalised library"
                     /clone_lib="BEMN"
                     /note="Vector: pCMV-Sport6; Life Tech Normalised library"
ORIGIN

  Query Match             3.4%;  Score 19;  DB 10;  Length 196;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        299 AGATGTACCAGGTGGAGTT 317
              |||||||||||||||||||
Db        103 AGATGTACCAGGTGGAGTT 121


RESULT 53
CB438594
LOCUS       CB438594                199 bp    mRNA    linear   EST 25-MAR-2003
DEFINITION  687245 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   CB438594
VERSION     CB438594.1  GI:29222764
KEYWORDS    EST.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 199)
  AUTHORS   Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
            Wray,J.E. and Keele,J.W.
  TITLE     A second set of bovine ESTs from pooled-tissue normalized libraries
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Plate: FQY8043  row: N  column: 24
            Seq primer: GTAATACGACTCACTATAGGG.
FEATURES             Location/Qualifiers
     source          1. .199
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 6BOV"
                     /note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
                     Library made with RNA pooled from multiple tissues
                     including liver, lung, hypothalamus, pituitary, and
                     placenta/endometrium."
ORIGIN

  Query Match             3.4%;  Score 19;  DB 4;  Length 199;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         21 CCACTCCCAAACCCTGCTG 39
              |||||||||||||||||||
Db         19 CCACTCCCAAACCCTGCTG 37


RESULT 54
CR583097
LOCUS       CR583097                219 bp    mRNA    linear   EST 26-JUL-2004
DEFINITION  CR583097 XGC-tailbud-head Xenopus tropicalis cDNA clone THdA028d23
            5', mRNA sequence.
ACCESSION   CR583097
VERSION     CR583097.1  GI:50583097
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 219)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Garrett,N. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (2004)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Croning MDR
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
             TROPICALIS_SEQUENCE_ID: THdA028d23.p1kbSP6
             This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Nigel Garrett.
            Seq primer: SP6.
FEATURES             Location/Qualifiers
     source          1. .219
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="THdA028d23"
                     /dev_stage="tailbud head (stage 28-30)"
                     /lab_host="Escherichia coli DH10B."
                     /clone_lib="XGC-tailbud-head"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from tailbud
                     head. EcoRI-NotI cut cDNA was then ligated into pCS107
                     with EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

  Query Match             3.4%;  Score 19;  DB 8;  Length 219;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        465 TTTTTATAAAACTAAAATC 483
              |||||||||||||||||||
Db        170 TTTTTATAAAACTAAAATC 188


RESULT 55
BB391337
LOCUS       BB391337                237 bp    mRNA    linear   EST 13-JUL-2000
DEFINITION  BB391337 RIKEN full-length enriched, 0 day neonate cerebellum Mus
            musculus cDNA clone C230074B09 3' similar to AB014577 Homo sapiens
            mRNA for KIAA0677 protein, mRNA sequence.
ACCESSION   BB391337
VERSION     BB391337.1  GI:9114288
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 237)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T.,
            Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
            Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
            Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
            Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C.,
            Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H.,
```

Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.

TITLE RIKEN Mouse ESTs (Konno,H., et al.)

JOURNAL Unpublished (2000)

COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

FEATURES Location/Qualifiers
source 1. .237
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="C230074B09"
/tissue_type="cerebellum"
/dev_stage="0 day neonate"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 0 day neonate cerebellum"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 479.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

ORIGIN

Query Match 3.4%; Score 19; DB 7; Length 237;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        299 AGATGTACCAGGTGGAGTT 317
              |||||||||||||||||||
Db         83 AGATGTACCAGGTGGAGTT 101
```

RESULT 56
CN094504/c

LOCUS CN094504 242 bp mRNA linear EST 31-MAR-2004

DEFINITION EC2BBA9DE06.g1 Xenopus tropicalis xtbs plasmid library Xenopus tropicalis cDNA clone xtbs09J12 5', mRNA sequence.

ACCESSION CN094504

VERSION CN094504.1 GI:45887200

KEYWORDS EST.

SOURCE Xenopus tropicalis (western clawed frog)

ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Silurana.

REFERENCE 1 (bases 1 to 242)

AUTHORS Thuret,R., Fierro,A.C., Coen,L., Perron,M., Demeneix,B., Wegnez,M., Gyapay,G., Weissenbach,J., Wincker,P., Mazabraud,A. and Pollet,N.

TITLE Exploring the nervous system transcriptome in the model Xenopus tropicalis using EST analysis

JOURNAL Unpublished (2004)

COMMENT Contact: Pollet N
Transgenese et Genetique des Amphibiens
CNRS UMR 8080
IBAIC bat 447, Universite Paris Sud, Orsay, F-91405, France
Tel: +33 169157272
Fax: +33 169156816
Email: Nicolas.Pollet@ibaic.u-psud.fr.

FEATURES Location/Qualifiers
source 1. .242
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/strain="Ivory Coast"
/db_xref="taxon:8364"
/clone="xtbs09J12"
/tissue_type="pool of brains and spinal cords from tadpoles at stages 51-52 and 61-62"
/dev_stage="stage 51-52 and 61-62"
/lab_host="E.coli DH10B"
/clone_lib="Xenopus tropicalis xtbs plasmid library"
/note="Vector: pCMVSPORT6_xtbs; Site_1: SfiI; Site_2: SfiI; Xenopus tropicalis polyA+ RNA was obtained from brain and spinal cord of tadpoles at stages 51-52 and 61-62. cDNAs were synthesized using the SMART system of CLONTECH and directionally cloned into pCMVSPORT6_xtbs, a modified version of pCMVSPORT6 allowing directional cloning using asymetric SfiI sites. For antisense RNA synthesis, use T7 promoter and for sense RNA use SP6 promoter. Library constructed by Dr. L. Coen and Prof. B. Demeneix (Museum National d'Histoire Naturelle and CNRS UMR 5166, Paris, France)."

ORIGIN

Query Match 3.4%; Score 19; DB 8; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        465 TTTTTATAAAACTAAAATC 483
              |||||||||||||||||||
Db         78 TTTTTATAAAACTAAAATC 60
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RESULT 57
AL640225/c

LOCUS AL640225 247 bp mRNA linear EST 07-NOV-2003

DEFINITION AL640225 XGC-neurula Xenopus tropicalis cDNA clone TNeu002k23 5', mRNA sequence.

ACCESSION AL640225

VERSION AL640225.2 GI:38219389

KEYWORDS EST.

SOURCE Xenopus tropicalis (western clawed frog)

ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Silurana.

REFERENCE 1 (bases 1 to 247)

AUTHORS Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.

```
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     On Nov 7, 2001 this sequence version replaced gi:16792356.
            Contact: Huckle E
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
            5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli DH10B
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TNeu002k23.p1kSP6
            Sequencing primer: SP6.
FEATURES             Location/Qualifiers
     source          1. .247
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TNeu002k23"
                     /dev_stage="neurula"
                     /lab_host="Escherichia coli DH10B"
                     /clone_lib="XGC-neurula"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from neurula.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

  Query Match             3.4%;  Score 19;  DB 1;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        465 TTTTTATAAAACTAAAATC 483
              |||||||||||||||||||
Db        101 TTTTTATAAAACTAAAATC 83


RESULT 58
BX668635
LOCUS       BX668635                247 bp    mRNA    linear   EST 07-MAY-2004
DEFINITION  BX668635 Sus Scrofa library (scac) Sus scrofa cDNA clone
            scac0028i.i.24 3prim, mRNA sequence.
ACCESSION   BX668635
VERSION     BX668635.1  GI:37977384
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 247)
  AUTHORS   Bonnet,A., Tosser-Klopp,G., Benne,F., Cabau,C., Villeger,S.,
            Soares,M., Bonaldo,F. and Hatey,F.
  TITLE     A Pig Normalised Multi-Tissue cDNA Library
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Tosser-Klopp G
            Genetique Animale
            Institut National de la Recherche Agronomique
            Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
            cedex, FRANCE
            Tel: 33 (0) 5.61.28.51.14
            Fax: 33 (0) 5.61.28.53.08
            Email: tosser@toulouse.inra.fr
            Sequence cleaned of vector, adaptator and repetitions. Contact us
            at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
            sequence.
            Plate: 0028  row: i  column: 24.
FEATURES             Location/Qualifiers
     source          1. .247
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /clone="scac0028i.i.24"
                     /tissue_type="mixed"
                     /clone_lib="Sus Scrofa library (scac)"
                     /note="Vector: pT7T3D-PacI; tissues: adipose tissue,
                     brain, kidney, liver, muscle, ovary, testis,  heart,
                     hypothalamus, pancreas, skin, spleen, thymus, placenta,
                     pituitary  gland, seminal vesicle, small intestine,
                     uterus, adrenals, bulbo uretral  gland, cerebral trunk,
                     epididymis, female gonad, gall-bladder,  hippocampus,
                     large intestine, male gonad, melanocytes, stomach, udder"
ORIGIN

  Query Match             3.4%;  Score 19;  DB 4;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        179 TGAATGAGAGTTGCCTGGC 197
              |||||||||||||||||||
Db        162 TGAATGAGAGTTGCCTGGC 180


RESULT 59
BB425487/c
LOCUS       BB425487                247 bp    mRNA    linear   EST 18-JUL-2000
DEFINITION  BB425487 RIKEN full-length enriched, 12 days embryo spinal cord Mus
            musculus cDNA clone C530046M16 3', mRNA sequence.
ACCESSION   BB425487
VERSION     BB425487.1  GI:9265214
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 247)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T.,
            Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
            Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
            Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
            Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C.,
            Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H.,
            Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K.,
            Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A.,
            Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watahiki,A.,
            Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A.,
            Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,
            Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length
            cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
            Okazaki,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
```

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          19-44 (1999)
           Please visit our web site (http://genome.rtc.riken.go.jp) for
          further details.
FEATURES             Location/Qualifiers
     source          1. .247
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="C530046M16"
                     /tissue_type="spinal cord"
                     /dev_stage="12 days embryo"
                     /lab_host="DH10B"
                     /clone_lib="RIKEN full-length enriched, 12 days embryo
                     spinal cord"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. Second strand cDNA was prepared with the
                     primer adapter of sequence [5'
                     GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA
                     was cleaved with XhoI and BamHI. Vector: a modified
                     pBluescript KS(+) after bulk excision from Lambda FLC I."
ORIGIN

  Query Match             3.4%;  Score 19;  DB 7;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        473 AAACTAAAATCAAGCTCTG 491
              |||||||||||||||||||
Db        104 AAACTAAAATCAAGCTCTG 86


RESULT 60
BX714043/c
LOCUS       BX714043                255 bp    mRNA    linear   EST 18-NOV-2003
DEFINITION  BX714043 XGC-tadpole Xenopus tropicalis cDNA clone TTpA016103 5',
            mRNA sequence.
ACCESSION   BX714043
VERSION     BX714043.1  GI:38385449
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 255)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Croning MDR
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TTpA016103.p1kSP6
            Sequencing primer: SP6
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Nigel Garrett.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from tadpole
            embryos. EcoRI-NotI cut cDNA was then ligated into pCS107 with
            EcoRI at the 5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli DH10B.
FEATURES             Location/Qualifiers
     source          1. .255
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TTpA016103"
                     /dev_stage="tadpole (stage 35-40)"
                     /lab_host="E. coli DH10B"
                     /clone_lib="XGC-tadpole"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from tadpole
                     embryos. EcoRI-NotI cut cDNA was then ligated into pCS107
                     with EcoRI at the 5' end and NotI at the 3' end"
ORIGIN

  Query Match             3.4%;  Score 19;  DB 4;  Length 255;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        465 TTTTTATAAAACTAAAATC 483
              |||||||||||||||||||
Db        243 TTTTTATAAAACTAAAATC 225


RESULT 61
BI703350
LOCUS       BI703350                265 bp    mRNA    linear   EST 18-SEP-2001
DEFINITION  fs85e10.x1 Zebrafish neuronal Danio rerio cDNA clone IMAGE:5076571
            3', mRNA sequence.
ACCESSION   BI703350
VERSION     BI703350.1  GI:15665979
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 265)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
            Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library constructed by S. Lin DNA Sequencing by: Washington
            University Genome Sequencing Center Clone distribution: the
            I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
            Seq primer: T7 from Gibco.
FEATURES             Location/Qualifiers
     source          1. .265
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:5076571"
                     /sex="mixed"
                     /dev_stage="adult"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="Zebrafish neuronal"
                     /note="Organ: brain; Vector: pBluescript (modified);
                     Site_1: DraIII(Y); Site_2: DRAIII(X); Library is cloned
                     directionally between the DraIII(X) and DraIII(Y) sites
                     and has been amplified. Library constructed by S. Lin. "
ORIGIN

  Query Match             3.4%;  Score 19;  DB 2;  Length 265;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy        412 CTGAATGTCAACAGTGTGA 430
              ||||||||||||||||||
Db        104 CTGAATGTCAACAGTGTGA 122


RESULT 62
AV338007
LOCUS       AV338007                267 bp    mRNA    linear   EST 11-NOV-1999
DEFINITION  AV338007 RIKEN full-length enriched, adult male olfactory bulb Mus
            musculus cDNA clone 6430407D11 3', mRNA sequence.
ACCESSION   AV338007
VERSION     AV338007.1  GI:6378059
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 267)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T.,
            Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F.,
            Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I.,
            Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M.,
            Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
            Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K.,
            Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y.,
            Suzuki,H., Suzuki,H., Takahashi,F., Tateno,M., Tominaga,N.,
            Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A.,
            Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al. 1999)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
            Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
            Hayashizaki,Y.
             Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
            Okazaki,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
             Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .267
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="6430407D11"
                     /sex="male"
                     /tissue_type="olfactory brain"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="RIKEN full-length enriched, adult male
                     olfactory bulb"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 10.0 and subtraction to Rot = 100.0. Second
                     strand cDNA was prepared with the primer adapter of
                     sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC
                     3']. cDNA was cloned into the XhoI and BamHI sites.
                     Vector: a modified pBluescript KS(+) after bulk excision
                     from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
                     BamHI"
ORIGIN

  Query Match             3.4%;  Score 19;  DB 1;  Length 267;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        307 CAGGTGGAGTTCAAGGCCA 325
              ||||||||||||||||||
Db        187 CAGGTGGAGTTCAAGGCCA 205


RESULT 63
AL777805/c
LOCUS       AL777805                276 bp    mRNA    linear   EST 12-NOV-2003
DEFINITION  AL777805 XGC-neurula Xenopus tropicalis cDNA clone TNeu077l17 5',
            mRNA sequence.
ACCESSION   AL777805
VERSION     AL777805.2  GI:38281824
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 276)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     On Jun 25, 2002 this sequence version replaced gi:21563509.
            Contact: Taylor R
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
            5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli DH10B
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TNeu077l17.p1cSP6
            Sequencing primer: SP6.
FEATURES             Location/Qualifiers
     source          1. .276
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TNeu077l17"
                     /dev_stage="neurula"
                     /lab_host="Escherichia coli DH10B"
                     /clone_lib="XGC-neurula"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from neurula.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

  Query Match             3.4%;  Score 19;  DB 1;  Length 276;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
```

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  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        465 TTTTTATAAAACTAAAATC 483
              |||||||||||||||||||
Db        117 TTTTTATAAAACTAAAATC 99


RESULT 64
BX683343
LOCUS       BX683343                280 bp    mRNA    linear   EST 14-NOV-2003
DEFINITION  BX683343 XGC-neurula Xenopus tropicalis cDNA clone TNeu077l17, mRNA
            sequence.
ACCESSION   BX683343
VERSION     BX683343.1  GI:38332463
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 280)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Croning MDR
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TNeu077l17.q1kT7
            Sequencing primer: T7
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
            5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli DH10B.
FEATURES             Location/Qualifiers
     source          1. .280
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TNeu077l17"
                     /dev_stage="neurula"
                     /lab_host="Escherichia coli DH10B"
                     /clone_lib="XGC-neurula"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from neurula.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

  Query Match             3.4%;  Score 19;  DB 4;  Length 280;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        465 TTTTTATAAAACTAAAATC 483
              |||||||||||||||||||
Db        174 TTTTTATAAAACTAAAATC 192


RESULT 65
AZ406693
LOCUS       AZ406693                283 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0176H05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0176H05 F, genomic survey sequence.
ACCESSION   AZ406693
VERSION     AZ406693.1  GI:10530706
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 283)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0176  row: H  column: 05
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 283.
FEATURES             Location/Qualifiers
     source          1. .283
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0176H05"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             3.4%;  Score 19;  DB 11;  Length 283;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        307 CAGGTGGAGTTCAAGGCCA 325
              |||||||||||||||||||
Db        179 CAGGTGGAGTTCAAGGCCA 197


RESULT 66
BQ392367
LOCUS       BQ392367                286 bp    mRNA    linear   EST 22-MAY-2002
DEFINITION  NISC_mq24a11.x1 NICHD_XGC_Emb5 Xenopus tropicalis cDNA clone
            IMAGE:5309109 3', mRNA sequence.
ACCESSION   BQ392367
VERSION     BQ392367.1  GI:21080054
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
```

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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 286)
  AUTHORS   NIH-XCG http://image.llnl.gov/image/html/xenopuslib_info.shtml.
  TITLE     National Institute of Child Health and Human Development, National
            Cancer Insitute, Xenopus Gene Collection
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation:
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
             DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC)
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            info@image.llnl.gov
            Plate: LLAM11783  row: B  column: 22
            Seq primer: -21M13 forward primer (ABI).
FEATURES             Location/Qualifiers
     source          1. .286
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="IMAGE:5309109"
                     /tissue_type="gastrula"
                     /dev_stage="embryo, stages 10-13"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NICHD_XGC_Emb5"
                     /note="Vector: pCMV-SPORT6.1; Site_1: NotI; Site_2: EcoRV;
                     Cloned unidirectionally. Primer: Oligo dT. Average insert
                     size 2.0 kb. Constructed by Invitrogen. Note: This is a
                     Xenopus Gene Collection (XGC) library."
ORIGIN

  Query Match             3.4%;  Score 19;  DB 3;  Length 286;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        465 TTTTTATAAAACTAAAATC 483
              |||||||||||||||||||
Db        210 TTTTTATAAAACTAAAATC 228


RESULT 67
AL643008
LOCUS       AL643008                287 bp    mRNA    linear   EST 07-NOV-2003
DEFINITION  AL643008 XGC-neurula Xenopus tropicalis cDNA clone TNeu016b16 5',
            mRNA sequence.
ACCESSION   AL643008
VERSION     AL643008.2  GI:38221579
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 287)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     On Nov 7, 2001 this sequence version replaced gi:16795133.
            Contact: Huckle E
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
            5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli DH10B
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TNeu016b16.p1kSP6
            Sequencing primer: SP6.
FEATURES             Location/Qualifiers
     source          1. .287
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TNeu016b16"
                     /dev_stage="neurula"
                     /lab_host="Escherichia coli DH10B"
                     /clone_lib="XGC-neurula"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from neurula.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

  Query Match             3.4%;  Score 19;  DB 1;  Length 287;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        465 TTTTTATAAAACTAAAATC 483
              |||||||||||||||||||
Db        219 TTTTTATAAAACTAAAATC 237


RESULT 68
BI703351/c
LOCUS       BI703351                290 bp    mRNA    linear   EST 18-SEP-2001
DEFINITION  fs85e10.y1 Zebrafish neuronal Danio rerio cDNA clone IMAGE:5076571
            5', mRNA sequence.
ACCESSION   BI703351
VERSION     BI703351.1  GI:15665980
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 290)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
            Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Other_ESTs: fs85e10.x1
            Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library constructed by S. Lin DNA Sequencing by: Washington
            University Genome Sequencing Center Clone distribution: the
            I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
            Seq primer: T3 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .290
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:5076571"
                     /sex="mixed"
                     /dev_stage="adult"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="Zebrafish neuronal"
                     /note="Organ: brain; Vector: pBluescript (modified);
                     Site_1: DraIII(Y); Site_2: DRAIII(X); Library is cloned
                     directionally between the DraIII(X) and DraIII(Y) sites
```

and has been amplified. Library constructed by S. Lin. "
ORIGIN

Query Match 3.4%; Score 19; DB 2; Length 290;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 412 CTGAATGTCAACAGTGTGA 430
||||||||||||||||||
Db 172 CTGAATGTCAACAGTGTGA 154

RESULT 69
BB460815/c
LOCUS BB460815 307 bp mRNA linear EST 21-JUL-2000
DEFINITION BB460815 RIKEN full-length enriched, 12 days embryo spinal ganglion Mus musculus cDNA clone D130068N23 3', mRNA sequence.
ACCESSION BB460815
VERSION BB460815.1 GI:9356308
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 307)
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Konno,H., et al.)
JOURNAL Unpublished (2000)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
FEATURES Location/Qualifiers
source 1. .307
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="D130068N23"
/tissue_type="spinal ganglion"
/dev_stage="12 days embryo"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 12 days embryo spinal ganglion"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."
ORIGIN

Query Match 3.4%; Score 19; DB 7; Length 307;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 226 GGGAGTTGCCTGGCCTCCA 244
||||||||||||||||||
Db 52 GGGAGTTGCCTGGCCTCCA 34

RESULT 70
BQ392345
LOCUS BQ392345 317 bp mRNA linear EST 22-MAY-2002
DEFINITION NISC_mq23h11.x1 NICHD_XGC_Emb5 Xenopus tropicalis cDNA clone IMAGE:5309444 3', mRNA sequence.
ACCESSION BQ392345
VERSION BQ392345.1 GI:21080032
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 317)
AUTHORS NIH-XCG http://image.llnl.gov/image/html/xenopuslib_info.shtml.
TITLE National Institute of Child Health and Human Development, National Cancer Insitute, Xenopus Gene Collection
JOURNAL Unpublished (2002)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation:
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Plate: LLAM11783 row: P column: 21
Seq primer: -21M13 forward primer (ABI).
FEATURES Location/Qualifiers
source 1. .317
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE:5309444"
/tissue_type="gastrula"
/dev_stage="embryo, stages 10-13"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHD_XGC_Emb5"
/note="Vector: pCMV-SPORT6.1; Site_1: NotI; Site_2: EcoRV; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.0 kb. Constructed by Invitrogen. Note: This is a Xenopus Gene Collection (XGC) library."
ORIGIN

```
  Query Match             3.4%;  Score 19;  DB 3;  Length 317;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        465 TTTTTATAAAACTAAAATC 483
              |||||||||||||||||||
Db        207 TTTTTATAAAACTAAAATC 225


RESULT 71
AG255889/c
LOCUS       AG255889                 330 bp    DNA     linear   GSS 19-JUL-2003
DEFINITION  Lotus corniculatus var. japonicus DNA, clone:LjT40h03_sfi, genomic
            survey sequence.
ACCESSION   AG255889
VERSION     AG255889.1  GI:26655726
KEYWORDS    GSS.
SOURCE      Lotus corniculatus var. japonicus (Lotus japonicus)
  ORGANISM  Lotus corniculatus var. japonicus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
            Lotus.
REFERENCE   1
  AUTHORS   Sato,S., Nakamura,Y. and Tabata,S.
  TITLE     Lotus japonicus TAC End sequences
  JOURNAL   Published Only in Database (2002)
REFERENCE   2  (bases 1 to 330)
  AUTHORS   Sato,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute,
            The First Laboratory for Plant Gene Research; 2-6-7
            Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan
            (E-mail:ssato@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/,
            Tel:81-438-52-3935(ex.2336), Fax:81-438-52-3934)
FEATURES             Location/Qualifiers
     source          1. .330
                     /organism="Lotus corniculatus var. japonicus"
                     /mol_type="genomic DNA"
                     /strain="Miyakojima MG-20"
                     /variety="japonicus"
                     /db_xref="taxon:34305"
                     /clone="LjT40h03_sfi"
                     /clone_lib="genomic TAC library"
                     /note="VECTOR:pYLTAC7
                     synonym: Lotus japonicus"
ORIGIN

  Query Match             3.4%;  Score 19;  DB 14;  Length 330;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        464 ATTTTTATAAAACTAAAAT 482
              |||||||||||||||||||
Db        243 ATTTTTATAAAACTAAAAT 225


RESULT 72
BQ392422
LOCUS       BQ392422                 334 bp    mRNA    linear   EST 22-MAY-2002
DEFINITION  NISC_mq24d03.x1 NICHD_XGC_Emb5 Xenopus tropicalis cDNA clone
            IMAGE:5309237 3', mRNA sequence.
ACCESSION   BQ392422
VERSION     BQ392422.1  GI:21080109
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 334)
  AUTHORS   NIH-XCG http://image.llnl.gov/image/html/xenopuslib_info.shtml.
  TITLE     National Institute of Child Health and Human Development, National
            Cancer Insitute, Xenopus Gene Collection
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation:
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
             DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC)
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            info@image.llnl.gov
            Plate: LLAM11783  row: H  column: 6
            Seq primer: -21M13 forward primer (ABI).
FEATURES             Location/Qualifiers
     source          1. .334
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="IMAGE:5309237"
                     /tissue_type="gastrula"
                     /dev_stage="embryo, stages 10-13"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NICHD_XGC_Emb5"
                     /note="Vector: pCMV-SPORT6.1; Site_1: NotI; Site_2: EcoRV;
                     Cloned unidirectionally. Primer: Oligo dT. Average insert
                     size 2.0 kb. Constructed by Invitrogen. Note: This is a
                     Xenopus Gene Collection (XGC) library."
ORIGIN

  Query Match             3.4%;  Score 19;  DB 3;  Length 334;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        465 TTTTTATAAAACTAAAATC 483
              |||||||||||||||||||
Db        171 TTTTTATAAAACTAAAATC 189


RESULT 73
AL849698/c
LOCUS       AL849698                 335 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AL849698 XGC-egg Xenopus tropicalis cDNA clone TEgg003k15 5', mRNA
            sequence.
ACCESSION   AL849698
VERSION     AL849698.2  GI:38560935
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 335)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     On Sep 15, 2002 this sequence version replaced gi:22869920.
            Contact: Taylor R
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TEgg003k15.p1kSP6
            Sequencing primer: SP6
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from egg.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
            5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli XL1-blue.
FEATURES             Location/Qualifiers
     source          1. .335
                     /organism="Xenopus tropicalis"
```

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                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TEgg003k15"
                     /dev_stage="egg"
                     /lab_host="Escherichia coli XL1-blue"
                     /clone_lib="XGC-egg"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from egg.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end"
ORIGIN

  Query Match             3.4%;  Score 19;  DB 1;  Length 335;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        465 TTTTTATAAAACTAAAATC 483
              |||||||||||||||||||
Db        189 TTTTTATAAAACTAAAATC 171


RESULT 74
CX358439
LOCUS       CX358439                350 bp    mRNA    linear   EST 28-SEP-2005
DEFINITION  JGI_XZT28.rev NIH_XGC_tropTad5 Xenopus tropicalis cDNA clone XZT28
            3', mRNA sequence.
ACCESSION   CX358439
VERSION     CX358439.1  GI:57126998
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 350)
  AUTHORS   Richardson,P., Lucas,S., Rokhsar,D., Detter,J.C., Ng,D.C.,
            Brokstein,P. and Lindquist,E.A.
  TITLE     DOE Joint Genome Institute Xenopus tropicalis EST project
  JOURNAL   Unpublished (2004)
COMMENT     Other_ESTs: JGI_XZT28.fwd
            Contact: Lindquist,E.A., Richardson,P.
            DOE Joint Genome Institute
            2800 Mitchell Drive, Walnut Creek, CA 94598, USA
            Tel: 925 296 5600
            Fax: 925 296 5710
            Email: cdna@jgi-psf.org
            Tissue Procurement: Richard M. Harland Laboratory, University of
            California, Berkeley: http://tropicalis.berkeley.edu/home
            cDNA Library Preparation: Richard M. Harland Laboratory, University
            of California, Berkeley
            cDNA Library Arrayed by: DOE Joint Genome Institute:
            http://www.jgi.doe.gov
            DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
            Clone Unavailable: The master plate for this cDNA clone no longer
            exists.
            Naming Conventions: EST name is generated by the concatenation of
            the JGI Clone Id and the direction of sequencing. The suffix '.rev'
            indicates a reverse sequencing read of the insert. It does not
            necessarily reflect the orientation of the insert.
            Poly-A: Based upon the presence of a run of 14 or more T residues
            at the beginning of the sequence, this clone was polyadenylated.
            The resulting Poly-T sequence has been removed.
            Small Insert: Based upon one or more sequencing reads of this clone
            where vector sequence was present at both ends, this clone has been
            determined to contain a cDNA insert on the order of 600-1000 bases.
            Plate: XZT 0001  row: g  column: 7
            High quality sequence stop: 171
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .350
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="XZT28"
                     /tissue_type="whole embryo"
                     /dev_stage="Tadpole (st. 36-41)"
                     /lab_host="E. coli XL1-Blue derivative, Stratagene
                     ElectroTen-Blue"
                     /clone_lib="NIH_XGC_tropTad5"
                     /note="Vector: pCS108; Site_1: SalI; Site_2: NotI; Tadpole
                     library constructed by Russell B. Fletcher in R. Harland's
                     lab using poly A RNA and oligo dT primers (Invitrogen
                     SuperScript Plasmid System for cDNA Synthesis and
                     Cloning). SalI (5' end) -NotI (3' end) cDNA was inserted
                     into vector pCS108
                     (http://mcb.berkeley.edu/labs/harland/pages/plasmids.html)
                     ."
ORIGIN

  Query Match             3.4%;  Score 19;  DB 9;  Length 350;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        465 TTTTTATAAAACTAAAATC 483
              |||||||||||||||||||
Db         11 TTTTTATAAAACTAAAATC 29


RESULT 75
BX708129
LOCUS       BX708129                351 bp    mRNA    linear   EST 17-NOV-2003
DEFINITION  BX708129 XGC-tadpole Xenopus tropicalis cDNA clone TTpA002b09 3',
            mRNA sequence.
ACCESSION   BX708129
VERSION     BX708129.1  GI:38370336
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 351)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Croning MDR
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TTpA002b09.q1kT7
            Sequencing primer: T7
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Nigel Garrett.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from tadpole
            embryos. EcoRI-NotI cut cDNA was then ligated into pCS107 with
            EcoRI at the 5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli DH10B.
FEATURES             Location/Qualifiers
     source          1. .351
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TTpA002b09"
                     /dev_stage="tadpole (stage 35-40)"
                     /lab_host="E. coli DH10B"
                     /clone_lib="XGC-tadpole"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from tadpole
                     embryos. EcoRI-NotI cut cDNA was then ligated into pCS107
                     with EcoRI at the 5' end and NotI at the 3' end"
ORIGIN

  Query Match             3.4%;  Score 19;  DB 4;  Length 351;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
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```
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        465 TTTTTATAAAACTAAAATC 483
              |||||||||||||||||||
Db        181 TTTTTATAAAACTAAAATC 199


RESULT 76
CN106168
LOCUS       CN106168                354 bp    mRNA    linear   EST 31-MAR-2004
DEFINITION  EC2CAA29AC03.b1 Xenopus tropicalis xthr plasmid library Xenopus
            tropicalis cDNA clone xthr29E05 3', mRNA sequence.
ACCESSION   CN106168
VERSION     CN106168.1  GI:45898864
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 354)
  AUTHORS   Thuret,R., Fierro,A.C., Coen,L., Perron,M., Demeneix,B., Wegnez,M.,
            Gyapay,G., Weissenbach,J., Wincker,P., Mazabraud,A. and Pollet,N.
  TITLE     Exploring the nervous system transcriptome in the model Xenopus
            tropicalis using EST analysis
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Pollet N
            Transgenese et Genetique des Amphibiens
            CNRS UMR 8080
            IBAIC bat 447, Universite Paris Sud, Orsay, F-91405, France
            Tel: +33 169157272
            Fax: +33 169156816
            Email: Nicolas.Pollet@ibaic.u-psud.fr.
FEATURES             Location/Qualifiers
     source          1. .354
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /strain="Ivory Coast"
                     /db_xref="taxon:8364"
                     /clone="xthr29E05"
                     /tissue_type="pool of heads and retinas from tailbud
                     stages 25-35"
                     /dev_stage="stage 25-35"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Xenopus tropicalis xthr plasmid library"
                     /note="Vector: pCMVSPORT6_xthr; Site_1: SfiI; Site_2:
                     SfiI; Xenopus tropicalis polyA+ RNA was obtained from pool
                     of heads and retinas from tailbud stages 25-35 cDNAs were
                     synthesized using the SMART system of CLONTECH and
                     directionally cloned into pCMVSPORT6_xthr, a modified
                     version of pCMVSPORT6 allowing directional cloning using
                     asymetric SfiI sites. For antisense RNA synthesis, use T7
                     promoter and for sense RNA use SP6 promoter. Library
                     constructed by Drs. N. Pollet, M. Perron, M. Wegnez, A.
                     Mazabraud (CNRS UMR 8080, Universite Paris Sud, Orsay,
                     France)."
ORIGIN

  Query Match             3.4%;  Score 19;  DB 8;  Length 354;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        465 TTTTTATAAAACTAAAATC 483
              |||||||||||||||||||
Db         87 TTTTTATAAAACTAAAATC 105


RESULT 77
AL855295
LOCUS       AL855295                361 bp    mRNA    linear   EST 02-DEC-2003
DEFINITION  AL855295 XGC-egg Xenopus tropicalis cDNA clone TEgg003k15 3', mRNA
            sequence.
ACCESSION   AL855295
VERSION     AL855295.2  GI:38630704
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 361)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     On Sep 15, 2002 this sequence version replaced gi:22875514.
            Contact: Taylor R
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TEgg003k15.q1kT7
            Sequencing primer: T7
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from egg.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
            5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli XL1-blue.
FEATURES             Location/Qualifiers
     source          1. .361
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TEgg003k15"
                     /dev_stage="egg"
                     /lab_host="Escherichia coli XL1-blue"
                     /clone_lib="XGC-egg"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from egg.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end"
ORIGIN

  Query Match             3.4%;  Score 19;  DB 1;  Length 361;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        465 TTTTTATAAAACTAAAATC 483
              |||||||||||||||||||
Db        173 TTTTTATAAAACTAAAATC 191


RESULT 78
DR612001/c
LOCUS       DR612001                365 bp    mRNA    linear   EST 11-JUL-2005
DEFINITION  EST1002129 FvH Gibberella moniliformis cDNA clone FVHAA26, mRNA
            sequence.
ACCESSION   DR612001
VERSION     DR612001.1  GI:70686649
KEYWORDS    EST.
SOURCE      Gibberella moniliformis
  ORGANISM  Gibberella moniliformis
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE   1  (bases 1 to 365)
  AUTHORS   Brown,D.W., Cheung,F., Proctor,R.H., Butchko,A.E., Zheng,L, Lee,Y.,
            Utterback,T., Smith,S., Feldblyum,T., Glenn,A.E., Plattner,R.D.,
            Kendra,D.F., Town,C.D. and Whitelaw,C.A.
  TITLE     Comparative analysis of 87,000 expressed sequence tags from the
            fumonisin-producing fungus Fusarium verticillioides
  JOURNAL   Fungal Genet. Biol. 42 (10), 848-861 (2005)
   PUBMED   16099185
COMMENT     Contact: Brown, D.W.
            USDA/ARS/NCAUR
            USDA
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            1815 N. University St, Peoria, IL 61604, USA
            Tel: 309 681 6230
            Fax: 309 681 6689
            Email: browndw@ncaur.usda.gov
            TIGR sequence name: FVHAA26TH
            Seq primer: AAT TAA CCC TCA CTA AAG GG.
FEATURES              Location/Qualifiers
     source           1. .365
                      /organism="Gibberella moniliformis"
                      /mol_type="mRNA"
                      /strain="m3125"
                      /db_xref="taxon:117187"
                      /clone="FVHAA26"
                      /tissue_type="mycelia"
                      /clone_lib="FvH"
                      /note="Vector: pBlueScript II SK(+) XR; Site_1: EcoRI;
                      Site_2: XhoI; anamorph: Fusarium verticillioides. Library
                      FvH was prepared from germinating conidia in an aqueous
                      extract of maize seedlings. The aqueous extract was
                      obtained by germinating surface-sterilized maize seeds for
                      four days on 1% water agar supplemented with 100 ug/ml
                      streptomycin sulfate. Under sterile conditions, 70 g of
                      excised roots and shoots from the resulting seedlings was
                      blended with 250 ml water, filtered once through Miracloth
                      (Calbiochem) and then again through #1 Whatman filter
                      paper. The extracts were inoculated to a spore
                      concentration of 5 x 106 conidia per ml and then incubated
                      for 10 hours at 30C with shaking at 200 RPM. Cultures were
                      vacuum filtered and the mycelial mats were frozen in
                      liquid nitrogen, ground to a powder, and then added to
                      TRIzol Reagent (Invitrogen, Carlsbad CA) at approximately
                      1 g mycelia per 10 ml TRIzol. The cDNA was directionally
                      ligated into the pBlueScript II SK(+) XR vector (cDNA
                      Synthesis Kit; Stratagene)."
ORIGIN

  Query Match             3.4%;  Score 19;  DB 10;  Length 365;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         96 CACTTCCGAAGAGATTGAT 114
              ||||||||||||||||||
Db        181 CACTTCCGAAGAGATTGAT 163


RESULT 79
DN068916
LOCUS       DN068916                 366 bp    mRNA    linear   EST 14-SEP-2005
DEFINITION  JGI_CABD5093.rev NIH_XGC_tropLun1 Xenopus tropicalis cDNA clone
            CABD5093 3', mRNA sequence.
ACCESSION   DN068916
VERSION     DN068916.1  GI:59657884
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 366)
  AUTHORS   Richardson,P., Lucas,S., Rokhsar,D., Detter,J.C., Ng,D.C.,
            Brokstein,P. and Lindquist,E.A.
  TITLE     DOE Joint Genome Institute Xenopus tropicalis EST project
  JOURNAL   Unpublished (2004)
COMMENT     Other_ESTs: JGI_CABD5093.fwd
            Contact: Lindquist,E.A., Richardson,P.
            DOE Joint Genome Institute
            2800 Mitchell Drive, Walnut Creek, CA 94598, USA
            Tel: 925 296 5600
            Fax: 925 296 5710
            Email: cdna@jgi-psf.org
            Tissue Procurement: Robert M. Grainger
            cDNA Library Preparation: Bruce Blumberg Laboratory, University of
            California, Irvine
            cDNA Library Arrayed by: DOE Joint Genome Institute:
            http://www.jgi.doe.gov
            DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
            Clone Unavailable: The master plate for this cDNA clone no longer
            exists.
            Naming Conventions: EST name is generated by the concatenation of
            the JGI Clone Id and the direction of sequencing. The suffix '.rev'
            indicates a reverse sequencing read of the insert. It does not
            necessarily reflect the orientation of the insert.
            Poly-A: Based upon the presence of a run of 14 or more T residues
            at the beginning of the sequence, this clone was polyadenylated.
            The resulting Poly-T sequence has been removed.
            Plate: CABD 0053  row: j  column: 1
            High quality sequence stop: 334
            POLYA=Yes.
FEATURES              Location/Qualifiers
     source           1. .366
                      /organism="Xenopus tropicalis"
                      /mol_type="mRNA"
                      /strain="N6 (Nigerian 6th generation inbred)"
                      /db_xref="taxon:8364"
                      /clone="CABD5093"
                      /tissue_type="Lung"
                      /dev_stage="Adult"
                      /lab_host="ElectroMAX DH10B T1 Phage Resistant cells"
                      /clone_lib="NIH_XGC_tropLun1"
                      /note="Vector: pCS107; Site_1: EcoRI; Site_2: XhoI; The
                      library was prepared from 5 ug of poly A+ RNA by oligo-dT
                      priming
                      (5'-ACTAGTGCGGCCGCCTAGGCCTCGAGTTTTTTTTTTTTTTTTV-3') and
                      Stratascript reverse transcriptase. After ligation of
                      EcoRI adapters (5'-AATTCGGCACGAGG-3') followed by kinasing
                      adapters and by XhoI digestion, the cDNA was size selected
                      by chromatography on Sepharose CL-2B columns and fractions
                      containing cDNAs larger than 1000 bp were ligated into
                      EcoRI/XhoI-digested pCS107. Reference for library
                      construction: Current Genomics 4, 635-644. Library
                      constructed by Michelle Tabb and Bruce Blumberg (Dept of
                      Developmental and Cell Biology, University of California,
                      Irvine)."
ORIGIN

  Query Match             3.4%;  Score 19;  DB 9;  Length 366;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        465 TTTTTATAAAACTAAAATC 483
              ||||||||||||||||||
Db        147 TTTTTATAAAACTAAAATC 165


RESULT 80
CR437136/c
LOCUS       CR437136                 379 bp    mRNA    linear   EST 19-JUN-2004
DEFINITION  CR437136 XGC-tailbud Xenopus tropicalis cDNA clone TTbA069f05 5',
            mRNA sequence.
ACCESSION   CR437136
VERSION     CR437136.1  GI:48962723
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 379)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Garrett,N. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (2004)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Croning MDR
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
```

```
           TROPICALIS_SEQUENCE_ID: TTbA069f05.p1kSP6
           This sequence is from a Xenopus Gene Collection (XGC) library
          constructed by Nigel Garrett.
          Seq primer: SP6.
FEATURES             Location/Qualifiers
     source          1. .379
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TTbA069f05"
                     /dev_stage="tailbud (stage 28-30)"
                     /lab_host="Escherichia coli DH10B."
                     /clone_lib="XGC-tailbud"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from tailbud.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

  Query Match             3.4%;  Score 19;  DB 8;  Length 379;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        465 TTTTTATAAAACTAAAATC 483
              |||||||||||||||||||
Db        233 TTTTTATAAAACTAAAATC 215


RESULT 81
CR560333
LOCUS       CR560333                386 bp    mRNA    linear   EST 19-JUL-2004
DEFINITION  CR560333 XGC-tailbud-head Xenopus tropicalis cDNA clone THdA003h06
            3', mRNA sequence.
ACCESSION   CR560333
VERSION     CR560333.1  GI:50390410
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Garrett,N. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (2004)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Croning MDR
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
             TROPICALIS_SEQUENCE_ID: THdA003h06.q1kT7
             This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Nigel Garrett.
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .386
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="THdA003h06"
                     /dev_stage="tailbud head (stage 28-30)"
                     /lab_host="Escherichia coli DH10B."
                     /clone_lib="XGC-tailbud-head"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from tailbud
                     head. EcoRI-NotI cut cDNA was then ligated into pCS107
                     with EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

  Query Match             3.4%;  Score 19;  DB 8;  Length 386;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        465 TTTTTATAAAACTAAAATC 483
              |||||||||||||||||||
Db        170 TTTTTATAAAACTAAAATC 188


RESULT 82
CR437137
LOCUS       CR437137                410 bp    mRNA    linear   EST 19-JUN-2004
DEFINITION  CR437137 XGC-tailbud Xenopus tropicalis cDNA clone TTbA069f05 3',
            mRNA sequence.
ACCESSION   CR437137
VERSION     CR437137.1  GI:48962724
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 410)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Garrett,N. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (2004)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Croning MDR
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
             TROPICALIS_SEQUENCE_ID: TTbA069f05.q1kT7
             This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Nigel Garrett.
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .410
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TTbA069f05"
                     /dev_stage="tailbud (stage 28-30)"
                     /lab_host="Escherichia coli DH10B."
                     /clone_lib="XGC-tailbud"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from tailbud.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

  Query Match             3.4%;  Score 19;  DB 8;  Length 410;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        465 TTTTTATAAAACTAAAATC 483
              |||||||||||||||||||
Db        178 TTTTTATAAAACTAAAATC 196


RESULT 83
BQ394236
LOCUS       BQ394236                421 bp    mRNA    linear   EST 22-MAY-2002
DEFINITION  NISC_ng08a11.x1 NICHD_XGC_Emb6 Xenopus tropicalis cDNA clone
            IMAGE:5382453 3', mRNA sequence.
ACCESSION   BQ394236
VERSION     BQ394236.1  GI:21081923
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 421)
  AUTHORS   NIH-XCG http://image.llnl.gov/image/html/xenopuslib_info.shtml.
  TITLE     National Institute of Child Health and Human Development, National
            Cancer Insitute, Xenopus Gene Collection
  JOURNAL   Unpublished (2002)
```

```
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation:
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
             DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC)
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            info@image.llnl.gov
            Plate: LLAM11974  row: B  column: 22
            Seq primer: -21M13 forward primer (ABI).
FEATURES              Location/Qualifiers
     source           1. .421
                      /organism="Xenopus tropicalis"
                      /mol_type="mRNA"
                      /db_xref="taxon:8364"
                      /clone="IMAGE:5382453"
                      /tissue_type="neurula"
                      /dev_stage="embryo, stages 14-19"
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="NICHD_XGC_Emb6"
                      /note="Vector: pCMV-SPORT6.1; Site_1: NotI; Site_2: EcoRV;
                      Cloned unidirectionally. Primer: Oligo dT. Average insert
                      size 2.1 kb. Constructed by Invitrogen. Note: This is a
                      Xenopus Gene Collection (XGC) library."
ORIGIN

  Query Match             3.4%;  Score 19;  DB 3;  Length 421;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        465 TTTTTATAAAACTAAAATC 483
              |||||||||||||||||||
Db        214 TTTTTATAAAACTAAAATC 232


RESULT 84
CX311082
LOCUS       CX311082                431 bp    mRNA    linear   EST 29-SEP-2005
DEFINITION  JGI_XZT11080.rev NIH_XGC_tropTad5 Xenopus tropicalis cDNA clone
            XZT11080 3', mRNA sequence.
ACCESSION   CX311082
VERSION     CX311082.1  GI:57035687
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 431)
  AUTHORS   Richardson,P., Lucas,S., Rokhsar,D., Detter,J.C., Ng,D.C.,
            Brokstein,P. and Lindquist,E.A.
  TITLE     DOE Joint Genome Institute Xenopus tropicalis EST project
  JOURNAL   Unpublished (2004)
COMMENT     Other_ESTs: JGI_XZT11080.fwd
            Contact: Lindquist,E.A., Richardson,P.
            DOE Joint Genome Institute
            2800 Mitchell Drive, Walnut Creek, CA 94598, USA
            Tel: 925 296 5600
            Fax: 925 296 5710
            Email: cdna@jgi-psf.org
            Tissue Procurement: Richard M. Harland Laboratory, University of
            California, Berkeley: http://tropicalis.berkeley.edu/home
            cDNA Library Preparation: Richard M. Harland Laboratory, University
            of California, Berkeley
            cDNA Library Arrayed by: DOE Joint Genome Institute:
            http://www.jgi.doe.gov
            DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
            Clone Unavailable: The master plate for this cDNA clone no longer
            exists.
            Naming Conventions: EST name is generated by the concatenation of
            the JGI Clone Id and the direction of sequencing. The suffix '.rev'
            indicates a reverse sequencing read of the insert. It does not
            necessarily reflect the orientation of the insert.
            Plate: XZT 0113  row: p  column: 10
            High quality sequence stop: 386.
FEATURES              Location/Qualifiers
     source           1. .431
                      /organism="Xenopus tropicalis"
                      /mol_type="mRNA"
                      /db_xref="taxon:8364"
                      /clone="XZT11080"
                      /tissue_type="whole embryo"
                      /dev_stage="Tadpole (st. 36-41)"
                      /lab_host="E. coli XL1-Blue derivative, Stratagene
                      ElectroTen-Blue"
                      /clone_lib="NIH_XGC_tropTad5"
                      /note="Vector: pCS108; Site_1: SalI; Site_2: NotI; Tadpole
                      library constructed by Russell B. Fletcher in R. Harland's
                      lab using poly A RNA and oligo dT primers (Invitrogen
                      SuperScript Plasmid System for cDNA Synthesis and
                      Cloning). SalI (5' end) -NotI (3' end) cDNA was inserted
                      into vector pCS108
                      (http://mcb.berkeley.edu/labs/harland/pages/plasmids.html)
                      ."
ORIGIN

  Query Match             3.4%;  Score 19;  DB 8;  Length 431;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        465 TTTTTATAAAACTAAAATC 483
              |||||||||||||||||||
Db         87 TTTTTATAAAACTAAAATC 105


RESULT 85
AL966626/c
LOCUS       AL966626                433 bp    mRNA    linear   EST 05-DEC-2003
DEFINITION  AL966626 XGC-gastrula Xenopus tropicalis cDNA clone TGas137b24 5',
            mRNA sequence.
ACCESSION   AL966626
VERSION     AL966626.2  GI:39021328
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 433)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     On Nov 27, 2002 this sequence version replaced gi:25790221.
            Contact: Taylor R
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TGas137b24.p1kSP6
            Sequencing primer: SP6
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from stages 10-13
            gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with
            EcoRI at the 5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli XL1- blue.
FEATURES              Location/Qualifiers
     source           1. .433
                      /organism="Xenopus tropicalis"
                      /mol_type="mRNA"
                      /db_xref="taxon:8364"
                      /clone="TGas137b24"
                      /dev_stage="gastrula (stages 10.5-12 mixed)"
                      /lab_host="Escherichia coli XL1-blue"
```

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                     /clone_lib="XGC-gastrula"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from stages
                     10-13 gastrulae.  EcoRI-NotI cut cDNA was then ligated
                     into pCS107 with EcoRI at the 5' end and NotI at the 3'
                     end."
ORIGIN

  Query Match             3.4%;  Score 19;  DB 1;  Length 433;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        465 TTTTTATAAAACTAAAATC 483
              |||||||||||||||||||
Db        205 TTTTTATAAAACTAAAATC 187


RESULT 86
CN106169/c
LOCUS       CN106169                 433 bp    mRNA    linear   EST 31-MAR-2004
DEFINITION  EC2CAA29AC03.g1 Xenopus tropicalis xthr plasmid library Xenopus
            tropicalis cDNA clone xthr29E05 5', mRNA sequence.
ACCESSION   CN106169
VERSION     CN106169.1  GI:45898865
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 433)
  AUTHORS   Thuret,R., Fierro,A.C., Coen,L., Perron,M., Demeneix,B., Wegnez,M.,
            Gyapay,G., Weissenbach,J., Wincker,P., Mazabraud,A. and Pollet,N.
  TITLE     Exploring the nervous system transcriptome in the model Xenopus
            tropicalis using EST analysis
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Pollet N
            Transgenese et Genetique des Amphibiens
            CNRS UMR 8080
            IBAIC bat 447, Universite Paris Sud, Orsay, F-91405, France
            Tel: +33 169157272
            Fax: +33 169156816
            Email: Nicolas.Pollet@ibaic.u-psud.fr.
FEATURES             Location/Qualifiers
     source          1. .433
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /strain="Ivory Coast"
                     /db_xref="taxon:8364"
                     /clone="xthr29E05"
                     /tissue_type="pool of heads and retinas from tailbud
                     stages 25-35"
                     /dev_stage="stage 25-35"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Xenopus tropicalis xthr plasmid library"
                     /note="Vector: pCMVSPORT6_xthr; Site_1: SfiI; Site_2:
                     SfiI; Xenopus tropicalis polyA+ RNA was obtained from pool
                     of heads and retinas from tailbud stages 25-35 cDNAs were
                     synthesized using the SMART system of CLONTECH and
                     directionally cloned into pCMVSPORT6_xthr, a modified
                     version of pCMVSPORT6 allowing directional cloning using
                     asymetric SfiI sites. For antisense RNA synthesis, use T7
                     promoter and for sense RNA use SP6 promoter. Library
                     constructed by Drs. N. Pollet, M. Perron, M. Wegnez, A.
                     Mazabraud (CNRS UMR 8080, Universite Paris Sud, Orsay,
                     France)."
ORIGIN

  Query Match             3.4%;  Score 19;  DB 8;  Length 433;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        465 TTTTTATAAAACTAAAATC 483
              |||||||||||||||||||
Db        267 TTTTTATAAAACTAAAATC 249


RESULT 87
CK989220/c
LOCUS       CK989220                 434 bp    mRNA    linear   EST 19-MAR-2004
DEFINITION  BgHC-23.76 BgHC Biomphalaria glabrata cDNA 5', mRNA sequence.
ACCESSION   CK989220
VERSION     CK989220.1  GI:45596257
KEYWORDS    EST.
SOURCE      Biomphalaria glabrata
  ORGANISM  Biomphalaria glabrata
            Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata;
            Basommatophora; Lymnaeoidea; Planorbidae; Biomphalaria.
REFERENCE   1  (bases 1 to 434)
  AUTHORS   Mitta,G., Galinier,R., Tisseyre,P., Allienne,J.-F.,
            Girerd-Chambaz,Y., Guillou,F., Bouchut,A. and Coustau,C.
  TITLE     Gene discovery and expression analysis of immune-relevant genes
            from Biomphalaria glabrata hemocytes
  JOURNAL   Dev. Comp. Immunol. 29 (5), 393-407 (2005)
   PUBMED   15707661
COMMENT     Contact: Mitta Guillaume
            Parasitologie fonctionnelle et evolutive.
            CNRS / Univ. Perpignan
            52 Ave Paul Alduy, Universite, 66 860 Perpignan cedex, France
            Tel: 33 3 68 66 21 88
            Fax: 33 3 68 66 22 81
            Email: mitta@univ-perp.fr
            Seq primer: CGAAGTTATCTCGACG.
FEATURES             Location/Qualifiers
     source          1. .434
                     /organism="Biomphalaria glabrata"
                     /mol_type="mRNA"
                     /isolate="Bg.Bra strain"
                     /db_xref="taxon:6526"
                     /sex="hermaphrodite"
                     /cell_type="Circulating hemocytes"
                     /clone_lib="BgHC"
                     /note="Vector: pDNR-LIB; The library was designed with 500
                     ng of total RNA using the creator SMART cDNA library
                     construction kit (Clontech)."
ORIGIN

  Query Match             3.4%;  Score 19;  DB 8;  Length 434;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        177 CATGAATGAGAGTTGCCTG 195
              |||||||||||||||||||
Db        139 CATGAATGAGAGTTGCCTG 121


RESULT 88
AQ928052/c
LOCUS       AQ928052                 436 bp    DNA     linear   GSS 21-DEC-1999
DEFINITION  RPCI-23-258G4.TJ RPCI-23 Mus musculus genomic clone RPCI-23-258G4,
            genomic survey sequence.
ACCESSION   AQ928052
VERSION     AQ928052.1  GI:6617055
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 436)
  AUTHORS   Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,
            Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de
            Jong,P. and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-23
  JOURNAL   Unpublished (1999)
COMMENT     Other_GSSs: RPCI-23-258G4.TV
```

```
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-23. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
            or from Resea ch Genetics (info@resgen.com). BAC end page:
            http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 258  row: G  column: 4
            Seq primer: SP6
            Class: BAC ends.
FEATURES              Location/Qualifiers
     source           1. .436
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="RPCI-23-258G4"
                      /sex="Female"
                      /lab_host="DH10B"
                      /clone_lib="RPCI-23"
                      /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
                      EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
                      brain genomic DNA was isolated and  partially digested
                      with a combination of EcoRI and EcoRI Methylase.   Size
                      selected DNA was cloned into the pBACe3.6 vector at the
                      EcoRI  sites.  The ligation products were transformed into
                      DH10B  electrocompetent cells (BRL Life Technologies).   "
ORIGIN

  Query Match              3.4%;  Score 19;  DB 11;  Length 436;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        307 CAGGTGGAGTTCAAGGCCA 325
              ||||||||||||||||||||
Db         38 CAGGTGGAGTTCAAGGCCA 20


RESULT 89
CF940887
LOCUS       CF940887                439 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  NcESTqab73f07.y1 Nc-1 Tachyzoite cDNA Library 2 Neospora caninum
            cDNA 5', mRNA sequence.
ACCESSION   CF940887
VERSION     CF940887.1  GI:38441457
KEYWORDS    EST.
SOURCE      Neospora caninum
  ORGANISM  Neospora caninum
            Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
            Sarcocystidae; Neospora.
REFERENCE   1  (bases 1 to 439)
  AUTHORS   Cole,R., Fogarty,S., Tang,K., Howe,D.K., Sibley,L.D., Clifton,S.,
            Marra,M., Hillier,L., Pape,D., Martin,J., Wylie,T., Theising,B.,
            Bowers,Y., Gibbons,M., Ritter,E., Bennet,J., Ronko,I.,
            Tsagareishvili,R., Fedele,M., Belaygorod,L., Franklin,C.,
            Carr,L.M., Grow,A., Maguire,L., Wadkins,J., Richey,J., Waterston,R.
            and Wilson,R.
  TITLE     USDA-WashU Neospora EST Project
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Sandy Clifton, Ph.D. - Neospora
            USDA-WashU Neospora EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Contact David Sibley (toxoest@borcim.wustl.edu) for further
            information relating to organism, libraries, or clone availability.
            Putative full length read
            vector to vector length is
            Seq primer: -40RP from Gibco.
FEATURES              Location/Qualifiers
     source           1. .439
                      /organism="Neospora caninum"
                      /mol_type="mRNA"
                      /db_xref="taxon:29176"
                      /dev_stage="Tachyzoite"
                      /lab_host="GC10 Competent Cells(PGC)"
                      /clone_lib="Nc-1 Tachyzoite cDNA Library 2"
                      /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
                      XhoI; The cDNA library was constructed by Keliang Tang,
                      and Robert Cole at Washington University. cDNA was
                      synthesized from poly mRNA using an oligo-dT primer
                      containing a XhoI site. Following second strand synthesis,
                      EcoRI adapters were ligated to the cDNA, and products were
                      size-selected on sephacryl S500. The cDNA were
                      directionally cloned into the EcoRI/XhoI prepared
                      pBluescript II SK+ vector, and electroporated into GC10
                      Competent Cells(PGC). The library may contain a small
                      percentage of host or bacterial contaminants."
ORIGIN

  Query Match              3.4%;  Score 19;  DB 5;  Length 439;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        366 TCTGGATCAAAACATGCTG 384
              ||||||||||||||||||||
Db        226 TCTGGATCAAAACATGCTG 244


RESULT 90
CR441087/c
LOCUS       CR441087                442 bp    mRNA    linear   EST 19-JUN-2004
DEFINITION  CR441087 XGC-tailbud Xenopus tropicalis cDNA clone TTbA078g04 5',
            mRNA sequence.
ACCESSION   CR441087
VERSION     CR441087.1  GI:48966674
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 442)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Garrett,N. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (2004)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Croning MDR
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
             TROPICALIS_SEQUENCE_ID: TTbA078g04.p1kSP6
             This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Nigel Garrett.
            Seq primer: SP6.
FEATURES              Location/Qualifiers
     source           1. .442
                      /organism="Xenopus tropicalis"
                      /mol_type="mRNA"
                      /db_xref="taxon:8364"
                      /clone="TTbA078g04"
                      /dev_stage="tailbud (stage 28-30)"
                      /lab_host="Escherichia coli DH10B."
                      /clone_lib="XGC-tailbud"
                      /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                      was oligo dT primed from 5ug of poly A+ RNA from tailbud.
                      EcoRI-NotI cut cDNA was then ligated into pCS107 with
                      EcoRI at the 5' end and NotI at the 3' end."
```

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ORIGIN

  Query Match             3.4%;  Score 19;  DB 8;  Length 442;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        465 TTTTTATAAAACTAAAATC 483
              |||||||||||||||||||
Db        296 TTTTTATAAAACTAAAATC 278


RESULT 91
BH310495/c
LOCUS       BH310495                450 bp    DNA     linear   GSS 03-DEC-2001
DEFINITION  CH230-168D7.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
            CH230-168D7, genomic survey sequence.
ACCESSION   BH310495
VERSION     BH310495.1  GI:17236186
KEYWORDS    GSS.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 450)
  AUTHORS   Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
            Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D.,
            Riggs,F., de Jong,P. and Fraser,C.M.
  TITLE     Rat BAC End Sequences from Library CHORI-230 EcoRI segment
  JOURNAL   Unpublished (1999)
COMMENT     Other_GSSs: CH230-168D7.TJ
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the rat BAC library CHORI-230
            (http://www.chori.org/bacpac/rat230.htm). For BAC library
            availability, please contact Pieter de Jong (pdejong@mail.cho.org).
            Clones may be purchased from BACPAC Resources
            (http://www.chori.org/bacpac/or ering_information.htm). BAC end
            page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
            Plate: 168  row: D  column: 7
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .450
                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /strain="BN/SsNHsd/MCW"
                     /db_xref="taxon:10116"
                     /clone="CH230-168D7"
                     /sex="Female"
                     /cell_type="Brain"
                     /clone_lib="CHORI-230 Segment 1"
                     /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
                     CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
                     Pieter de Jong"
ORIGIN

  Query Match             3.4%;  Score 19;  DB 11;  Length 450;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        315 GTTCAAGGCCATGAATGCA 333
              |||||||||||||||||||
Db        164 GTTCAAGGCCATGAATGCA 146


RESULT 92
BX691929
LOCUS       BX691929                456 bp    mRNA    linear   EST 14-NOV-2003
DEFINITION  BX691929 XGC-neurula Xenopus tropicalis cDNA clone TNeu104p22 3',
            mRNA sequence.
ACCESSION   BX691929
VERSION     BX691929.1  GI:38341049
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Croning MDR
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TNeu104p22.q1kT7
            Sequencing primer: T7
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
            5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli DH10B.
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TNeu104p22"
                     /dev_stage="neurula"
                     /lab_host="Escherichia coli DH10B"
                     /clone_lib="XGC-neurula"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from neurula.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

  Query Match             3.4%;  Score 19;  DB 4;  Length 456;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        465 TTTTTATAAAACTAAAATC 483
              |||||||||||||||||||
Db        376 TTTTTATAAAACTAAAATC 394


RESULT 93
AQ583994
LOCUS       AQ583994                459 bp    DNA     linear   GSS 07-JUN-1999
DEFINITION  RPCI-11-451K12.TJ RPCI-11 Homo sapiens genomic clone
            RPCI-11-451K12, genomic survey sequence.
ACCESSION   AQ583994
VERSION     AQ583994.1  GI:5011104
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 459)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
            Venter,J.C.
  TITLE     Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Other_GSSs: RPCI-11-451K12.TV
```

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            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genet cs (info@resgen.com). BAC end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: SP6
            Class: BAC ends.
FEATURES              Location/Qualifiers
     source           1. .459
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="GDB:7673051"
                      /db_xref="taxon:9606"
                      /clone="RPCI-11-451K12"
                      /sex="Male"
                      /cell_type="Lymphocytes"
                      /clone_lib="RPCI-11"
                      /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                      RPCI11 Human Male BAC Library"
ORIGIN

  Query Match             3.4%;  Score 19;  DB 11;  Length 459;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        429 GACTGTGCCACAGAACTCC 447
              ||||||||||||||||||
Db        278 GACTGTGCCACAGAACTCC 296


RESULT 94
AL677765/c
LOCUS       AL677765                 465 bp    mRNA    linear   EST 10-NOV-2003
DEFINITION  AL677765 XGC-neurula Xenopus tropicalis cDNA clone TNeu059h04 5',
            mRNA sequence.
ACCESSION   AL677765
VERSION     AL677765.2  GI:38250638
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 465)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     On Mar 18, 2002 this sequence version replaced gi:19534139.
            Contact: Taylor R
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
            5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli DH10B
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TNeu059h04.p1cSP6
            Sequencing primer: SP6.
FEATURES              Location/Qualifiers
     source           1. .465
                      /organism="Xenopus tropicalis"
                      /mol_type="mRNA"
                      /db_xref="taxon:8364"
                      /clone="TNeu059h04"
                      /dev_stage="neurula"
                      /lab_host="Escherichia coli DH10B"
                      /clone_lib="XGC-neurula"
                      /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                      was oligo dT primed from 5ug of poly A+ RNA from neurula.
                      EcoRI-NotI cut cDNA was then ligated into pCS107 with
                      EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

  Query Match             3.4%;  Score 19;  DB 1;  Length 465;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        465 TTTTTATAAAACTAAAATC 483
              |||||||||||||||||||
Db        306 TTTTTATAAAACTAAAATC 288


RESULT 95
CJ319407
LOCUS       CJ319407                 466 bp    mRNA    linear   EST 28-SEP-2005
DEFINITION  CJ319407 RIKEN full-length enriched mouse cDNA library, Rathke's
            pouches 14.5 days embryo Mus musculus cDNA clone M230025A08 3',
            mRNA sequence.
ACCESSION   CJ319407
VERSION     CJ319407.1  GI:76543602
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 466)
  AUTHORS   The FANTOM Consortium and RIKEN Genome Exploration Research Group
            and Genome Science Group (Genome Network Project Core Group).
  TITLE     The transcriptional landscape of the mammalian genome
  JOURNAL   Science 309 (5740), 1559-1563 (2005)
   PUBMED   16141072
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. Tissues were provided by Michelle Brinkmeier
            and Sally Camper ( Dept. Human Genetics University of Michigan
            Medical School 4301 MSRB 3 1500 W. Medical Center Dr. Ann Arbor,MI
            48109-0638 USA ) whose assistance we gratefully acknowledge.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/.
FEATURES              Location/Qualifiers
     source           1. .466
                      /organism="Mus musculus"
                      /mol_type="mRNA"
                      /db_xref="taxon:10090"
                      /clone="M230025A08"
                      /tissue_type="Rathke's pouches"
                      /dev_stage="14.5 days embryo"
                      /clone_lib="RIKEN full-length enriched mouse cDNA library,
                      Rathke's pouches 14.5 days embryo"
ORIGIN

  Query Match             3.4%;  Score 19;  DB 5;  Length 466;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
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  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        307 CAGGTGGAGTTCAAGGCCA 325
              ||||||||||||||||||
Db        387 CAGGTGGAGTTCAAGGCCA 405


RESULT 96
BQ523107
LOCUS       BQ523107                 471 bp    mRNA    linear   EST 10-JUN-2002
DEFINITION  NISC_nl20d03.x1 NICHD_XGC_Emb7 Xenopus tropicalis cDNA clone
            IMAGE:5379125 3', mRNA sequence.
ACCESSION   BQ523107
VERSION     BQ523107.1  GI:21381976
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 471)
  AUTHORS   NIH-XCG http://image.llnl.gov/image/html/xenopuslib_info.shtml.
  TITLE     National Institute of Child Health and Human Development, National
            Cancer Insitute, Xenopus Gene Collection
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation:
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
             DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC)
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            info@image.llnl.gov
            Plate: LLAM11965  row: H  column: 6
            Seq primer: -21M13 forward primer (ABI).
FEATURES             Location/Qualifiers
     source          1. .471
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="IMAGE:5379125"
                     /tissue_type="tailbud"
                     /dev_stage="embryo, stages 20-27"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NICHD_XGC_Emb7"
                     /note="Vector: pCMV-SPORT6.1; Site_1: NotI; Site_2: EcoRV;
                     Cloned unidirectionally. Primer: Oligo dT. Average insert
                     size 2.1 kb. Constructed by Invitrogen. Note: This is a
                     Xenopus Gene Collection (XGC) library."
ORIGIN

  Query Match             3.4%;  Score 19;  DB 3;  Length 471;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        465 TTTTTATAAAACTAAAATC 483
              |||||||||||||||||||
Db        200 TTTTTATAAAACTAAAATC 218


RESULT 97
BG371292
LOCUS       BG371292                 472 bp    mRNA    linear   EST 09-MAR-2001
DEFINITION  dac43b03.x1 RIKEN Xenopus egg Xenopus laevis cDNA clone
            IMAGE:4432828 3' similar to SW:ES1_HUMAN P30042 ES1 PROTEIN HOMOLOG
            PRECURSOR ;, mRNA sequence.
ACCESSION   BG371292
VERSION     BG371292.1  GI:13267829
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Xenopus.
REFERENCE   1  (bases 1 to 472)
  AUTHORS   Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L.,
            Pape,D., Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y.,
            Person,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Xenopus EST project, 1999
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Sandy Clifton, Ph.D.
            WashU Xenopus EST project, 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Library constructed by Piero Carninci (RIKEN, Genome Science
            Laboratory, Japan: http://genome.rtc.riken.go.jp/) using egg RNA
            supplied by Marc Kirschner (Harvard Medical School, Dept. of Cell
            Biology) DNA Sequencing by: Washington University Genome Sequencing
            Center
             Clone distribution: Xenopus clones from this library are available
            through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
            Trace considered overall poor quality
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .472
                     /organism="Xenopus laevis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8355"
                     /clone="IMAGE:4432828"
                     /tissue_type="egg (unfertilized)"
                     /lab_host="DH10B"
                     /clone_lib="RIKEN Xenopus egg"
                     /note="Vector: pCS2G (custom); Site_1: BamHI; Site_2:
                     XhoI; cDNA oligo-dT primed using oligo
                     5'-GAGAGAGAGAGGATCCAATACTGGAGAGTTTTTTTTTTTTTTVN-3'  and
                     directionally cloned into XhoI and BamHI sites using the
                     5' adaptor
                     5'-AGAGAGAGAGCTCGAGCTCTAATAAGGTGACACTATAGAACCA-3'.  Size
                     selection was done automatically by the cloning vector
                     (lambda FLC-II,  P. Carninci et al., unpublished). Library
                     was amplified at the phage stage  and normalized (RoT
                     value = 5). This library was constructed using the
                     CapTrapper method and Trehalose thermoactivated reverse
                     transcriptase to  enrich for full-length clones. Library
                     constructed by Piero Carninci (RIKEN,  Genome Science
                     Laboratory, Japan: http://genome.rtc.riken.go.jp/) using
                     egg  RNA supplied by Marc Kirschner (Harvard Medical
                     School, Dept. of Cell  Biology). References: Methods
                     Enzymol.303:19-44 and Genome Res. 10:1617-1630  Please
                     contact Marc Kirschner (marc@hms.harvard.edu) for
                     information on  obtaining aliquots of this cDNA library."
ORIGIN

  Query Match             3.4%;  Score 19;  DB 2;  Length 472;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         21 CCACTCCCAAACCCTGCTG 39
              |||||||||||||||||||
Db        376 CCACTCCCAAACCCTGCTG 394


RESULT 98
CV865967
LOCUS       CV865967                 474 bp    mRNA    linear   EST 31-DEC-2005
DEFINITION  PDUts1024D12 Porcine testis cDNA library I Sus scrofa cDNA clone
            PDUts1024D12 5' similar to homologue to ref|NM_014663.1| Homo
            sapiens jumonji domain containing 2A (JMJD2A), mRNA, mRNA sequence.
ACCESSION   CV865967
VERSION     CV865967.1  GI:84119927
```

```
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 474)
  AUTHORS   Lee,W.C., Lin,E.-C., Huang,M.C., Chiou,S.H., Sun,H.S., Huang,S.Y.,
            Chuang,C.K., Chen,M.Y., Liu,M.L., Hsu,M.C., Yang,K.T., Fan,Y.H.,
            Lin,J.H., Liu,C.C., Huang,C.H., Chen,Y.C. and Lin,D.T.
  TITLE     Porcine testis EST project
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Wen-Chuan Lee
            Division of Biotechnology
            Animal Technology Institute Taiwan
            P.O.BOX 23, Chunan 35099, Miaoli, Taiwan, R.O.C.
            Tel: 886 37 585833
            Fax: 886 37 585829
            Email: wen-chuan@mail.atit.org.tw
            The EST project for testis from Duroc was granted by Council of
            Agriculture, Taiwan. Material with normal function was tested by
            Divisions of Biotechnology and Animal Resources, Animal Technology
            Institute Taiwan (ATIT). Library was constructed and EST clones
            were sequenced by Institutes of Veterinary Microbiology and Animal
            Production, National Chung-Hsing University. Bioinformatic work was
            conducted by a network from ATIT, National Cheng-Kung University,
            and Chung-Hua University. The sequences were stored in a database
            'Tropical Pig Bioinformatic Center'. Bases called and all trimmed
            with phred v0.020425.c. Vector identified and masked by
            cross_match. Sequences were cleaned of vector, adaptors and
            repetitions.
            Plate: 24  row: D  column: 12
            Seq primer: T7 promoter primer
            High quality sequence stop: 474
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .474
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /strain="Duroc"
                     /db_xref="taxon:9823"
                     /clone="PDUts1024D12"
                     /sex="male"
                     /dev_stage="adult, 1 year of age"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="Porcine testis cDNA library I"
                     /note="Organ: testis; Vector: pSPORT1; Site_1: NotI;
                     Site_2: SalI; Material with normal function was tested by
                     Divisions of Biotechnology and Animal Resources, Animal
                     Technology Institute Taiwan (ATIT). First strand cDNA was
                     primed with a NotI-oligo(dT) primer and 2nd strand cDNA
                     was synthesized by using nick translational replacement of
                     the mRNA. Double-strand cDNA was added with SalI adapter,
                     then digested with NotI and cloned into the NotI and SalI
                     sites of pSPORT1 vector."
ORIGIN

  Query Match             3.4%;  Score 19;  DB 8;  Length 474;
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Qy        299 AGATGTACCAGGTGGAGTT 317
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Db        234 AGATGTACCAGGTGGAGTT 252


RESULT 99
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DEFINITION  mi37e03.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA
            clone IMAGE:465724 5', mRNA sequence.
ACCESSION   AA032893
VERSION     AA032893.1  GI:1504286
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 475)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:279540
            Seq primer: -28M13 rev2 from Amersham
            High quality sequence stop: 465.
FEATURES             Location/Qualifiers
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                     /tissue_type="embryo"
                     /dev_stage="13.5-14.5dpc total fetus"
                     /lab_host="DH10B"
                     /clone_lib="Soares mouse embryo NbME13.5 14.5"
                     /note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI;
                     1st strand cDNA was primed with a Not I - oligo(dT) primer
                     [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGGAAATTTTTTTTTTTTTTTTTTTTTTT
                     T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
                     14.5dpc embryos [total RNA provided by  Minoru Ko, Wayne
                     State Univ., from 2 ]; double-stranded cDNA was ligated to
                     Eco RI adaptors (Pharmacia), digested with Not I and
                     cloned into the Not I and Eco RI sites of the modified
                     pT7T3 vector. Library went through one round of
                     normalization, and was constructed by Bento Soares and
                     M.Fatima Bonaldo.  "
ORIGIN

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  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        299 AGATGTACCAGGTGGAGTT 317
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RESULT 100
BX684618
LOCUS       BX684618                477 bp    mRNA    linear   EST 14-NOV-2003
DEFINITION  BX684618 XGC-neurula Xenopus tropicalis cDNA clone TNeu061h07 3',
            mRNA sequence.
ACCESSION   BX684618
VERSION     BX684618.1  GI:38333738
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
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            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 477)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Croning MDR
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TNeu061h07.q1kT7
            Sequencing primer: T7
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
            5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli DH10B.
FEATURES             Location/Qualifiers
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                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from neurula.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

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  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        465 TTTTTATAAAACTAAAATC 483
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Db        181 TTTTTATAAAACTAAAATC 199


Search completed: June 10, 2006, 14:53:58
Job time : 3439.62 secs
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2006, 22:44:33 ; Search time 127.538 Seconds
(without alignments)
8230.433 Million cell updates/sec

Title: US-10-821-670A-101
Perfect score: 561
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1403666 seqs, 935554401 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2806514

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 200 summaries

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	3	558	99.5	666	3	US-09-917-265A-32	Sequence 32, Appl
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	5	510	90.9	1533	3	US-09-917-265A-43	Sequence 43, Appl
c	6	510	90.9	1533	3	US-09-917-265A-45	Sequence 45, Appl
	7	510	90.9	1599	3	US-09-917-265A-38	Sequence 38, Appl
c	8	510	90.9	1599	3	US-09-917-265A-40	Sequence 40, Appl
	9	507	90.4	591	3	US-09-917-265A-35	Sequence 35, Appl
c	10	507	90.4	591	3	US-09-917-265A-37	Sequence 37, Appl
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	12	494	88.1	591	3	US-09-302-495-9	Sequence 9, Appli
	13	494	88.1	591	3	US-10-079-616-9	Sequence 9, Appli
	14	494	88.1	1441	3	US-09-011-143-8	Sequence 8, Appli
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	25	81	14.4	669	3	US-09-079-984A-12	Sequence 12, Appl
	26	81	14.4	669	3	US-09-390-729-2	Sequence 2, Appli
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	48	65	11.6	1026	3	US-09-023-655-1041	Sequence 1041, Ap
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	75	27	4.8	2013	3	US-09-634-368-11	Sequence 11, Appl
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c	91	20	3.6	20	3	US-09-851-520-31	Sequence 31, Appl
c	92	20	3.6	20	3	US-09-851-520-39	Sequence 39, Appl
c	93	20	3.6	20	3	US-09-851-520-40	Sequence 40, Appl
c	94	20	3.6	20	3	US-09-851-520-41	Sequence 41, Appl
c	95	20	3.6	20	3	US-09-851-520-42	Sequence 42, Appl
c	96	20	3.6	20	3	US-09-851-520-45	Sequence 45, Appl

c 97	20	3.6	20	3	US-09-851-520-57	Sequence 57, Appl
c 98	20	3.6	20	3	US-09-851-520-58	Sequence 58, Appl
c 99	19	3.4	20	3	US-09-851-520-59	Sequence 59, Appl
c 100	19	3.4	39	2	US-08-184-009-198	Sequence 198, App
c 101	19	3.4	39	2	US-08-458-356-198	Sequence 198, App
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c 103	19	3.4	39	3	US-09-079-984A-10	Sequence 10, Appl
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c 116	18	3.2	18	4	US-09-341-700A-1646	Sequence 1646, Ap
c 117	18	3.2	18	4	US-09-341-700A-1647	Sequence 1647, Ap
c 118	18	3.2	18	4	US-09-341-700A-1652	Sequence 1652, Ap
c 119	18	3.2	22	3	US-09-917-265A-94	Sequence 94, Appl
c 120	18	3.2	409	3	US-09-189-060B-13	Sequence 13, Appl
121	18	3.2	415	3	US-09-189-060B-15	Sequence 15, Appl
122	18	3.2	495	3	US-09-328-352-1301	Sequence 1301, Ap
c 123	18	3.2	1095	3	US-09-248-796A-894	Sequence 894, App
124	18	3.2	2925	4	US-10-094-749-256	Sequence 256, App
125	18	3.2	3327	4	US-09-880-107-3432	Sequence 3432, Ap
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c 133	17	3.0	29	3	US-09-826-025-20	Sequence 20, Appl
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161	17	3.0	601	3	US-09-949-016-116083	Sequence 116083,
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c 170	17	3.0	624	3	US-10-120-988-351	Sequence 351, App
171	17	3.0	645	3	US-09-248-796A-13889	Sequence 13889, A
172	17	3.0	666	3	US-09-949-016-4938	Sequence 4938, Ap
173	17	3.0	666	4	US-09-880-107-3375	Sequence 3375, Ap
174	17	3.0	696	3	US-09-107-532A-2085	Sequence 2085, Ap
c 175	17	3.0	826	2	US-08-631-200-10	Sequence 10, Appl
c 176	17	3.0	826	2	US-08-829-553-10	Sequence 10, Appl
c 177	17	3.0	826	2	US-08-922-267A-10	Sequence 10, Appl
c 178	17	3.0	826	2	US-08-936-707A-10	Sequence 10, Appl
c 179	17	3.0	826	2	US-08-936-706A-10	Sequence 10, Appl
c 180	17	3.0	826	3	US-09-248-203-10	Sequence 10, Appl
c 181	17	3.0	826	3	US-09-406-071-10	Sequence 10, Appl
c 182	17	3.0	826	3	US-09-814-986-10	Sequence 10, Appl
c 183	17	3.0	1097	3	US-09-976-594-115	Sequence 115, App
184	17	3.0	1176	3	US-09-543-681A-4120	Sequence 4120, Ap
c 185	17	3.0	1500	3	US-09-134-000C-3021	Sequence 3021, Ap
186	17	3.0	1617	2	US-08-467-963C-25	Sequence 25, Appl
187	17	3.0	1617	2	US-08-838-189D-25	Sequence 25, Appl
188	17	3.0	1617	3	US-08-852-344D-25	Sequence 25, Appl
189	17	3.0	1617	3	US-08-344-639E-25	Sequence 25, Appl
c 190	17	3.0	1770	3	US-09-540-236-1478	Sequence 1478, Ap
191	17	3.0	1844	2	US-08-467-963C-1	Sequence 1, Appli
192	17	3.0	1844	2	US-08-838-189D-1	Sequence 1, Appli
193	17	3.0	1844	3	US-08-852-344D-1	Sequence 1, Appli
194	17	3.0	1844	3	US-08-344-639E-1	Sequence 1, Appli
195	17	3.0	1844	3	US-08-467-969A-1	Sequence 1, Appli
196	17	3.0	1844	3	US-08-467-961A-1	Sequence 1, Appli
197	17	3.0	1844	3	US-08-001-554A-1	Sequence 1, Appli
198	17	3.0	2845	3	US-10-104-047-292	Sequence 292, App
c 199	17	3.0	3312	3	US-09-669-751-259	Sequence 259, App
200	17	3.0	11026	3	US-09-949-016-16680	Sequence 16680, A

ALIGNMENTS

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RESULT 1
US-09-917-265A-101
; Sequence 101, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 101
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(561)
US-09-917-265A-101

  Query Match             100.0%;  Score 561;  DB 3;  Length 561;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-277;
  Matches  561;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
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Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db        541 ATGAGCTATCTGAATGCTTCC 561
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RESULT 2
US-09-917-265A-103/c
; Sequence 103, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 103
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265A-103

Query Match 100.0%; Score 561; DB 3; Length 561;
Best Local Similarity 100.0%; Pred. No. 1.5e-277;
Matches 561; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1
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RESULT 3
US-09-917-265A-32
; Sequence 32, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(666)
US-09-917-265A-32

Query Match 99.5%; Score 558; DB 3; Length 666;
Best Local Similarity 100.0%; Pred. No. 5.3e-276;
Matches 558; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648

Qy        544 AGCTATCTGAATGCTTCC 561
                |||||||||||||||||
Db        649 AGCTATCTGAATGCTTCC 666
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RESULT 4
US-09-917-265A-34/c
; Sequence 34, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265A-34

Query Match 99.5%; Score 558; DB 3; Length 666;
Best Local Similarity 100.0%; Pred. No. 5.3e-276;
Matches 558; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        544 AGCTATCTGAATGCTTCC 561
                |||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1
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RESULT 5
US-09-917-265A-43
; Sequence 43, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)
US-09-917-265A-43

Query Match 90.9%; Score 510; DB 3; Length 1533;
Best Local Similarity 99.8%; Pred. No. 2.2e-251;
Matches 560; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1032

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1092

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1093 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1152

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1153 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1212

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1213 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1272

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1273 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1332

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1333 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1392

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1393 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1452

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1453 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1512

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db       1513 ATGAGCTATCTGAATGCTTCC 1533
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RESULT 6
US-09-917-265A-45/c
; Sequence 45, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265A-45

Query Match 90.9%; Score 510; DB 3; Length 1533;
Best Local Similarity 99.8%; Pred. No. 2.2e-251;
Matches 560; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82
```

```
Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1
```

RESULT 7
US-09-917-265A-38
; Sequence 38, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1599)
US-09-917-265A-38

Query Match 90.9%; Score 510; DB 3; Length 1599;
Best Local Similarity 99.8%; Pred. No. 2.2e-251;
Matches 560; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1098

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1158

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1218

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1219 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1278

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1338

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1398

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1458

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1459 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1518

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1519 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1578
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```
Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db       1579 ATGAGCTATCTGAATGCTTCC 1599
```

RESULT 8
US-09-917-265A-40/c
; Sequence 40, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265A-40

Query Match 90.9%; Score 510; DB 3; Length 1599;
Best Local Similarity 99.8%; Pred. No. 2.2e-251;
Matches 560; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              ||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1
```

RESULT 9
US-09-917-265A-35
; Sequence 35, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(591)
US-09-917-265A-35

Query Match 90.4%; Score 507; DB 3; Length 591;
Best Local Similarity 99.8%; Pred. No. 7.5e-250;
Matches 557; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573

Qy        544 AGCTATCTGAATGCTTCC 561
              ||||||||||||||||||
Db        574 AGCTATCTGAATGCTTCC 591
```

RESULT 10
US-09-917-265A-37/c
; Sequence 37, Application US/09917265A

```
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-37

  Query Match             90.4%;  Score 507;  DB 3;  Length 591;
  Best Local Similarity   99.8%;  Pred. No. 7.5e-250;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        544 AGCTATCTGAATGCTTCC 561
              |||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1


RESULT 11
US-09-011-143-9
; Sequence 9, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  591 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-9

  Query Match             88.1%;  Score 494;  DB 3;  Length 591;
  Best Local Similarity   99.8%;  Pred. No. 3.5e-243;
  Matches  544;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
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Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        454 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATC 513

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573

Qy        544 AGCTA 548
              |||||
Db        574 AGCTA 578


RESULT 12
US-09-302-495-9
; Sequence 9, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 591 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-302-495-9

  Query Match             88.1%;  Score 494;  DB 3;  Length 591;
  Best Local Similarity   99.8%;  Pred. No. 3.5e-243;
  Matches  544;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
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Db         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        454 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATC 513

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573

Qy        544 AGCTA 548
              |||||
Db        574 AGCTA 578


RESULT 13
US-10-079-616-9
; Sequence 9, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
```

```
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 591 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-079-616-9

  Query Match             88.1%;  Score 494;  DB 3;  Length 591;
  Best Local Similarity   99.8%;  Pred. No. 3.5e-243;
  Matches  544;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
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Db        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
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Db        454 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATC 513

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573

Qy        544 AGCTA 548
              |||||
Db        574 AGCTA 578


RESULT 14
US-09-011-143-8
; Sequence 8, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1441 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-8

  Query Match             88.1%;  Score 494;  DB 3;  Length 1441;
  Best Local Similarity   99.8%;  Pred. No. 3.5e-243;
  Matches  544;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 310

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 370

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 430

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 490

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 550

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        551 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 610

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
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Db        611 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 670

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
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Db        671 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATC 730
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Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
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Db        731 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 790

Qy        544 AGCTA 548
              |||||
Db        791 AGCTA 795


RESULT 15
US-09-302-495-8
; Sequence 8, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1441 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-302-495-8

  Query Match             88.1%;  Score 494;  DB 3;  Length 1441;
  Best Local Similarity   99.8%;  Pred. No. 3.5e-243;
  Matches  544;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 310

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 370

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 430

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 490

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 550

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
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Db        551 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 610

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 670

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
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Db        671 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATC 730

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
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Db        731 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 790

Qy        544 AGCTA 548
              |||||
Db        791 AGCTA 795


RESULT 16
US-10-079-616-8
; Sequence 8, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
```

```
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;    INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1441 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-079-616-8

  Query Match             88.1%;  Score 494;  DB 3;  Length 1441;
  Best Local Similarity   99.8%;  Pred. No. 3.5e-243;
  Matches  544;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 310

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 370

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 430

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 490

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 550

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        551 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 610

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 670

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
              ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        671 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATC 730

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        731 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 790

Qy        544 AGCTA 548
              |||||
Db        791 AGCTA 795


RESULT 17
US-09-011-143-26
; Sequence 26, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  26:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  689 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-26

  Query Match             39.4%;  Score 221;  DB 3;  Length 689;
  Best Local Similarity   99.2%;  Pred. No. 3.3e-103;
  Matches  371;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        175 ACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGC 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 ACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGC 345

Qy        235 CTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGAC 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 CTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGAC 405

Qy        295 TTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAA 354
              |||||||||||||||||||||||||||||||||||||||||||||| | ||||||||||||
Db        406 TTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAA 465

Qy        355 AGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTG 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 AGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTG 525

Qy        415 AATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAA 474
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        526 AATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAA 585

Qy        475 ACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAAT 534
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAAT 645

Qy        535 AGAATGATGAGCTA 548
              ||||||||||||||
Db        646 AGAATGATGAGCTA 659


RESULT 18
US-09-302-495-26
; Sequence 26, Application US/09302495
; Patent No. 6518045
;  GENERAL INFORMATION:
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;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/302,495
;            FILING DATE: 30-Apr-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 26:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 689 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-302-495-26

  Query Match            39.4%;  Score 221;  DB 3;  Length 689;
  Best Local Similarity   99.2%;  Pred. No. 3.3e-103;
  Matches  371;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        175 ACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGC 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 ACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGC 345

Qy        235 CTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGAC 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 CTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGAC 405

Qy        295 TTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAA 354
              |||||||||||||||||||||||||||||||||||||||||||| | ||||||||||||
Db        406 TTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAA 465

Qy        355 AGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTG 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 AGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTG 525

Qy        415 AATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAA 474
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        526 AATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAA 585

Qy        475 ACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAAT 534
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAAT 645

Qy        535 AGAATGATGAGCTA 548
              ||||||||||||||
Db        646 AGAATGATGAGCTA 659


RESULT 19
US-10-079-616-26
; Sequence 26, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 26:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 689 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-079-616-26

  Query Match            39.4%;  Score 221;  DB 3;  Length 689;
  Best Local Similarity   99.2%;  Pred. No. 3.3e-103;
  Matches  371;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        175 ACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGC 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 ACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGC 345

Qy        235 CTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGAC 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 CTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGAC 405

Qy        295 TTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAA 354
              |||||||||||||||||||||||||||||||||||||||||||| | ||||||||||||
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Db        406 TTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAA 465

Qy        355 AGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTG 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 AGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTG 525

Qy        415 AATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAA 474
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        526 AATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAA 585

Qy        475 ACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAAT 534
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAAT 645

Qy        535 AGAATGATGAGCTA 548
              ||||||||||||||
Db        646 AGAATGATGAGCTA 659


RESULT 20
US-09-917-265A-49
; Sequence 49, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(591)
US-09-917-265A-49

  Query Match             14.4%;  Score 81;  DB 3;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 2e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        223 CTGGCTTCCAGAGAGATCTCT 243


RESULT 21
US-09-917-265A-51/c
; Sequence 51, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-51

  Query Match             14.4%;  Score 81;  DB 3;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 2e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 22
US-09-917-265A-46
; Sequence 46, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
US-09-917-265A-46

  Query Match             14.4%;  Score 81;  DB 3;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 2e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 23
US-09-917-265A-48/c
; Sequence 48, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
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; SEQ ID NO 48
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-48

  Query Match             14.4%;  Score 81;  DB 3;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 2e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 24
US-09-079-984A-2
; Sequence 2, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,984A
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  669 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 666
;      IDENTIFICATION METHOD:  Similarity
US-09-079-984A-2

  Query Match             14.4%;  Score 81;  DB 3;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 2e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 25
US-09-079-984A-12
; Sequence 12, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,984A
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  669 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 666
;      IDENTIFICATION METHOD:  Similarity
US-09-079-984A-12

  Query Match             14.4%;  Score 81;  DB 3;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 2e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 26
US-09-390-729-2
; Sequence 2, Application US/09390729
```

```
; Patent No. 6562334
; GENERAL INFORMATION:
;   APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;   APPLICANT:  Yamada, Katsushige
;   TITLE OF INVENTION:  Canine interleukin 12, a production method
;   TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;   TITLE OF INVENTION:  method using it
;   NUMBER OF SEQUENCES:  16
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Miller & Christenbury Intellectual Property
;     ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;     STREET:  1600 Market Street, 39th Floor
;     CITY:  Philadelphia
;     STATE:  PA
;     COUNTRY:  USA
;     ZIP:  19103
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy Disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  WordPerfect 5.1
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/390,729
;     FILING DATE:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  09/079,984
;     FILING DATE:  15-MAY-1998
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Austin R. Miller
;     REGISTRATION NUMBER:  16,602
;     REFERENCE/DOCKET NUMBER:  1051-98
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (215) 563-1810
;     TELEFAX:  (215) 568-6946
; INFORMATION FOR SEQ ID NO:  2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  669 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  double
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  cDNA to mRNA
;   ORIGINAL SOURCE:
;     ORGANISM:  Canis familiaris
;   FEATURE:
;     NAME/KEY:  Canine IL12
;     LOCATION:  1 to 666
;     IDENTIFICATION METHOD:  Similarity
US-09-390-729-2

  Query Match             14.4%;  Score 81;  DB 3;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 2e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 27
US-09-390-729-12
; Sequence 12, Application US/09390729
; Patent No. 6562334
; GENERAL INFORMATION:
;   APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;   APPLICANT:  Yamada, Katsushige
;   TITLE OF INVENTION:  Canine interleukin 12, a production method
;   TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;   TITLE OF INVENTION:  method using it
;   NUMBER OF SEQUENCES:  16
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Miller & Christenbury Intellectual Property
;     ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;     STREET:  1600 Market Street, 39th Floor
;     CITY:  Philadelphia
;     STATE:  PA
;     COUNTRY:  USA
;     ZIP:  19103
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy Disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  WordPerfect 5.1
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/390,729
;     FILING DATE:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  09/079,984
;     FILING DATE:  15-MAY-1998
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Austin R. Miller
;     REGISTRATION NUMBER:  16,602
;     REFERENCE/DOCKET NUMBER:  1051-98
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (215) 563-1810
;     TELEFAX:  (215) 568-6946
; INFORMATION FOR SEQ ID NO:  12:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  669 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  double
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  cDNA to mRNA
;   ORIGINAL SOURCE:
;     ORGANISM:  Canis familiaris
;   FEATURE:
;     NAME/KEY:  Canine IL12
;     LOCATION:  1 to 666
;     IDENTIFICATION METHOD:  Similarity
US-09-390-729-12

  Query Match             14.4%;  Score 81;  DB 3;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 2e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 28
US-09-917-265A-104
; Sequence 104, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 104
;   LENGTH: 1455
;   TYPE: DNA
```

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;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (232)..(897)
US-09-917-265A-104

  Query Match             14.4%;  Score 81;  DB 3;  Length 1455;
  Best Local Similarity   100.0%;  Pred. No. 2e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 528

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        529 CTGGCTTCCAGAGAGATCTCT 549


RESULT 29
US-09-917-265A-106/c
; Sequence 106, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 106
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-106

  Query Match             14.4%;  Score 81;  DB 3;  Length 1455;
  Best Local Similarity   100.0%;  Pred. No. 2e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 928

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        927 CTGGCTTCCAGAGAGATCTCT 907


RESULT 30
US-09-917-265A-66
; Sequence 66, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-09-917-265A-66

  Query Match             14.4%;  Score 81;  DB 3;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 2e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1105 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1164

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db       1165 CTGGCTTCCAGAGAGATCTCT 1185


RESULT 31
US-09-917-265A-68/c
; Sequence 68, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-68

  Query Match             14.4%;  Score 81;  DB 3;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 2e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 32
US-09-917-265A-61
; Sequence 61, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
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;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-09-917-265A-61

  Query Match            14.4%;  Score 81;  DB 3;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 2e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1230

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db       1231 CTGGCTTCCAGAGAGATCTCT 1251


RESULT 33
US-09-917-265A-63/c
; Sequence 63, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-63

  Query Match            14.4%;  Score 81;  DB 3;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 2e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 34
US-09-949-016-20385
; Sequence 20385, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20385
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-20385

  Query Match            11.6%;  Score 65;  DB 3;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 159

Qy        514 ATTCG 518
              |||||
Db        160 ATTCG 164


RESULT 35
US-09-949-016-87352
; Sequence 87352, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 87352
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-87352

  Query Match            11.6%;  Score 65;  DB 3;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 159

Qy        514 ATTCG 518
              |||||
Db        160 ATTCG 164


RESULT 36
US-08-186-529-3
; Sequence 3, Application US/08186529
; Patent No. 5573764
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
```

```
;       ZIP:  02140
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/186,529
;       FILING DATE:
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  McDaniels, Patricia A.
;       REGISTRATION NUMBER:  33,194
;       REFERENCE/DOCKET NUMBER:  GI 5225
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-498-8401
;       TELEFAX:  617-876-5851
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  660 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     ORIGINAL SOURCE:
;       ORGANISM:  Homo sapiens
;       CELL TYPE:  Lymphoblast
;       CELL LINE:  RPMI 8866
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..660
US-08-186-529-3

  Query Match             11.6%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        514 ATTCG 518
              |||||
Db        610 ATTCG 614


RESULT 37
US-08-640-386A-3
; Sequence 3, Application US/08640386A
; Patent No. 5756085
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/640,386A
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;      REFERENCE/DOCKET NUMBER:  GI 5225A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8224
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  660 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Lymphoblast
;      CELL LINE:  RPMI 8866
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..660
US-08-640-386A-3

  Query Match             11.6%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        514 ATTCG 518
              |||||
Db        610 ATTCG 614


RESULT 38
US-08-184-009-199
; Sequence 199, Application US/08184009
; Patent No. 5833975
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/184,009
;      FILING DATE:  19-JAN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  199:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  721 base pairs
;      TYPE:  nucleic acid
```

```
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-184-009-199

  Query Match             11.6%;  Score 65;  DB 2;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy        514 ATTCG 518
              |||||
Db        671 ATTCG 675


RESULT 39
US-08-458-356-199
; Sequence 199, Application US/08458356
; Patent No. 5942235
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,356
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  199:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  721 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-458-356-199

  Query Match             11.6%;  Score 65;  DB 2;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy        514 ATTCG 518
              |||||
Db        671 ATTCG 675


RESULT 40
US-08-460-736-199
; Sequence 199, Application US/08460736
; Patent No. 6265189
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,736
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  199:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  721 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-460-736-199

  Query Match             11.6%;  Score 65;  DB 3;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy        514 ATTCG 518
              |||||
Db        671 ATTCG 675


RESULT 41
US-09-535-370-199
; Sequence 199, Application US/09535370
; Patent No. 6537594
;   GENERAL INFORMATION:
;       APPLICANT: Paoletti, Enzo
;                  Tartaglia, James
;                  Cox, William I.
;       TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
;       NUMBER OF SEQUENCES: 217
```

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;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Curtis, Morris & Safford
;             STREET: 530 Fifth Avenue
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10036
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/535,370
;             FILING DATE: 24-Mar-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/460,736
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Frommer, William S.
;             REGISTRATION NUMBER: 25,506
;             REFERENCE/DOCKET NUMBER: 454310-2530
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 840-3333
;             TELEFAX: (212) 840-0712
;             TELEX: 425066CURTMS
;   INFORMATION FOR SEQ ID NO: 199:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 721 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 199:
US-09-535-370-199

  Query Match             11.6%;  Score 65;  DB 3;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy        514 ATTCG 518
              |||||
Db        671 ATTCG 675


RESULT 42
US-09-663-667-199
; Sequence 199, Application US/09663667
; Patent No. 6780407
;   GENERAL INFORMATION:
;        APPLICANT: Paoletti, Enzo
;                   Tartaglia, James
;                   Cox, William I.
;        TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
;        NUMBER OF SEQUENCES: 217
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Curtis, Morris & Safford
;             STREET: 530 Fifth Avenue
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10036
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/663,667
;             FILING DATE: 15-Sep-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/184,009
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Frommer, William S.
;             REGISTRATION NUMBER: 25,506
;             REFERENCE/DOCKET NUMBER: 454310-2530
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 840-3333
;             TELEFAX: (212) 840-0712
;             TELEX: 425066CURTMS
;   INFORMATION FOR SEQ ID NO: 199:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 721 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 199:
US-09-663-667-199

  Query Match             11.6%;  Score 65;  DB 3;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy        514 ATTCG 518
              |||||
Db        671 ATTCG 675


RESULT 43
US-08-848-760B-21
; Sequence 21, Application US/08848760B
; Patent No. 6248721
;   GENERAL INFORMATION:
;        APPLICANT: Chang, Lung-Ji
;        TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
;        NUMBER OF SEQUENCES: 33
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
;             STREET: 2421 N.W. 41st Street, Suite A-1
;             CITY: Gainesville
;             STATE: Florida
;             COUNTRY: United States of America
;             ZIP: 32606
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/848,760B
;             FILING DATE: 25-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/838,702
;             FILING DATE: 09-APR-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: PACE, DORAN R.
;             REGISTRATION NUMBER: 38,261
;             REFERENCE/DOCKET NUMBER: CNG-100C1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (352) 375-8100
;             TELEFAX: (352) 372-5800
;   INFORMATION FOR SEQ ID NO: 21:
;        SEQUENCE CHARACTERISTICS:
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;             LENGTH: 762 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: other nucleic acid
;             DESCRIPTION: /desc = "DNA"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-08-848-760B-21

  Query Match            11.6%;  Score 65;  DB 3;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        514 ATTCG 518
              |||||
Db        712 ATTCG 716


RESULT 44
US-09-826-025-21
; Sequence 21, Application US/09826025
; Patent No. 6730512
;  GENERAL INFORMATION:
;       APPLICANT: Chang, Lung-Ji
;       TITLE OF INVENTION: Combination Immunogene Therapy
;       NUMBER OF SEQUENCES: 25
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Medlen & Carroll, LLP
;            STREET: 220 Montgomery Street, Suite 2200
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: United States of America
;            ZIP: 94104
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/826,025
;            FILING DATE: 04-Apr-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/838,702
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Ingolia, Diane E.
;            REGISTRATION NUMBER: 40,027
;            REFERENCE/DOCKET NUMBER: CHANG-02687
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 705-8410
;            TELEFAX: (415) 397-8338
;  INFORMATION FOR SEQ ID NO: 21:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 762 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: other nucleic acid
;            DESCRIPTION: /desc = "DNA"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-826-025-21

  Query Match            11.6%;  Score 65;  DB 3;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        514 ATTCG 518
              |||||
Db        712 ATTCG 716


RESULT 45
US-09-543-679A-2890
; Sequence 2890, Application US/09543679A
; Patent No. 7034007
;  GENERAL INFORMATION:
;       APPLICANT: NYCE, Jonathan W.
;       TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                           COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                           OF AIRWAY DISORDERS ASSOCIATED WITH
;                           BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;       NUMBER OF SEQUENCES: 3111
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;            STREET: 7 Clarke Drive
;            CITY: Cranbury
;            STATE: NJ
;            COUNTRY: USA
;            ZIP: 08512
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD-R
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: N/A
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/543,679A
;            FILING DATE: 13-Apr-2000
;            CLASSIFICATION: UNKNOWN
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/127,958
;            FILING DATE: 1998-08-03
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Amzel, Viviana
;            REGISTRATION NUMBER: 30,930
;            REFERENCE/DOCKET NUMBER: EPI-0067191b
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 609-409-3035
;            TELEFAX: 413-254-9245
;            TELEX: <Unknown>
;  INFORMATION FOR SEQ ID NO: 2890:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 762 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2890:
US-09-543-679A-2890

  Query Match            11.6%;  Score 65;  DB 5;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        514 ATTCG 518
              |||||
Db        712 ATTCG 716


RESULT 46
US-09-949-016-2462
; Sequence 2462, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
```

```
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2462
;   LENGTH: 1019
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-2462

  Query Match             11.6%;  Score 65;  DB 3;  Length 1019;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        712 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 771

Qy        514 ATTCG 518
              |||||
Db        772 ATTCG 776


RESULT 47
US-08-751-767A-1
; Sequence 1, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1026 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  170..826
US-08-751-767A-1

  Query Match             11.6%;  Score 65;  DB 2;  Length 1026;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 778

Qy        514 ATTCG 518
              |||||
Db        779 ATTCG 783


RESULT 48
US-09-023-655-1041
; Sequence 1041, Application US/09023655
; Patent No. 6607879
;  GENERAL INFORMATION:
;    APPLICANT:  Cocks, Benjamin G.
;    APPLICANT:  Susan G. Stuart
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1508
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/023,655
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0001 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  1041:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1026 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GENBANK
;      CLONE:  g180623
US-09-023-655-1041

  Query Match             11.6%;  Score 65;  DB 3;  Length 1026;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 778
```

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Qy        514 ATTCG 518
              |||||
Db        779 ATTCG 783


RESULT 49
US-09-949-016-130
; Sequence 130, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 130
;   LENGTH: 1026
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-130

  Query Match             11.6%;  Score 65;  DB 3;  Length 1026;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 778

Qy        514 ATTCG 518
              |||||
Db        779 ATTCG 783


RESULT 50
US-09-634-368-6
; Sequence 6, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 1287
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: human Fc-p35
;   OTHER INFORMATION: fusion protein coding sequence
US-09-634-368-6

  Query Match             11.6%;  Score 65;  DB 3;  Length 1287;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1177 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1236

Qy        514 ATTCG 518
              |||||
Db       1237 ATTCG 1241


RESULT 51
US-08-684-687-3
; Sequence 3, Application US/08684687
; Patent No. 5830451
;  GENERAL INFORMATION:
;    APPLICANT:  KIEFF, ELLIOTT D.
;    APPLICANT:  DEVERGNE, ODILE
;    TITLE OF INVENTION:  A NOVEL HAEMATOPOIETIC CYTOKINE AND USES
;    TITLE OF INVENTION:  THEREFOR
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  WOLF, GREENFIELD & SACKS, P.C.
;      STREET:  600 ATLANTIC AVENUE
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/684,687
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,092
;      FILING DATE:  11-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  GATES, EDWARD R.
;      REGISTRATION NUMBER:  31,616
;      REFERENCE/DOCKET NUMBER:  B0801/7051
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1316 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  HOMO SAPIENS
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  102..863
US-08-684-687-3

  Query Match             11.6%;  Score 65;  DB 2;  Length 1316;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 812

Qy        514 ATTCG 518
              |||||
Db        813 ATTCG 817
```

```
RESULT 52
US-09-851-520-3
; Sequence 3, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
;   LENGTH: 1316
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (102)...(863)
US-09-851-520-3

  Query Match             11.6%;  Score 65;  DB 3;  Length 1316;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 812

Qy        514 ATTCG 518
              |||||
Db        813 ATTCG 817


RESULT 53
US-08-265-087-3
; Sequence 3, Application US/08265087
; Patent No. 5571515
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/265,087
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1364 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  101..859
US-08-265-087-3

  Query Match             11.6%;  Score 65;  DB 2;  Length 1364;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 811

Qy        514 ATTCG 518
              |||||
Db        812 ATTCG 816


RESULT 54
US-08-621-493-3
; Sequence 3, Application US/08621493
; Patent No. 5723127
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/621,493
;      FILING DATE:  25-MAR-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1364 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  101..859
US-08-621-493-3

  Query Match             11.6%;  Score 65;  DB 2;  Length 1364;
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  Best Local Similarity   100.0%;  Pred. No. 3.2e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 811

Qy        514 ATTCG 518
              |||||
Db        812 ATTCG 816


RESULT 55
US-08-965-688-3
; Sequence 3, Application US/08965688
; Patent No. 5976539
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/965,688
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/621,493
;      FILING DATE:  25-MAR-1996
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1364 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  101..859
US-08-965-688-3

  Query Match            11.6%;  Score 65;  DB 2;  Length 1364;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 811

Qy        514 ATTCG 518
              |||||
Db        812 ATTCG 816


RESULT 56
US-09-260-173-3
; Sequence 3, Application US/09260173
; Patent No. 6168923
;   GENERAL INFORMATION:
;        APPLICANT: Scott, Phillip
;                   Trinchieri, Giorgio
;        TITLE OF INVENTION: Compositions and Methods for Use of
;                            IL-12 as an Adjuvant
;        NUMBER OF SEQUENCES: 4
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Howson and Howson
;             STREET: Spring House Corporate Center, PO Box 457
;             CITY: Spring House
;             STATE: Pennsylvania
;             COUNTRY: USA
;             ZIP: 19477
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/260,173
;             FILING DATE: 01-Mar-1999
;             CLASSIFICATION: <Unknown>
;                             17-JUN-1994
;                             18-APR-1994
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/965,688
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: 08/265,087
;             FILING DATE: 17-JUN-1994
;             APPLICATION NUMBER: US 08/229,282
;             FILING DATE: 18-APR-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Bak, Mary E.
;             REGISTRATION NUMBER: 31,215
;             REFERENCE/DOCKET NUMBER: WST51AUSA
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 215-540-9206
;             TELEFAX: 215-540-5818
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1364 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: unknown
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  101..859
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-260-173-3

  Query Match            11.6%;  Score 65;  DB 3;  Length 1364;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 811

Qy        514 ATTCG 518
              |||||
Db        812 ATTCG 816


RESULT 57
```

```
US-09-924-703-5
; Sequence 5, Application US/09924703
; Patent No. 6555658
; GENERAL INFORMATION:
;  APPLICANT: TRINCHIERI, GIORGIO
;  APPLICANT:  PERUSSIA, BICE
;  APPLICANT:  CLARK, STEVEN C.
;  APPLICANT:  WONG, GORDON G.
;  APPLICANT:  HEWICK, RODNEY
;  APPLICANT:  KOBAYASHI, MICHIKO
;  TITLE OF INVENTION: ANTIBODIES TO NATURAL KILLER STIMULATORY FACTOR
;  FILE REFERENCE: 01142.0142.0100
;  CURRENT APPLICATION NUMBER: US/09/924,703
;  CURRENT FILING DATE:  2001-08-09
;  PRIOR APPLICATION NUMBER: 09/325,958
;  PRIOR FILING DATE: 1999-06-04
;  PRIOR APPLICATION NUMBER: 08/858,000
;  PRIOR FILING DATE: 1997-05-16
;  PRIOR APPLICATION NUMBER: 08/403,013
;  PRIOR FILING DATE: 1995-03-13
;  PRIOR APPLICATION NUMBER: 07/584,941
;  PRIOR FILING DATE: 1990-09-18
;  PRIOR APPLICATION NUMBER: 07/307,817
;  PRIOR FILING DATE: 1989-02-07
;  PRIOR APPLICATION NUMBER: 07/269,945
;  PRIOR FILING DATE: 1988-11-10
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 1395
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
;   OTHER INFORMATION: sequence of the 30 kD subunit of NKSF
;   NAME/KEY: CDS
;   LOCATION: (114)..(872)
US-09-924-703-5

  Query Match             11.6%;  Score 65;  DB 3;  Length 1395;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        765 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 824

Qy        514 ATTCG 518
              |||||
Db        825 ATTCG 829


RESULT 58
US-08-751-767A-11
; Sequence 11, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1560 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1557
US-08-751-767A-11

  Query Match             11.6%;  Score 65;  DB 2;  Length 1560;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1450 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1509

Qy        514 ATTCG 518
              |||||
Db       1510 ATTCG 1514


RESULT 59
US-08-751-767A-9
; Sequence 9, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1623 base pairs
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```
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..1620
US-08-751-767A-9

  Query Match             11.6%;  Score 65;  DB 2;  Length 1623;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1513 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1572

Qy        514 ATTCG 518
              |||||
Db       1573 ATTCG 1577


RESULT 60
US-09-310-842-2
; Sequence 2, Application US/09310842A
; Patent No. 6451593
; GENERAL INFORMATION:
;  APPLICANT: Wittig, Prof. Burghardt
;  APPLICANT: Junghans, Claas
;  TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
;  TITLE OF INVENTION: Therapy
;  FILE REFERENCE: XI 597/99
;  CURRENT APPLICATION NUMBER: US/09/310,842A
;  CURRENT FILING DATE: 1999-05-12
;  EARLIER APPLICATION NUMBER: DE 196 48 625.4
;  EARLIER FILING DATE: 1996-11-13
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 1645
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (1)..(1645)
;   OTHER INFORMATION: Interleukin-12 (IL-12, p35-subunit); Oligo DNA
;   OTHER INFORMATION: Dumbbell
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1)..(2)
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at
;   OTHER INFORMATION: position 1 to 2  can be modified with amino or caroxy
;   OTHER INFORMATION: features
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1644)..(1645)
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1644
;   OTHER INFORMATION: to 1645  can be modified with amino or caroxy features
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Strandness: both;  nucleic
;   OTHER INFORMATION: acid (linear),  hypothetical: No. 6451593 anti-sense: No
US-09-310-842-2

  Query Match             11.6%;  Score 65;  DB 3;  Length 1645;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1284 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1343

Qy        514 ATTCG 518
              |||||
Db       1344 ATTCG 1348


RESULT 61
US-09-543-679A-2893
; Sequence 2893, Application US/09543679A
; Patent No. 7034007
;   GENERAL INFORMATION:
;       APPLICANT: NYCE, Jonathan W.
;       TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                           COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                           OF AIRWAY DISORDERS ASSOCIATED WITH
;                           BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;       NUMBER OF SEQUENCES: 3111
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;            STREET: 7 Clarke Drive
;            CITY: Cranbury
;            STATE: NJ
;            COUNTRY: USA
;            ZIP: 08512
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD-R
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: N/A
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/543,679A
;            FILING DATE: 13-Apr-2000
;            CLASSIFICATION: UNKNOWN
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/127,958
;            FILING DATE: 1998-08-03
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Amzel, Viviana
;            REGISTRATION NUMBER: 30,930
;            REFERENCE/DOCKET NUMBER: EPI-0067191b
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 609-409-3035
;            TELEFAX: 413-254-9245
;            TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2893:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 4521 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2893:
US-09-543-679A-2893

  Query Match             11.6%;  Score 65;  DB 5;  Length 4521;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        514 ATTCG 518
              |||||
Db        712 ATTCG 716


RESULT 62
US-08-751-767A-7
; Sequence 7, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
```

```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6139 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3222..4841
US-08-751-767A-7

  Query Match             11.6%;  Score 65;  DB 2;  Length 6139;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4734 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 4793

Qy        514 ATTCG 518
              |||||
Db       4794 ATTCG 4798


RESULT 63
US-09-949-016-11872
; Sequence 11872, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11872
;   LENGTH: 10764
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-11872

  Query Match             11.6%;  Score 65;  DB 3;  Length 10764;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8457 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 8516

Qy        514 ATTCG 518
              |||||
Db       8517 ATTCG 8521


RESULT 64
US-09-949-016-14204
; Sequence 14204, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14204
;   LENGTH: 10765
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-14204

  Query Match             11.6%;  Score 65;  DB 3;  Length 10765;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8457 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 8516

Qy        514 ATTCG 518
              |||||
Db       8517 ATTCG 8521


RESULT 65
US-09-949-016-20381
; Sequence 20381, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20381
;   LENGTH: 601
;   TYPE: DNA
```

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;   ORGANISM: Human
US-09-949-016-20381

  Query Match             10.0%;  Score 56;  DB 3;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-18;
  Matches   56;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        103 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 158
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 199


RESULT 66
US-09-949-016-87348
; Sequence 87348, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 87348
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-87348

  Query Match             10.0%;  Score 56;  DB 3;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-18;
  Matches   56;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        103 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 158
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 199


RESULT 67
US-09-011-143-24
; Sequence 24, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  79 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-24

  Query Match             7.7%;  Score 43;  DB 3;  Length 79;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-12;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        117 TGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGC 159
              |||||||||||||||||||||||||||||||||||||||||||
Db          1 TGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGC 43


RESULT 68
US-09-302-495-24
; Sequence 24, Application US/09302495
; Patent No. 6518045
;  GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/302,495
;            FILING DATE: 30-Apr-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
```

```
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 24:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 79 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-302-495-24

  Query Match             7.7%;  Score 43;  DB 3;  Length 79;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-12;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        117 TGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGC 159
              |||||||||||||||||||||||||||||||||||||||||||
Db          1 TGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGC 43


RESULT 69
US-10-079-616-24
; Sequence 24, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 24:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 79 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-079-616-24

  Query Match             7.7%;  Score 43;  DB 3;  Length 79;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-12;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        117 TGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGC 159
              |||||||||||||||||||||||||||||||||||||||||||
Db          1 TGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGC 43


RESULT 70
US-09-917-265A-91
; Sequence 91, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91
;   LENGTH: 39
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-917-265A-91

  Query Match             5.3%;  Score 30;  DB 3;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 3e-05;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAA 30
              ||||||||||||||||||||||||||||||
Db         10 GGGATGTTCCAGTGCCTCAACCACTCCCAA 39


RESULT 71
US-09-634-368-1
; Sequence 1, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 582
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine p35
;   OTHER INFORMATION: coding sequence for mature protein
US-09-634-368-1

  Query Match             4.8%;  Score 27;  DB 3;  Length 582;
  Best Local Similarity   100.0%;  Pred. No. 0.001;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        283 ATCTATGAGGACTTGAAGATGTACCAG 309
              |||||||||||||||||||||||||||
Db        301 ATCTATGAGGACTTGAAGATGTACCAG 327
```

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RESULT 72
US-08-385-335A-10
; Sequence 10, Application US/08385335A
; Patent No. 5891680
;  GENERAL INFORMATION:
;    APPLICANT:  Lieschke, Graham J.
;    APPLICANT:  Mulligan, Richard C.
;    TITLE OF INVENTION:  Bioactive Fusion Proteins
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/385,335A
;      FILING DATE:  08-FEB-1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  WHI95-01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-861-6240
;      TELEFAX:  617-861-9540
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  713 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-08-385-335A-10

  Query Match             4.8%;  Score 27;  DB 2;  Length 713;
  Best Local Similarity   100.0%;  Pred. No. 0.001;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        283 ATCTATGAGGACTTGAAGATGTACCAG 309
              |||||||||||||||||||||||||||
Db        413 ATCTATGAGGACTTGAAGATGTACCAG 439


RESULT 73
US-09-634-368-5
; Sequence 5, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 1278
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: Fc-p35 fusion protein coding sequence
US-09-634-368-5

  Query Match             4.8%;  Score 27;  DB 3;  Length 1278;
  Best Local Similarity   100.0%;  Pred. No. 0.00099;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        283 ATCTATGAGGACTTGAAGATGTACCAG 309
              |||||||||||||||||||||||||||
Db        997 ATCTATGAGGACTTGAAGATGTACCAG 1023


RESULT 74
US-09-634-368-12
; Sequence 12, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 1569
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p35-linker-p40 fusion protein coding sequence
US-09-634-368-12

  Query Match             4.8%;  Score 27;  DB 3;  Length 1569;
  Best Local Similarity   100.0%;  Pred. No. 0.00099;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        283 ATCTATGAGGACTTGAAGATGTACCAG 309
              |||||||||||||||||||||||||||
Db        301 ATCTATGAGGACTTGAAGATGTACCAG 327


RESULT 75
US-09-634-368-11
; Sequence 11, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 2013
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p35-linker-p40-IL-2 fusion protein coding sequence
US-09-634-368-11

  Query Match             4.8%;  Score 27;  DB 3;  Length 2013;
  Best Local Similarity   100.0%;  Pred. No. 0.00098;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        283 ATCTATGAGGACTTGAAGATGTACCAG 309
```

```
                    ||||||||||||||||||||||||||
Db        301 ATCTATGAGGACTTGAAGATGTACCAG 327


RESULT 76
US-09-634-368-13
; Sequence 13, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 13
;   LENGTH: 2709
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: Fc-p35-linker-p40-IL-2 fusion protein coding
;   OTHER INFORMATION: sequence
US-09-634-368-13

  Query Match             4.8%;  Score 27;  DB 3;  Length 2709;
  Best Local Similarity   100.0%;  Pred. No. 0.00098;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        283 ATCTATGAGGACTTGAAGATGTACCAG 309
                    ||||||||||||||||||||||||||
Db        997 ATCTATGAGGACTTGAAGATGTACCAG 1023


RESULT 77
US-08-659-206A-4
; Sequence 4, Application US/08659206A
; Patent No. 5922685
;  GENERAL INFORMATION:
;    APPLICANT:  Rakhmilevich, Alexander
;    TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/659,206A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  110229.91144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6295 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "plasmid pWRG3196"
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(955..1260, 1334..1675)
;      OTHER INFORMATION:  /product= "p35 gene product"
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2377..3384
;      OTHER INFORMATION:  /product= "p40 gene product"
US-08-659-206A-4

  Query Match             4.8%;  Score 27;  DB 2;  Length 6295;
  Best Local Similarity   100.0%;  Pred. No. 0.00097;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        283 ATCTATGAGGACTTGAAGATGTACCAG 309
                    ||||||||||||||||||||||||||
Db       1394 ATCTATGAGGACTTGAAGATGTACCAG 1420


RESULT 78
US-08-659-206A-1
; Sequence 1, Application US/08659206A
; Patent No. 5922685
;  GENERAL INFORMATION:
;    APPLICANT:  Rakhmilevich, Alexander
;    TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/659,206A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  110229.91144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7287 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Plasmid DNA"
;    IMMEDIATE SOURCE:
;      CLONE:  pWRG3169
;    FEATURE:
;      NAME/KEY:  promoter
;      LOCATION:  1..628
;    FEATURE:
;      NAME/KEY:  iDNA
;      LOCATION:  629..810
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(953..1258, 1332..1673)
```

```
;      OTHER INFORMATION:  /product= "p35 gene product"
;    FEATURE:
;      NAME/KEY:  polyA_site
;      LOCATION:  1797..2024
;    FEATURE:
;      NAME/KEY:  promoter
;      LOCATION:  2110..2737
;    FEATURE:
;      NAME/KEY:  iDNA
;      LOCATION:  2738..2919
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2983..3990
;      OTHER INFORMATION:  /product= "p40 gene product"
;    FEATURE:
;      NAME/KEY:  polyA_site
;      LOCATION:  4075..4306
US-08-659-206A-1

  Query Match             4.8%;  Score 27;  DB 2;  Length 7287;
  Best Local Similarity   100.0%;  Pred. No. 0.00097;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        283 ATCTATGAGGACTTGAAGATGTACCAG 309
              |||||||||||||||||||||||||||
Db       1392 ATCTATGAGGACTTGAAGATGTACCAG 1418


RESULT 79
US-09-917-265A-90/c
; Sequence 90, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90
;   LENGTH: 27
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-917-265A-90

  Query Match             4.3%;  Score 24;  DB 3;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.036;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        538 ATGATGAGCTATCTGAATGCTTCC 561
              ||||||||||||||||||||||||
Db         27 ATGATGAGCTATCTGAATGCTTCC 4


RESULT 80
US-09-011-143-25/c
; Sequence 25, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  36 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-25

  Query Match             4.3%;  Score 24;  DB 3;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 0.036;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        316 TTCAAGGCCATGAATGCAAAGCTG 339
              ||||||||||||||||||||||||
Db         36 TTCAAGGCCATGAATGCAAAGCTG 13


RESULT 81
US-09-302-495-25/c
; Sequence 25, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
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;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 25:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 36 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-302-495-25

  Query Match             4.3%;  Score 24;  DB 3;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 0.036;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        316 TTCAAGGCCATGAATGCAAAGCTG 339
              ||||||||||||||||||||||||
Db         36 TTCAAGGCCATGAATGCAAAGCTG 13


RESULT 82
US-10-079-616-25/c
; Sequence 25, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 25:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 36 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-10-079-616-25

  Query Match             4.3%;  Score 24;  DB 3;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 0.036;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        316 TTCAAGGCCATGAATGCAAAGCTG 339
              ||||||||||||||||||||||||
Db         36 TTCAAGGCCATGAATGCAAAGCTG 13


RESULT 83
US-09-917-265A-92/c
; Sequence 92, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92
;   LENGTH: 41
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-917-265A-92

  Query Match             4.3%;  Score 24;  DB 3;  Length 41;
  Best Local Similarity   100.0%;  Pred. No. 0.036;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        538 ATGATGAGCTATCTGAATGCTTCC 561
              ||||||||||||||||||||||||
Db         41 ATGATGAGCTATCTGAATGCTTCC 18


RESULT 84
US-08-859-998-383
; Sequence 383, Application US/08859998
; Patent No. 5994076
;  GENERAL INFORMATION:
;    APPLICANT:  Chenchik, Alex
;    APPLICANT:  Jokhadze, George
;    APPLICANT:  Bibilashvilli, Robert
;    TITLE OF INVENTION:  METHOD OF ASSAYING DIFFERENTIAL
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1375
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  2200 Sand Hill Road, Suite 100
;      CITY:  Menlo Park
;      STATE:  CA
;      COUNTRY:  US
```

```
;       ZIP:  94025
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  Windows95
;       SOFTWARE:  FastSEQ for Windows Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/859,998
;       FILING DATE:  21-MAY-1997
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Field, Bret E.
;       REGISTRATION NUMBER:  37,620
;       REFERENCE/DOCKET NUMBER:  09096/002001
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-322-5070
;       TELEFAX:  415-854-0875
;   INFORMATION FOR SEQ ID NO:  383:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  32 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA
;     FEATURE:
;       OTHER INFORMATION:  oligonucleotide primer
US-08-859-998-383

  Query Match             3.7%;  Score 21;  DB 2;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        301 ATGTACCAGGTGGAGTTCAAG 321
              |||||||||||||||||||||
Db          1 ATGTACCAGGTGGAGTTCAAG 21


RESULT 85
US-09-225-928-383
; Sequence 383, Application US/09225928
; Patent No. 6352829
;   GENERAL INFORMATION:
;       APPLICANT: Chenchik, Alex
;                  Jokhadze, George
;                  Bibilashvilli, Robert
;       TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
;                           EXPRESSION
;       NUMBER OF SEQUENCES: 1375
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Fish & Richardson, P.C.
;            STREET: 2200 Sand Hill Road, Suite 100
;            CITY: Menlo Park
;            STATE: CA
;            COUNTRY: US
;            ZIP: 94025
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: Windows95
;            SOFTWARE: FastSEQ for Windows Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/225,928
;            FILING DATE: 05-Jan-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/859,998
;            FILING DATE: 21-MAY-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Field, Bret E.
;            REGISTRATION NUMBER: 37,620
;            REFERENCE/DOCKET NUMBER: 09096/002001
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 415-322-5070
;            TELEFAX: 415-854-0875
;   INFORMATION FOR SEQ ID NO: 383:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 32 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       FEATURE:
;            OTHER INFORMATION:  oligonucleotide primer
;       SEQUENCE DESCRIPTION: SEQ ID NO: 383:
US-09-225-928-383

  Query Match             3.7%;  Score 21;  DB 3;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        301 ATGTACCAGGTGGAGTTCAAG 321
              |||||||||||||||||||||
Db          1 ATGTACCAGGTGGAGTTCAAG 21


RESULT 86
US-09-225-201B-383
; Sequence 383, Application US/09225201B
; Patent No. 6489455
;   GENERAL INFORMATION:
;       APPLICANT: Chenchik, Alex
;                  Jokhadze, George
;                  Bibilashvilli, Robert
;       TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
;                           EXPRESSION
;       NUMBER OF SEQUENCES: 1375
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Fish & Richardson, P.C.
;            STREET: 2200 Sand Hill Road, Suite 100
;            CITY: Menlo Park
;            STATE: CA
;            COUNTRY: US
;            ZIP: 94025
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: Windows95
;            SOFTWARE: FastSEQ for Windows Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/225,201B
;            FILING DATE: 05-Jan-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/859,998
;            FILING DATE: 21-MAY-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Field, Bret E.
;            REGISTRATION NUMBER: 37,620
;            REFERENCE/DOCKET NUMBER: 09096/002001
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 415-322-5070
;            TELEFAX: 415-854-0875
;   INFORMATION FOR SEQ ID NO: 383:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 32 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       FEATURE:
;            OTHER INFORMATION:  oligonucleotide primer
;       SEQUENCE DESCRIPTION: SEQ ID NO: 383:
US-09-225-201B-383
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  Query Match             3.7%;  Score 21;  DB 3;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        301 ATGTACCAGGTGGAGTTCAAG 321
              |||||||||||||||||||||
Db          1 ATGTACCAGGTGGAGTTCAAG 21


RESULT 87
US-08-012-543-13
; Sequence 13, Application US/08012543
; Patent No. 5596072
;  GENERAL INFORMATION:
;    APPLICANT:  Culpepper, Janice
;    APPLICANT:  McKenzie, Andrew
;    APPLICANT:  Dang, Warren
;    APPLICANT:  de Waal Malefyt, Rene
;    APPLICANT:  Heath, Andrew
;    APPLICANT:  Aversa, Gregorio
;    APPLICANT:  Briere, Francine
;    APPLICANT:  Banchereau, Jacques
;    APPLICANT:  de Vries, Jan
;    APPLICANT:  Zurawski, Gerard
;    TITLE OF INVENTION:  Human Interleukin-13
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DNAX Research Institute
;      STREET:  901 California Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/012,543
;      FILING DATE:  01-FEB-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/933,416
;      FILING DATE:  21-AUG-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  DX0302K1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-852-9196
;      TELEFAX:  415-496-1200
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-012-543-13

  Query Match             3.6%;  Score 20;  DB 2;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        223 AATGGGAGTTGCCTGGCCTC 242
              ||||||||||||||||||||
Db          1 AATGGGAGTTGCCTGGCCTC 20


RESULT 88
US-08-621-841-19
; Sequence 19, Application US/08621841
; Patent No. 6096869
;  GENERAL INFORMATION:
;    APPLICANT:  Stanley, Margaret A.
;    APPLICANT:  Scarpini, Cinzia G.
;    TITLE OF INVENTION:  TREATMENT OF PAPILLOMAVIRUS-ASSOCIATED
;    TITLE OF INVENTION:  LESIONS
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/621,841
;      FILING DATE:  22-MAR-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9505784.0
;      FILING DATE:  22-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dreger, Walter H.
;      REGISTRATION NUMBER:  24,190
;      REFERENCE/DOCKET NUMBER:  A-63316
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 781-1989
;      TELEFAX:  (415) 398-3249
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-621-841-19

  Query Match             3.6%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        219 AACTAATGGGAGTTGCCTGG 238
              ||||||||||||||||||||
Db          1 AACTAATGGGAGTTGCCTGG 20


RESULT 89
US-08-621-841-52/c
; Sequence 52, Application US/08621841
; Patent No. 6096869
;  GENERAL INFORMATION:
;    APPLICANT:  Stanley, Margaret A.
;    APPLICANT:  Scarpini, Cinzia G.
;    TITLE OF INVENTION:  TREATMENT OF PAPILLOMAVIRUS-ASSOCIATED
;    TITLE OF INVENTION:  LESIONS
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
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;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/621,841
;       FILING DATE:  22-MAR-1996
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 9505784.0
;       FILING DATE:  22-MAR-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Dreger, Walter H.
;       REGISTRATION NUMBER:  24,190
;       REFERENCE/DOCKET NUMBER:  A-63316
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 781-1989
;       TELEFAX:  (415) 398-3249
;   INFORMATION FOR SEQ ID NO:  52:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  20 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
US-08-621-841-52

  Query Match             3.6%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        483 CAAGCTCTGCATACTTCTTC 502
              ||||||||||||||||||||
Db         20 CAAGCTCTGCATACTTCTTC 1


RESULT 90
US-09-851-520-28/c
; Sequence 28, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 28
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-520-28

  Query Match             3.6%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         63 GAAGGCCAGACAAACTCTAG 82
              ||||||||||||||||||||
Db         20 GAAGGCCAGACAAACTCTAG 1


RESULT 91
US-09-851-520-31/c
; Sequence 31, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 31
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-520-31

  Query Match             3.6%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        136 AAAACCAGCACAGTGGAGGC 155
              ||||||||||||||||||||
Db         20 AAAACCAGCACAGTGGAGGC 1


RESULT 92
US-09-851-520-39/c
; Sequence 39, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 39
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-520-39

  Query Match             3.6%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        223 AATGGGAGTTGCCTGGCCTC 242
              ||||||||||||||||||||
Db         20 AATGGGAGTTGCCTGGCCTC 1


RESULT 93
US-09-851-520-40/c
; Sequence 40, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 40
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-520-40

  Query Match             3.6%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy        230 GTTGCCTGGCCTCCAGAAAG 249
              ||||||||||||||||||||
Db         20 GTTGCCTGGCCTCCAGAAAG 1


RESULT 94
US-09-851-520-41/c
; Sequence 41, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 41
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-520-41

  Query Match             3.6%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        236 TGGCCTCCAGAAAGACCTCT 255
              ||||||||||||||||||||
Db         20 TGGCCTCCAGAAAGACCTCT 1


RESULT 95
US-09-851-520-42/c
; Sequence 42, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 42
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-520-42

  Query Match             3.6%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        241 TCCAGAAAGACCTCTTTTAT 260
              ||||||||||||||||||||
Db         20 TCCAGAAAGACCTCTTTTAT 1


RESULT 96
US-09-851-520-45/c
; Sequence 45, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 45
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-520-45

  Query Match             3.6%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        299 AGATGTACCAGGTGGAGTTC 318
              ||||||||||||||||||||
Db         20 AGATGTACCAGGTGGAGTTC 1


RESULT 97
US-09-851-520-57/c
; Sequence 57, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 57
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-520-57

  Query Match             3.6%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        458 AACCGGATTTTTATAAAACT 477
              ||||||||||||||||||||
Db         20 AACCGGATTTTTATAAAACT 1


RESULT 98
US-09-851-520-58/c
; Sequence 58, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 58
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-520-58

  Query Match             3.6%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        491 GCATACTTCTTCATGCTTTC 510
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```
                    ||||||||||||||||||||
Db         20 GCATACTTCTTCATGCTTTC 1


RESULT 99
US-09-851-520-59/c
; Sequence 59, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 59
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-520-59

  Query Match             3.4%;  Score 19;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        500 TTCATGCTTTCAGAATTCG 518
                ||||||||||||||||||||
Db         20 TTCATGCTTTCAGAATTCG 2


RESULT 100
US-08-184-009-198/c
; Sequence 198, Application US/08184009
; Patent No. 5833975
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/184,009
;      FILING DATE:  19-JAN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  198:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  39 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-184-009-198

  Query Match             3.4%;  Score 19;  DB 2;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        543 GAGCTATCTGAATGCTTCC 561
                ||||||||||||||||||||
Db         34 GAGCTATCTGAATGCTTCC 16


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OM nucleic - nucleic search, using sw model

Run on: June 9, 2006, 23:31:05 ; Search time 943.018 Seconds
(without alignments)
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Title: US-10-821-670A-101
Perfect score: 561
Sequence: 1 gggatgttccagtgcctcaa.....tgagctatctgaatgcttcc 561

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 18892170 seqs, 6143817638 residues

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Minimum DB seq length: 0
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Post-processing: Listing first 200 summaries

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9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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c	2	561	100.0	561	3	US-09-917-265-103	Sequence 103, App
	3	561	100.0	561	9	US-10-821-670-101	Sequence 101, App
c	4	561	100.0	561	9	US-10-821-670-103	Sequence 103, App
	5	558	99.5	666	3	US-09-917-265-32	Sequence 32, Appl
c	6	558	99.5	666	3	US-09-917-265-34	Sequence 34, Appl
	7	558	99.5	666	9	US-10-821-670-32	Sequence 32, Appl
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ALIGNMENTS

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; Sequence 101, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(561)
;   OTHER INFORMATION:
US-09-917-265-101

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RESULT 2
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; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
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US-09-917-265-103

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Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
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Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1


RESULT 3
US-10-821-670-101
; Sequence 101, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 101
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(561)
US-10-821-670-101

  Query Match            100.0%;  Score 561;  DB 9;  Length 561;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-289;
  Matches  561;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
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Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db        541 ATGAGCTATCTGAATGCTTCC 561
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RESULT 4
US-10-821-670-103/c
; Sequence 103, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 103
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Felis catus
US-10-821-670-103

Query Match 100.0%; Score 561; DB 9; Length 561;
Best Local Similarity 100.0%; Pred. No. 7.1e-289;
Matches 561; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1
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RESULT 5
US-09-917-265-32
; Sequence 32, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(666)
; OTHER INFORMATION:
US-09-917-265-32

Query Match 99.5%; Score 558; DB 3; Length 666;
Best Local Similarity 100.0%; Pred. No. 2.9e-287;
Matches 558; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468

Qy         364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528

Qy         424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588

Qy         484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648

Qy         544 AGCTATCTGAATGCTTCC 561
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Db         649 AGCTATCTGAATGCTTCC 666


RESULT 6
US-09-917-265-34/c
; Sequence 34, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-34

  Query Match             99.5%;  Score 558;  DB 3;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-287;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy          64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy         124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy         184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy         244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy         304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy         364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy         424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         138 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy         484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy         544 AGCTATCTGAATGCTTCC 561
              ||||||||||||||||||
Db          18 AGCTATCTGAATGCTTCC 1


RESULT 7
US-10-821-670-32
; Sequence 32, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
US-10-821-670-32

  Query Match             99.5%;  Score 558;  DB 9;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-287;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168

Qy          64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228

Qy         124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288

Qy         184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348

Qy         244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408

Qy         304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468

Qy         364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528

Qy         424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
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Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648

Qy        544 AGCTATCTGAATGCTTCC 561
              |||||||||||||||||
Db        649 AGCTATCTGAATGCTTCC 666


RESULT 8
US-10-821-670-34/c
; Sequence 34, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-34

  Query Match             99.5%;  Score 558;  DB 9;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-287;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        544 AGCTATCTGAATGCTTCC 561
              ||||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1


RESULT 9
US-09-917-265-43
; Sequence 43, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
;   OTHER INFORMATION:
US-09-917-265-43

  Query Match             90.9%;  Score 510;  DB 3;  Length 1533;
  Best Local Similarity   99.8%;  Pred. No. 1.4e-261;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1032

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1092

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1093 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1152

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1153 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1212

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1213 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1272

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1273 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1332

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1333 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1392

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1393 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1452

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1453 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1512

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              ||||||||||||||||||||
Db       1513 ATGAGCTATCTGAATGCTTCC 1533
```

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RESULT 10
US-09-917-265-45/c
; Sequence 45, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-45

  Query Match             90.9%;  Score 510;  DB 3;  Length 1533;
  Best Local Similarity   99.8%;  Pred. No. 1.4e-261;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1


RESULT 11
US-10-821-670-43
; Sequence 43, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-10-821-670-43

  Query Match             90.9%;  Score 510;  DB 9;  Length 1533;
  Best Local Similarity   99.8%;  Pred. No. 1.4e-261;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1032

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1092

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1093 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1152

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1153 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1212

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1213 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1272

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1273 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1332

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1333 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1392

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1393 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1452

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1453 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1512

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db       1513 ATGAGCTATCTGAATGCTTCC 1533


RESULT 12
US-10-821-670-45/c
; Sequence 45, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
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;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-45

  Query Match            90.9%;  Score 510;  DB 9;  Length 1533;
  Best Local Similarity   99.8%;  Pred. No. 1.4e-261;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1


RESULT 13
US-09-917-265-38
; Sequence 38, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
US-09-917-265-38

  Query Match            90.9%;  Score 510;  DB 3;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 1.4e-261;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1098

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1158

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1218

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1219 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1278

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1338

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1398

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1458

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1459 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1518

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1519 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1578

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db       1579 ATGAGCTATCTGAATGCTTCC 1599


RESULT 14
US-09-917-265-40/c
; Sequence 40, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
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;   ORGANISM: Felis catus
US-09-917-265-40

  Query Match             90.9%;  Score 510;  DB 3;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 1.4e-261;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1


RESULT 15
US-10-821-670-38
; Sequence 38, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-10-821-670-38

  Query Match             90.9%;  Score 510;  DB 9;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 1.4e-261;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1098

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1158

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1218

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1219 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1278

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1338

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1398

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1458

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1459 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1518

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1519 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1578

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db       1579 ATGAGCTATCTGAATGCTTCC 1599


RESULT 16
US-10-821-670-40/c
; Sequence 40, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-40

  Query Match             90.9%;  Score 510;  DB 9;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 1.4e-261;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1
```

RESULT 17
US-09-917-265-35
; Sequence 35, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(591)
; OTHER INFORMATION:
US-09-917-265-35

Query Match 90.4%; Score 507; DB 3; Length 591;
Best Local Similarity 99.8%; Pred. No. 5.4e-260;
Matches 557; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573

Qy        544 AGCTATCTGAATGCTTCC 561
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Db        574 AGCTATCTGAATGCTTCC 591
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RESULT 18
US-09-917-265-37/c
; Sequence 37, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265-37

Query Match 90.4%; Score 507; DB 3; Length 591;
Best Local Similarity 99.8%; Pred. No. 5.4e-260;
Matches 557; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379
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Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        544 AGCTATCTGAATGCTTCC 561
              |||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1
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RESULT 19
US-10-821-670-35
; Sequence 35, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(591)
US-10-821-670-35

Query Match 90.4%; Score 507; DB 9; Length 591;
Best Local Similarity 99.8%; Pred. No. 5.4e-260;
Matches 557; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573

Qy        544 AGCTATCTGAATGCTTCC 561
              |||||||||||||||||
Db        574 AGCTATCTGAATGCTTCC 591
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RESULT 20
US-10-821-670-37/c
; Sequence 37, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Felis catus
US-10-821-670-37

Query Match 90.4%; Score 507; DB 9; Length 591;
Best Local Similarity 99.8%; Pred. No. 5.4e-260;
Matches 557; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
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Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
              ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        544 AGCTATCTGAATGCTTCC 561
              ||||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1


RESULT 21
US-10-079-616-9
; Sequence 9, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 591 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-079-616-9

  Query Match             88.1%;  Score 494;  DB 6;  Length 591;
  Best Local Similarity   99.8%;  Pred. No. 4.9e-253;
  Matches  544;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
              ||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db        454 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATC 513

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573

Qy        544 AGCTA 548
              |||||
Db        574 AGCTA 578


RESULT 22
US-10-079-616-8
; Sequence 8, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
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;              APPLICATION NUMBER: 09/011,143
;              FILING DATE: 04-FEB-1998
;              APPLICATION NUMBER: PCT/JP97/01824
;              FILING DATE: 29-MAY-1997
;              APPLICATION NUMBER: JP 165249/1996
;              FILING DATE: 04-JUN-1996
;         ATTORNEY/AGENT INFORMATION:
;              NAME: BROWDY, Roger L.
;              REGISTRATION NUMBER: 25,618
;              REFERENCE/DOCKET NUMBER: IMAMURA=1
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: 202-628-5197
;              TELEFAX: 202-737-3528
;    INFORMATION FOR SEQ ID NO: 8:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 1441 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;         MOLECULE TYPE: cDNA
;         SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-079-616-8

  Query Match             88.1%;  Score 494;  DB 6;  Length 1441;
  Best Local Similarity   99.8%;  Pred. No. 4.9e-253;
  Matches  544;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 310

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 370

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 430

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 490

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 550

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        551 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 610

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 670

Qy        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        671 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATC 730

Qy        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        731 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 790

Qy        544 AGCTA 548
              |||||
Db        791 AGCTA 795


RESULT 23
US-10-079-616-26
; Sequence 26, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;    INFORMATION FOR SEQ ID NO: 26:
;         SEQUENCE CHARACTERISTICS:
;             LENGTH: 689 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;         MOLECULE TYPE: cDNA
;         SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-079-616-26

  Query Match             39.4%;  Score 221;  DB 6;  Length 689;
  Best Local Similarity   99.2%;  Pred. No. 4.9e-107;
  Matches  371;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        175 ACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGC 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 ACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGC 345

Qy        235 CTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGAC 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 CTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGAC 405

Qy        295 TTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAA 354
              |||||||||||||||||||||||||||||||||||||||||||||| | ||||||||||||
Db        406 TTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAA 465

Qy        355 AGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTG 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 AGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTG 525

Qy        415 AATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAA 474
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        526 AATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAA 585

Qy        475 ACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAAT 534
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        586 ACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAAT 645

Qy        535 AGAATGATGAGCTA 548
              ||||||||||||||
Db        646 AGAATGATGAGCTA 659


RESULT 24
US-10-041-672C-2
; Sequence 2, Application US/10041672C
; Publication No. US20030157059A1
; GENERAL INFORMATION:
;  APPLICANT: Mologen Forschungs-, Entwicklungs- und Vetriebs GmbH
;  APPLICANT:  Universitat Zurich
;  TITLE OF INVENTION: FELINE INTERLEUKIN-12 AS IMMUNOSTIMULANT
;  FILE REFERENCE: NHL-NP-36
;  CURRENT APPLICATION NUMBER: US/10/041,672C
;  CURRENT FILING DATE:  2002-01-08
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 669
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: feline IL-12 p35
US-10-041-672C-2

  Query Match             34.8%;  Score 195;  DB 7;  Length 669;
  Best Local Similarity   99.0%;  Pred. No. 4e-93;
  Matches  395;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168

Qy         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        169 AAGGCCAGACAAACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228

Qy        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAAT 288

Qy        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243
              |||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCC 348

Qy        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408

Qy        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468

Qy        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 402
              |||||||||||||||||||||||||||||||||||||||
Db        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 507


RESULT 25
US-09-917-265-49
; Sequence 49, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(591)
;   OTHER INFORMATION:
US-09-917-265-49

  Query Match             14.4%;  Score 81;  DB 3;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        223 CTGGCTTCCAGAGAGATCTCT 243


RESULT 26
US-09-917-265-51/c
; Sequence 51, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-51

  Query Match             14.4%;  Score 81;  DB 3;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 27
US-10-821-670-49
; Sequence 49, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
```

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;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(591)
US-10-821-670-49

  Query Match            14.4%;  Score 81;  DB 9;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        223 CTGGCTTCCAGAGAGATCTCT 243


RESULT 28
US-10-821-670-51/c
; Sequence 51, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-51

  Query Match            14.4%;  Score 81;  DB 9;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 29
US-09-917-265-46
; Sequence 46, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
;   OTHER INFORMATION:
US-09-917-265-46

  Query Match            14.4%;  Score 81;  DB 3;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 30
US-09-917-265-48/c
; Sequence 48, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-48

  Query Match            14.4%;  Score 81;  DB 3;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 31
US-10-821-670-46
; Sequence 46, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
```

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;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
US-10-821-670-46

  Query Match            14.4%;  Score 81;  DB 9;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 32
US-10-821-670-48/c
; Sequence 48, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-48

  Query Match            14.4%;  Score 81;  DB 9;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 33
US-09-917-265-104
; Sequence 104, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (232)..(897)
;   OTHER INFORMATION:
US-09-917-265-104

  Query Match            14.4%;  Score 81;  DB 3;  Length 1455;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 528

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        529 CTGGCTTCCAGAGAGATCTCT 549


RESULT 34
US-09-917-265-106/c
; Sequence 106, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 106
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-106

  Query Match            14.4%;  Score 81;  DB 3;  Length 1455;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 928

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        927 CTGGCTTCCAGAGAGATCTCT 907


RESULT 35
US-10-821-670-104
; Sequence 104, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
```

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;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 104
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (232)..(897)
US-10-821-670-104

  Query Match             14.4%;  Score 81;  DB 9;  Length 1455;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 528

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        529 CTGGCTTCCAGAGAGATCTCT 549


RESULT 36
US-10-821-670-106/c
; Sequence 106, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 106
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-106

  Query Match             14.4%;  Score 81;  DB 9;  Length 1455;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 928

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        927 CTGGCTTCCAGAGAGATCTCT 907


RESULT 37
US-09-917-265-66
; Sequence 66, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
;   OTHER INFORMATION:
US-09-917-265-66

  Query Match             14.4%;  Score 81;  DB 3;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1105 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1164

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db       1165 CTGGCTTCCAGAGAGATCTCT 1185


RESULT 38
US-09-917-265-68/c
; Sequence 68, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-68

  Query Match             14.4%;  Score 81;  DB 3;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 39
US-10-821-670-66
; Sequence 66, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
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; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-10-821-670-66

  Query Match             14.4%;  Score 81;  DB 9;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1105 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1164

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db       1165 CTGGCTTCCAGAGAGATCTCT 1185


RESULT 40
US-10-821-670-68/c
; Sequence 68, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-68

  Query Match             14.4%;  Score 81;  DB 9;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 41
US-09-917-265-61
; Sequence 61, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
US-09-917-265-61

  Query Match             14.4%;  Score 81;  DB 3;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1230

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db       1231 CTGGCTTCCAGAGAGATCTCT 1251


RESULT 42
US-09-917-265-63/c
; Sequence 63, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-63

  Query Match             14.4%;  Score 81;  DB 3;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 43
US-10-821-670-61
; Sequence 61, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
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;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-10-821-670-61

  Query Match            14.4%;  Score 81;  DB 9;  Length 1599;
  Best Local Similarity  100.0%;  Pred. No. 3.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1230

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db       1231 CTGGCTTCCAGAGAGATCTCT 1251


RESULT 44
US-10-821-670-63/c
; Sequence 63, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-63

  Query Match            14.4%;  Score 81;  DB 9;  Length 1599;
  Best Local Similarity  100.0%;  Pred. No. 3.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        193 CTGGCTTCCAGAGAGATCTCT 213
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 45
US-10-041-672C-8
; Sequence 8, Application US/10041672C
; Publication No. US20030157059A1
; GENERAL INFORMATION:
;  APPLICANT: Mologen Forschungs-, Entwicklungs- und Vetriebs GmbH
;  APPLICANT:  Universitat Zurich
;  TITLE OF INVENTION: FELINE INTERLEUKIN-12 AS IMMUNOSTIMULANT
;  FILE REFERENCE: NHL-NP-36
;  CURRENT APPLICATION NUMBER: US/10/041,672C
;  CURRENT FILING DATE:  2002-01-08
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 71
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer f12p35-1-lang
US-10-041-672C-8

  Query Match            12.7%;  Score 71;  DB 7;  Length 71;
  Best Local Similarity  100.0%;  Pred. No. 8.2e-27;
  Matches   71;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        380 TGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCAC 439
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCAC 60

Qy        440 AGAACTCCTCC 450
              ||||||||||||
Db         61 AGAACTCCTCC 71


RESULT 46
US-10-741-601-946
; Sequence 946, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 946
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-946

  Query Match            11.6%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 72

Qy        514 ATTCG 518
              |||||
Db         73 ATTCG 77


RESULT 47
US-10-741-601-947
; Sequence 947, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 947
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-947

  Query Match            11.6%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
```

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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 80

Qy        514 ATTCG 518
                 |||||
Db         81 ATTCG 85


RESULT 48
US-10-741-601-951
; Sequence 951, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 951
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-951

  Query Match             11.6%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 181

Qy        514 ATTCG 518
                 |||||
Db        182 ATTCG 186


RESULT 49
US-10-741-601-955
; Sequence 955, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 955
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-955

  Query Match             11.6%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 72

Qy        514 ATTCG 518
                 |||||
Db         73 ATTCG 77


RESULT 50
US-10-741-601-957
; Sequence 957, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 957
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-957

  Query Match             11.6%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 80

Qy        514 ATTCG 518
                 |||||
Db         81 ATTCG 85


RESULT 51
US-10-741-601-960
; Sequence 960, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 960
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-960

  Query Match             11.6%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 181

Qy        514 ATTCG 518
                 |||||
Db        182 ATTCG 186


RESULT 52
US-10-741-601-7417
; Sequence 7417, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
```

```
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7417
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-7417

  Query Match            11.6%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 72

Qy        514 ATTCG 518
              |||||
Db         73 ATTCG 77


RESULT 53
US-10-741-601-7418
; Sequence 7418, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7418
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-7418

  Query Match            11.6%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 80

Qy        514 ATTCG 518
              |||||
Db         81 ATTCG 85


RESULT 54
US-10-741-601-7431
; Sequence 7431, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7431
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-7431

  Query Match            11.6%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 181

Qy        514 ATTCG 518
              |||||
Db        182 ATTCG 186


RESULT 55
US-10-741-601-11370/c
; Sequence 11370, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11370
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-11370

  Query Match            11.6%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 130

Qy        514 ATTCG 518
              |||||
Db        129 ATTCG 125


RESULT 56
US-10-741-601-11372/c
; Sequence 11372, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11372
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-11372

  Query Match            11.6%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 122

Qy        514 ATTCG 518
```

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              |||||
Db        121 ATTCG 117


RESULT 57
US-10-741-601-11417/c
; Sequence 11417, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11417
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-11417

  Query Match             11.6%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 21

Qy        514 ATTCG 518
              |||||
Db         20 ATTCG 16


RESULT 58
US-10-741-600-3487
; Sequence 3487, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3487
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-3487

  Query Match             11.6%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 72

Qy        514 ATTCG 518
              |||||
Db         73 ATTCG 77


RESULT 59
US-10-741-600-3488
; Sequence 3488, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3488
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-3488

  Query Match             11.6%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 80

Qy        514 ATTCG 518
              |||||
Db         81 ATTCG 85


RESULT 60
US-10-741-600-3492
; Sequence 3492, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3492
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-3492

  Query Match             11.6%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 181

Qy        514 ATTCG 518
              |||||
Db        182 ATTCG 186


RESULT 61
US-10-741-600-3496
; Sequence 3496, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3496
```

```
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-3496

  Query Match            11.6%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 72

Qy        514 ATTCG 518
              |||||
Db         73 ATTCG 77


RESULT 62
US-10-741-600-3498
; Sequence 3498, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3498
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-3498

  Query Match            11.6%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 80

Qy        514 ATTCG 518
              |||||
Db         81 ATTCG 85


RESULT 63
US-10-741-600-3501
; Sequence 3501, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3501
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-3501

  Query Match            11.6%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 181

Qy        514 ATTCG 518
              |||||
Db        182 ATTCG 186


RESULT 64
US-10-741-600-20963
; Sequence 20963, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20963
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-20963

  Query Match            11.6%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 72

Qy        514 ATTCG 518
              |||||
Db         73 ATTCG 77


RESULT 65
US-10-741-600-20964
; Sequence 20964, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20964
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-20964

  Query Match            11.6%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 80

Qy        514 ATTCG 518
              |||||
Db         81 ATTCG 85
```

```
RESULT 66
US-10-741-600-20992
; Sequence 20992, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20992
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-20992

  Query Match             11.6%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 181

Qy        514 ATTCG 518
              |||||
Db        182 ATTCG 186


RESULT 67
US-10-741-600-28831/c
; Sequence 28831, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28831
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-28831

  Query Match             11.6%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 130

Qy        514 ATTCG 518
              |||||
Db        129 ATTCG 125


RESULT 68
US-10-741-600-28833/c
; Sequence 28833, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28833
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-28833

  Query Match             11.6%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 122

Qy        514 ATTCG 518
              |||||
Db        121 ATTCG 117


RESULT 69
US-10-741-600-28877/c
; Sequence 28877, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28877
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-28877

  Query Match             11.6%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 21

Qy        514 ATTCG 518
              |||||
Db         20 ATTCG 16


RESULT 70
US-10-995-561-1976
; Sequence 1976, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1976
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
```

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US-10-995-561-1976

  Query Match             11.6%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 72

Qy        514 ATTCG 518
              |||||
Db         73 ATTCG 77


RESULT 71
US-10-995-561-1977
; Sequence 1977, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1977
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-1977

  Query Match             11.6%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 80

Qy        514 ATTCG 518
              |||||
Db         81 ATTCG 85


RESULT 72
US-10-995-561-1981
; Sequence 1981, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1981
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-1981

  Query Match             11.6%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 181

Qy        514 ATTCG 518
              |||||
Db        182 ATTCG 186


RESULT 73
US-10-995-561-1986
; Sequence 1986, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1986
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-1986

  Query Match             11.6%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 72

Qy        514 ATTCG 518
              |||||
Db         73 ATTCG 77


RESULT 74
US-10-995-561-1988
; Sequence 1988, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1988
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-1988

  Query Match             11.6%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 80

Qy        514 ATTCG 518
              |||||
Db         81 ATTCG 85
```

```
RESULT 75
US-10-995-561-1991
; Sequence 1991, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1991
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-1991

  Query Match             11.6%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 181

Qy        514 ATTCG 518
              |||||
Db        182 ATTCG 186


RESULT 76
US-10-995-561-18302
; Sequence 18302, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18302
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-18302

  Query Match             11.6%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 72

Qy        514 ATTCG 518
              |||||
Db         73 ATTCG 77


RESULT 77
US-10-995-561-18303
; Sequence 18303, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18303
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-18303

  Query Match             11.6%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 80

Qy        514 ATTCG 518
              |||||
Db         81 ATTCG 85


RESULT 78
US-10-995-561-18335
; Sequence 18335, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18335
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-18335

  Query Match             11.6%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 181

Qy        514 ATTCG 518
              |||||
Db        182 ATTCG 186


RESULT 79
US-10-995-561-26362/c
; Sequence 26362, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
```

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;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26362
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-26362

  Query Match             11.6%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 21

Qy        514 ATTCG 518
              |||||
Db         20 ATTCG 16


RESULT 80
US-10-995-561-26545/c
; Sequence 26545, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26545
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-26545

  Query Match             11.6%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 130

Qy        514 ATTCG 518
              |||||
Db        129 ATTCG 125


RESULT 81
US-10-995-561-26548/c
; Sequence 26548, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26548
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-26548

  Query Match             11.6%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 122

Qy        514 ATTCG 518
              |||||
Db        121 ATTCG 117


RESULT 82
US-10-995-561-73346/c
; Sequence 73346, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73346
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-73346

  Query Match             11.6%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 130

Qy        514 ATTCG 518
              |||||
Db        129 ATTCG 125


RESULT 83
US-10-995-561-73349/c
; Sequence 73349, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73349
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-73349

  Query Match             11.6%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 122
```

```
Qy        514 ATTCG 518
              |||||
Db        121 ATTCG 117


RESULT 84
US-10-995-561-73383/c
; Sequence 73383, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73383
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-73383

  Query Match             11.6%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 21

Qy        514 ATTCG 518
              |||||
Db         20 ATTCG 16


RESULT 85
US-09-754-014-6
; Sequence 6, Application US/09754014
; Patent No. US20020119940A1
;   GENERAL INFORMATION:
;        APPLICANT: Jeff No. US20020119940A1dstrom
;                   Bruce Freimark
;                   Deepa Deshpande
;        TITLE OF INVENTION: GENE EXPRESSION AND DELIVERY SYTEMS
;                            AND USES
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                     Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 90071-2066
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                          storage
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: IBM P.C. DOS 5.0
;             SOFTWARE: FastSEQ for Windows 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/754,014
;             FILING DATE: 03-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/948,958
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Berkman, Charles S.
;             REGISTRATION NUMBER: 38,077
;             REFERENCE/DOCKET NUMBER: 226/284
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 660 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-754-014-6

  Query Match             11.6%;  Score 65;  DB 3;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        514 ATTCG 518
              |||||
Db        610 ATTCG 614


RESULT 86
US-09-836-866-4
; Sequence 4, Application US/09836866
; Patent No. US20020123473A1
;   GENERAL INFORMATION:
;        APPLICANT: No. US20020123473A1dstrom, Jeff
;                   Freimark, Bruce
;                   Deshpande, Deepa
;        TITLE OF INVENTION: IL-12 GENE EXPRESSION AND
;                            DELIVERY SYTEMS AND USES
;        NUMBER OF SEQUENCES: 8
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                     Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 90071-2066
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                          storage
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: IBM P.C. DOS 5.0
;             SOFTWARE: FastSEQ for Windows 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/836,866
;             FILING DATE: 16-Apr-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/949,160
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Warburg, Richard J.
;             REGISTRATION NUMBER: 32,327
;             REFERENCE/DOCKET NUMBER: 226/285
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 660 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
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;             TOPOLOGY: linear
;         SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-836-866-4

  Query Match             11.6%;  Score 65;  DB 3;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        514 ATTCG 518
              |||||
Db        610 ATTCG 614


RESULT 87
US-10-267-384-199
; Sequence 199, Application US/10267384
; Publication No. US20030198623A1
;   GENERAL INFORMATION:
;        APPLICANT: Paoletti, Enzo
;                   Tartaglia, James
;                   Cox, William I.
;        TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
;        NUMBER OF SEQUENCES: 217
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Curtis, Morris & Safford
;             STREET: 530 Fifth Avenue
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10036
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/267,384
;             FILING DATE: 09-Oct-2002
;             CLASSIFICATION: 435
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Frommer, William S.
;             REGISTRATION NUMBER: 25,506
;             REFERENCE/DOCKET NUMBER: 454310-2530
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 840-3333
;             TELEFAX: (212) 840-0712
;             TELEX: 425066CURTMS
;   INFORMATION FOR SEQ ID NO: 199:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 721 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 199:
US-10-267-384-199

  Query Match             11.6%;  Score 65;  DB 7;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy        514 ATTCG 518
              |||||
Db        671 ATTCG 675


RESULT 88
US-09-826-025-21
; Sequence 21, Application US/09826025
; Patent No. US20020162123A1
;   GENERAL INFORMATION:
;        APPLICANT: Chang, Lung-Ji
;        TITLE OF INVENTION: Combination Immunogene Therapy
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Medlen & Carroll, LLP
;             STREET: 220 Montgomery Street, Suite 2200
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: United States of America
;             ZIP: 94104
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/826,025
;             FILING DATE: 04-Apr-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/838,702
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ingolia, Diane E.
;             REGISTRATION NUMBER: 40,027
;             REFERENCE/DOCKET NUMBER: CHANG-02687
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 705-8410
;             TELEFAX: (415) 397-8338
;   INFORMATION FOR SEQ ID NO: 21:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 762 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: other nucleic acid
;             DESCRIPTION: /desc = "DNA"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-826-025-21

  Query Match             11.6%;  Score 65;  DB 3;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        514 ATTCG 518
              |||||
Db        712 ATTCG 716


RESULT 89
US-10-785-577-21
; Sequence 21, Application US/10785577
; Publication No. US20040237129A1
;   GENERAL INFORMATION:
;        APPLICANT: Chang, Lung-Ji
;        TITLE OF INVENTION: Combination Immunogene Therapy
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Medlen & Carroll, LLP
;             STREET: 220 Montgomery Street, Suite 2200
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: United States of America
```

```
;            ZIP: 94104
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/785,577
;            FILING DATE: 23-Feb-2004
;            CLASSIFICATION: 424
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/838,702
;            FILING DATE: 9-Apr-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Ingolia, Diane E.
;            REGISTRATION NUMBER: 40,027
;            REFERENCE/DOCKET NUMBER: CHANG-02687
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 705-8410
;            TELEFAX: (415) 397-8338
;   INFORMATION FOR SEQ ID NO: 21:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 762 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: other nucleic acid
;            DESCRIPTION: /desc = "DNA"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-10-785-577-21

  Query Match             11.6%;  Score 65;  DB 9;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        514 ATTCG 518
              |||||
Db        712 ATTCG 716


RESULT 90
US-10-688-845-57
; Sequence 57, Application US/10688845
; Publication No. US20040247578A1
; GENERAL INFORMATION:
;  APPLICANT: Lotze, Michael T
;  APPLICANT:  Tahara, Hideaki
;  TITLE OF INVENTION: Methods And Reagents For Inducing Immunity
;  FILE REFERENCE: UPT-004
;  CURRENT APPLICATION NUMBER: US/10/688,845
;  CURRENT FILING DATE:  2003-10-15
;  PRIOR APPLICATION NUMBER: 60/418,865
;  PRIOR FILING DATE: 2002-10-15
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
;   LENGTH: 762
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-688-845-57

  Query Match             11.6%;  Score 65;  DB 9;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        514 ATTCG 518
              |||||
Db        712 ATTCG 716


RESULT 91
US-10-373-456-19
; Sequence 19, Application US/10373456
; Publication No. US20040009146A1
; GENERAL INFORMATION:
;  APPLICANT: Podhajcer, Osvaldo
;  TITLE OF INVENTION: Anti-Tumor Vaccine and Method
;  FILE REFERENCE: 1423P-US/101141-14
;  CURRENT APPLICATION NUMBER: US/10/373,456
;  CURRENT FILING DATE:  2003-02-25
;  PRIOR APPLICATION NUMBER: US 60/359,836
;  PRIOR FILING DATE: 2002-02-26
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 811
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-373-456-19

  Query Match             11.6%;  Score 65;  DB 7;  Length 811;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 557

Qy        514 ATTCG 518
              |||||
Db        558 ATTCG 562


RESULT 92
US-10-349-507-4
; Sequence 4, Application US/10349507
; Publication No. US20030199002A1
; GENERAL INFORMATION:
;  APPLICANT: Hekimi , Siegfried
;  APPLICANT:  Jiang , Ning
;  APPLICANT:  Benard, Claire
;  APPLICANT:  Kebir , Hania
;  APPLICANT:  McCright, Brenton
;  APPLICANT:  Lakowski , Bernard
;  TITLE OF INVENTION: CLK-2 NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
;  FILE REFERENCE: 11202-006-999
;  CURRENT APPLICATION NUMBER: US/10/349,507
;  CURRENT FILING DATE:  2003-01-22
;  PRIOR APPLICATION NUMBER: 10/312,187
;  PRIOR FILING DATE: 2002-12-20
;  PRIOR APPLICATION NUMBER: PCT/CA01/00913
;  PRIOR FILING DATE: 2001-06-20
;  PRIOR APPLICATION NUMBER: 60/213,174
;  PRIOR FILING DATE: 2000-06-22
;  PRIOR APPLICATION NUMBER: 60/254,932
;  PRIOR FILING DATE: 2000-12-13
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 856
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (170)...(826)
US-10-349-507-4

  Query Match             11.6%;  Score 65;  DB 7;  Length 856;
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```
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 778

Qy        514 ATTCG 518
              |||||
Db        779 ATTCG 783


RESULT 93
US-10-267-565-4
; Sequence 4, Application US/10267565
; Publication No. US20030204059A1
; GENERAL INFORMATION:
;  APPLICANT: Gately, Maurice
;  APPLICANT:  Gubler, Ulrich
;  APPLICANT:  Hulmes, Jeffery
;  APPLICANT:  Podlaski, Frank
;  APPLICANT:  Stern, Alvin
;  TITLE OF INVENTION: PURIFICATION AND CHARACTERIZATION OF CYTOTOXIC
;  TITLE OF INVENTION:  LYMPHOCYTE MATURATION FACTOR AND MONOCLONAL
;  TITLE OF INVENTION:  ANTIBODIES THERETO
;  FILE REFERENCE: 11126-005
;  CURRENT APPLICATION NUMBER: US/10/267,565
;  CURRENT FILING DATE:  2003-01-23
;  PRIOR APPLICATION NUMBER: 09/401,839
;  PRIOR FILING DATE: 1999-09-22
;  PRIOR APPLICATION NUMBER: 08/459,151
;  PRIOR FILING DATE: 1995-06-02
;  PRIOR APPLICATION NUMBER: 08/205,011
;  PRIOR FILING DATE: 1994-03-02
;  PRIOR APPLICATION NUMBER: 07/857,023
;  PRIOR FILING DATE: 1992-03-24
;  PRIOR APPLICATION NUMBER: 07/572,284
;  PRIOR FILING DATE: 1990-08-27
;  PRIOR APPLICATION NUMBER: 07/520,935
;  PRIOR FILING DATE: 1990-05-09
;  PRIOR APPLICATION NUMBER: 07/455,708
;  PRIOR FILING DATE: 1989-12-22
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 856
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (170)...(826)
US-10-267-565-4

  Query Match             11.6%;  Score 65;  DB 7;  Length 856;
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Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
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Db        719 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 778

Qy        514 ATTCG 518
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Db        779 ATTCG 783


RESULT 94
US-10-373-456-17
; Sequence 17, Application US/10373456
; Publication No. US20040009146A1
; GENERAL INFORMATION:
;  APPLICANT: Podhajcer, Osvaldo
;  TITLE OF INVENTION: Anti-Tumor Vaccine and Method
;  FILE REFERENCE: 1423P-US/101141-14
;  CURRENT APPLICATION NUMBER: US/10/373,456
;  CURRENT FILING DATE:  2003-02-25
;  PRIOR APPLICATION NUMBER: US 60/359,836
;  PRIOR FILING DATE: 2002-02-26
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
;   LENGTH: 868
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-373-456-17

  Query Match             11.6%;  Score 65;  DB 7;  Length 868;
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Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
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Db        561 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 620

Qy        514 ATTCG 518
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Db        621 ATTCG 625


RESULT 95
US-10-172-399-5
; Sequence 5, Application US/10172399
; Publication No. US20030045495A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Chuan-Yuan
;  APPLICANT:  Dewhirst, Mark
;  APPLICANT:  Huang, Qian
;  TITLE OF INVENTION: A METHOD FOR SELECTIVE EXPRESSION OF THERAPEUTIC GENES BY HYPERTHI
;  FILE REFERENCE: 180-129
;  CURRENT APPLICATION NUMBER: US/10/172,399
;  CURRENT FILING DATE:  2002-06-14
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 1026
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (170)..(829)
US-10-172-399-5

  Query Match             11.6%;  Score 65;  DB 6;  Length 1026;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
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Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
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Db        719 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 778

Qy        514 ATTCG 518
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Db        779 ATTCG 783


RESULT 96
US-10-641-643-1041
; Sequence 1041, Application US/10641643
; Publication No. US20040077003A1
;   GENERAL INFORMATION:
;        APPLICANT: Cocks, Benjamin G.
;                   Susan G. Stuart
;                   Jeffrey J. Seilhamer
;        TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
;                            GENE EXPRESSION
;        NUMBER OF SEQUENCES: 1508
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;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
;            STREET: 3174 PORTER DRIVE
;            CITY: PALO ALTO
;            STATE: CALIFORNIA
;            COUNTRY: USA
;            ZIP: 94304
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/641,643
;            FILING DATE: 14-Aug-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: <Unknown>
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Zeller, Karen J.
;            REGISTRATION NUMBER: 37,071
;            REFERENCE/DOCKET NUMBER: PA-0001 US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (650) 855-0555
;            TELEFAX: (650) 845-4166
;   INFORMATION FOR SEQ ID NO: 1041:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1026 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       IMMEDIATE SOURCE:
;            LIBRARY: GENBANK
;            CLONE: g180623
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1041 :
US-10-641-643-1041

  Query Match             11.6%;  Score 65;  DB 8;  Length 1026;
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Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
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Db        719 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 778

Qy        514 ATTCG 518
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Db        779 ATTCG 783


RESULT 97
US-10-603-064-6
; Sequence 6, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
;  APPLICANT: Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION: Multiple Cytokine Protein Complexes
;  FILE REFERENCE: LEX-010
;  CURRENT APPLICATION NUMBER: US/10/603,064
;  CURRENT FILING DATE:  2003-06-24
;  PRIOR APPLICATION NUMBER: US/09/634,368
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: 60/147,924
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 1287
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: human Fc-p35
;   OTHER INFORMATION: fusion protein coding sequence
US-10-603-064-6

  Query Match             11.6%;  Score 65;  DB 8;  Length 1287;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
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Db       1177 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1236

Qy        514 ATTCG 518
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Db       1237 ATTCG 1241


RESULT 98
US-10-476-960-3
; Sequence 3, Application US/10476960
; Publication No. US20040248828A1
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Isis Pharmaceuticals, Inc.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTSP-0392
;  CURRENT APPLICATION NUMBER: US/10/476,960
;  CURRENT FILING DATE:  2003-11-05
;  PRIOR APPLICATION NUMBER: 09/851,520
;  PRIOR FILING DATE: 2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
;   LENGTH: 1316
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (102)...(863)
US-10-476-960-3

  Query Match             11.6%;  Score 65;  DB 9;  Length 1316;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
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Db        753 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 812

Qy        514 ATTCG 518
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Db        813 ATTCG 817


RESULT 99
US-11-089-191-3
; Sequence 3, Application US/11089191
; Publication No. US20050261228A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Susan Gregory
;  APPLICANT:  Ronnie C. Hanecak
;  APPLICANT:  Kevin P. Anderson
;  APPLICANT:  Ming-Yi Chiang
;  APPLICANT:  Vickie Brown-Driver
;  APPLICANT:  David J. Ecker
;  APPLICANT:  Timothy Vickers
;  APPLICANT:  Jacqueline Wyatt
;  APPLICANT:  Eric G. Marcusson
;  APPLICANT:  Nicholas M. Dean
;  APPLICANT:  Sanjay Bhanot
```

```
;  APPLICANT:  Elizabeth J. Ackermann
;  APPLICANT:  Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: BNDL-0021US.P1
;  CURRENT APPLICATION NUMBER: US/11/089,191
;  CURRENT FILING DATE:  2005-03-23
;  PRIOR APPLICATION NUMBER: 10/476,960
;  PRIOR FILING DATE: 2003-11-07
;  PRIOR APPLICATION NUMBER: PCT/US02/13871
;  PRIOR FILING DATE: 2002-05-01
;  PRIOR APPLICATION NUMBER: 09/851,520
;  PRIOR FILING DATE: 2001-05-07
;  PRIOR APPLICATION NUMBER: 10/67,236
;  PRIOR FILING DATE: 2003-09-17
;  PRIOR APPLICATION NUMBER: 10/038,335
;  PRIOR FILING DATE: 2002-01-02
;  PRIOR APPLICATION NUMBER: 09/299,058
;  PRIOR FILING DATE: 1999-04-23
;  PRIOR APPLICATION NUMBER: 08/403,888
;  PRIOR FILING DATE: 1995-06-12
;  PRIOR APPLICATION NUMBER: PCT/US93/09297
;  PRIOR FILING DATE: 1993-09-29
;  PRIOR APPLICATION NUMBER: 07/954,185
;  PRIOR FILING DATE: 1992-09-29
;  PRIOR APPLICATION NUMBER: 10/515,546
;  PRIOR FILING DATE: 2004-11-23
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
;   LENGTH: 1316
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (102)...(863)
US-11-089-191-3

  Query Match             11.6%;  Score 65;  DB 15;  Length 1316;
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Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
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Db        753 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 812

Qy        514 ATTCG 518
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Db        813 ATTCG 817


RESULT 100
US-09-924-703-5
; Sequence 5, Application US/09924703
; Patent No. US20020137898A1
; GENERAL INFORMATION:
;  APPLICANT: TRINCHIERI, GIORGIO
;  APPLICANT:  PERUSSIA, BICE
;  APPLICANT:  CLARK, STEVEN C.
;  APPLICANT:  WONG, GORDON G.
;  APPLICANT:  HEWICK, RODNEY
;  APPLICANT:  KOBAYASHI, MICHIKO
;  TITLE OF INVENTION: ANTIBODIES TO NATURAL KILLER STIMULATORY FACTOR
;  FILE REFERENCE: 01142.0142.0100
;  CURRENT APPLICATION NUMBER: US/09/924,703
;  CURRENT FILING DATE:  2001-08-09
;  PRIOR APPLICATION NUMBER: 09/325,958
;  PRIOR FILING DATE: 1999-06-04
;  PRIOR APPLICATION NUMBER: 08/858,000
;  PRIOR FILING DATE: 1997-05-16
;  PRIOR APPLICATION NUMBER: 08/403,013
;  PRIOR FILING DATE: 1995-03-13
;  PRIOR APPLICATION NUMBER: 07/584,941
;  PRIOR FILING DATE: 1990-09-18
;  PRIOR APPLICATION NUMBER: 07/307,817
;  PRIOR FILING DATE: 1989-02-07
;  PRIOR APPLICATION NUMBER: 07/269,945
;  PRIOR FILING DATE: 1988-11-10
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 1395
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
;   OTHER INFORMATION: sequence of the 30 kD subunit of NKSF
;   NAME/KEY: CDS
;   LOCATION: (114)..(872)
US-09-924-703-5

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Qy        454 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 513
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Qy        514 ATTCG 518
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Db        825 ATTCG 829


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OM nucleic - nucleic search, using sw model

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8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	18	3.2	22	7	US-11-266-409-9	Sequence 9, Appli
	2	18	3.2	2324	7	US-11-293-697-1624	Sequence 1624, Ap
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c	4	17	3.0	2024	7	US-11-293-697-1253	Sequence 1253, Ap
c	5	17	3.0	5298	7	US-11-217-529-1583	Sequence 1583, Ap
	6	16	2.9	360	6	US-10-488-619-237	Sequence 237, App
	7	16	2.9	569	6	US-10-488-619-2250	Sequence 2250, Ap
c	8	16	2.9	807	6	US-10-488-619-2249	Sequence 2249, Ap
	9	16	2.9	861	7	US-11-217-529-585	Sequence 585, App
	10	16	2.9	1159	6	US-10-953-349-19286	Sequence 19286, A
c	11	16	2.9	1203	6	US-10-953-349-36627	Sequence 36627, A
c	12	16	2.9	1437	7	US-11-183-218-9	Sequence 9, Appli
	13	16	2.9	1536	6	US-10-471-571A-2411	Sequence 2411, Ap
	14	16	2.9	1575	6	US-10-953-349-16963	Sequence 16963, A
	15	16	2.9	1676	6	US-10-953-349-34653	Sequence 34653, A
	16	16	2.9	1859	7	US-11-293-697-326	Sequence 326, App
c	17	16	2.9	1944	7	US-11-217-529-78920	Sequence 78920, A
c	18	16	2.9	2243	6	US-10-511-937-2883	Sequence 2883, Ap
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	20	16	2.9	4293	7	US-11-217-529-76344	Sequence 76344, A
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	22	16	2.9	6383	6	US-10-511-937-2838	Sequence 2838, Ap
	23	16	2.9	138941	6	US-10-489-730-10	GENERAL INFORMATI
c	24	16	2.9	138941	6	US-10-489-730-10	GENERAL INFORMATI
c	25	15	2.7	25	7	US-11-217-529-105697	Sequence 105697,
	26	15	2.7	25	7	US-11-217-529-155757	Sequence 155757,
c	27	15	2.7	25	7	US-11-217-529-191540	Sequence 191540,
c	28	15	2.7	25	7	US-11-217-529-191845	Sequence 191845,
c	29	15	2.7	400	6	US-10-488-619-2364	Sequence 2364, Ap
	30	15	2.7	418	6	US-10-488-619-857	Sequence 857, App
	31	15	2.7	425	6	US-10-473-173-354	Sequence 354, App
	32	15	2.7	425	6	US-10-488-619-858	Sequence 858, App
	33	15	2.7	438	6	US-10-488-619-2365	Sequence 2365, Ap
	34	15	2.7	441	6	US-10-488-619-1356	Sequence 1356, Ap
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	36	15	2.7	510	7	US-11-217-529-79785	Sequence 79785, A
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c	39	15	2.7	612	7	US-11-217-529-77395	Sequence 77395, A
	40	15	2.7	630	6	US-10-953-349-12334	Sequence 12334, A
	41	15	2.7	630	6	US-10-953-349-25972	Sequence 25972, A
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	43	15	2.7	778	6	US-10-953-349-355	Sequence 355, App
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	46	15	2.7	906	7	US-11-217-529-174189	Sequence 174189,
	47	15	2.7	1046	6	US-10-953-349-39221	Sequence 39221, A
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	50	15	2.7	1176	7	US-11-217-529-79991	Sequence 79991, A
	51	15	2.7	1190	6	US-10-953-349-26534	Sequence 26534, A
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	58	15	2.7	1406	6	US-10-953-349-3438	Sequence 3438, Ap
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	60	15	2.7	1504	6	US-10-953-349-10170	Sequence 10170, A
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	63	15	2.7	1821	6	US-10-953-349-1943	Sequence 1943, Ap
	64	15	2.7	1869	6	US-10-953-349-12445	Sequence 12445, A
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	67	15	2.7	2151	7	US-11-293-697-153	Sequence 153, App
	68	15	2.7	2205	7	US-11-293-697-56	Sequence 56, Appl
	69	15	2.7	2241	7	US-11-217-529-2489	Sequence 2489, Ap
c	70	15	2.7	2400	7	US-11-217-529-80988	Sequence 80988, A
c	71	15	2.7	2537	7	US-11-293-697-2092	Sequence 2092, Ap
c	72	15	2.7	2650	7	US-11-293-697-749	Sequence 749, App
	73	15	2.7	4533	7	US-11-217-529-1172	Sequence 1172, Ap
	74	15	2.7	5171	6	US-10-501-834-216	Sequence 216, App
	75	15	2.7	5703	7	US-11-217-529-191092	Sequence 191092,
c	76	15	2.7	5734	6	US-10-505-928-28	Sequence 28, Appl
c	77	15	2.7	5874	7	US-11-313-450-15	Sequence 15, Appl
c	78	15	2.7	6826	6	US-10-505-928-330	Sequence 330, App
	79	15	2.7	128361	6	US-10-505-928-151	Sequence 151, App
c	80	15	2.7	261789	7	US-11-260-842-1	Sequence 1, Appli
	81	14	2.5	25	7	US-11-217-529-26117	Sequence 26117, A
	82	14	2.5	25	7	US-11-217-529-40959	Sequence 40959, A
	83	14	2.5	25	7	US-11-217-529-124406	Sequence 124406,
c	84	14	2.5	25	7	US-11-217-529-136455	Sequence 136455,
c	85	14	2.5	25	7	US-11-217-529-148494	Sequence 148494,
c	86	14	2.5	50	6	US-10-511-937-3058	Sequence 3058, Ap
c	87	14	2.5	258	6	US-10-471-571A-1747	Sequence 1747, Ap
c	88	14	2.5	312	7	US-11-217-529-5872	Sequence 5872, Ap
c	89	14	2.5	330	7	US-11-217-529-76063	Sequence 76063, A
	90	14	2.5	360	6	US-10-471-571A-127	Sequence 127, App
	91	14	2.5	381	7	US-11-217-529-166773	Sequence 166773,
c	92	14	2.5	410	6	US-10-473-173-293	Sequence 293, App
	93	14	2.5	426	6	US-10-488-619-2658	Sequence 2658, Ap
	94	14	2.5	449	6	US-10-473-173-445	Sequence 445, App
	95	14	2.5	453	7	US-11-217-529-82632	Sequence 82632, A
	96	14	2.5	467	6	US-10-488-619-943	Sequence 943, App
c	97	14	2.5	470	6	US-10-473-173-454	Sequence 454, App
	98	14	2.5	510	7	US-11-217-529-3168	Sequence 3168, Ap

99	14	2.5	541	6	US-10-488-619-949	Sequence 949, App
100	14	2.5	552	7	US-11-301-554-137	Sequence 137, App
101	14	2.5	555	7	US-11-217-529-76962	Sequence 76962, A
c 102	14	2.5	569	6	US-10-488-619-2455	Sequence 2455, Ap
103	14	2.5	578	6	US-10-488-619-1525	Sequence 1525, Ap
c 104	14	2.5	581	6	US-10-488-619-1940	Sequence 1940, Ap
105	14	2.5	586	6	US-10-488-619-1222	Sequence 1222, Ap
c 106	14	2.5	605	6	US-10-488-619-1416	Sequence 1416, Ap
107	14	2.5	606	6	US-10-488-619-2488	Sequence 2488, Ap
c 108	14	2.5	614	7	US-11-301-554-1307	Sequence 1307, Ap
c 109	14	2.5	615	7	US-11-217-529-81209	Sequence 81209, A
c 110	14	2.5	627	6	US-10-471-571A-3259	Sequence 3259, Ap
c 111	14	2.5	649	6	US-10-953-349-16024	Sequence 16024, A
112	14	2.5	667	6	US-10-953-349-26444	Sequence 26444, A
c 113	14	2.5	669	7	US-11-257-062-21	Sequence 21, Appl
114	14	2.5	714	7	US-11-217-529-173285	Sequence 173285,
c 115	14	2.5	717	6	US-10-471-571A-1489	Sequence 1489, Ap
116	14	2.5	747	6	US-10-953-349-30349	Sequence 30349, A
c 117	14	2.5	756	6	US-10-488-619-2529	Sequence 2529, Ap
c 118	14	2.5	756	7	US-11-217-529-173433	Sequence 173433,
119	14	2.5	759	7	US-11-217-529-5972	Sequence 5972, Ap
c 120	14	2.5	768	6	US-10-471-571A-1189	Sequence 1189, Ap
c 121	14	2.5	788	6	US-10-953-349-25425	Sequence 25425, A
122	14	2.5	795	7	US-11-217-529-190902	Sequence 190902,
123	14	2.5	810	6	US-10-488-619-2332	Sequence 2332, Ap
124	14	2.5	810	6	US-10-953-349-9058	Sequence 9058, Ap
125	14	2.5	818	6	US-10-488-619-2757	Sequence 2757, Ap
c 126	14	2.5	831	7	US-11-217-529-80137	Sequence 80137, A
c 127	14	2.5	847	6	US-10-953-349-6957	Sequence 6957, Ap
128	14	2.5	856	6	US-10-953-349-25491	Sequence 25491, A
c 129	14	2.5	884	6	US-10-953-349-297	Sequence 297, App
c 130	14	2.5	889	6	US-10-953-349-13941	Sequence 13941, A
131	14	2.5	909	6	US-10-953-349-26362	Sequence 26362, A
c 132	14	2.5	925	6	US-10-953-349-28311	Sequence 28311, A
c 133	14	2.5	932	6	US-10-953-349-22368	Sequence 22368, A
c 134	14	2.5	933	6	US-10-471-571A-5273	Sequence 5273, Ap
c 135	14	2.5	948	7	US-11-217-529-2070	Sequence 2070, Ap
c 136	14	2.5	956	6	US-10-953-349-3171	Sequence 3171, Ap
137	14	2.5	995	6	US-10-953-349-16178	Sequence 16178, A
c 138	14	2.5	1000	6	US-10-953-349-22396	Sequence 22396, A
139	14	2.5	1010	6	US-10-953-349-18832	Sequence 18832, A
c 140	14	2.5	1014	7	US-11-321-475-1	Sequence 1, Appli
c 141	14	2.5	1017	7	US-11-217-529-1998	Sequence 1998, Ap
c 142	14	2.5	1023	6	US-10-471-571A-255	Sequence 255, App
143	14	2.5	1032	7	US-11-217-529-4293	Sequence 4293, Ap
c 144	14	2.5	1040	6	US-10-953-349-7739	Sequence 7739, Ap
145	14	2.5	1044	6	US-10-953-349-14244	Sequence 14244, A
c 146	14	2.5	1083	6	US-10-471-571A-1795	Sequence 1795, Ap
147	14	2.5	1087	6	US-10-953-349-14786	Sequence 14786, A
148	14	2.5	1097	6	US-10-953-349-101	Sequence 101, App
c 149	14	2.5	1106	6	US-10-953-349-1012	Sequence 1012, Ap
150	14	2.5	1125	7	US-11-217-529-76126	Sequence 76126, A
151	14	2.5	1125	7	US-11-217-529-81925	Sequence 81925, A
c 152	14	2.5	1133	6	US-10-953-349-7324	Sequence 7324, Ap
c 153	14	2.5	1160	6	US-10-953-349-14240	Sequence 14240, A
c 154	14	2.5	1174	6	US-10-953-349-7440	Sequence 7440, Ap
155	14	2.5	1176	7	US-11-121-154-118	Sequence 118, App
c 156	14	2.5	1177	6	US-10-196-749-381	Sequence 381, App
c 157	14	2.5	1177	7	US-11-101-316-129	Sequence 129, App
c 158	14	2.5	1178	6	US-10-953-349-17819	Sequence 17819, A
159	14	2.5	1185	7	US-11-217-529-5626	Sequence 5626, Ap
c 160	14	2.5	1197	7	US-11-122-986-301	Sequence 301, App
c 161	14	2.5	1197	7	US-11-122-986-303	Sequence 303, App
162	14	2.5	1212	6	US-10-953-349-20909	Sequence 20909, A
163	14	2.5	1227	6	US-10-713-648A-43	Sequence 43, Appl
c 164	14	2.5	1253	6	US-10-953-349-1509	Sequence 1509, Ap
165	14	2.5	1266	7	US-11-217-529-4799	Sequence 4799, Ap
166	14	2.5	1272	7	US-11-217-529-1909	Sequence 1909, Ap
c 167	14	2.5	1274	6	US-10-953-349-28054	Sequence 28054, A
168	14	2.5	1284	7	US-11-217-529-5325	Sequence 5325, Ap
c 169	14	2.5	1284	7	US-11-217-529-77448	Sequence 77448, A
170	14	2.5	1307	6	US-10-953-349-20901	Sequence 20901, A
171	14	2.5	1310	6	US-10-953-349-10264	Sequence 10264, A
c 172	14	2.5	1318	6	US-10-953-349-17559	Sequence 17559, A
c 173	14	2.5	1320	6	US-10-953-349-33465	Sequence 33465, A
174	14	2.5	1325	6	US-10-953-349-24008	Sequence 24008, A
175	14	2.5	1357	6	US-10-953-349-10776	Sequence 10776, A
176	14	2.5	1376	6	US-10-953-349-2456	Sequence 2456, Ap
177	14	2.5	1388	7	US-11-268-011-2	Sequence 2, Appli
178	14	2.5	1419	6	US-10-953-349-19413	Sequence 19413, A
179	14	2.5	1422	7	US-11-217-529-76672	Sequence 76672, A
c 180	14	2.5	1434	6	US-10-953-349-23886	Sequence 23886, A
181	14	2.5	1461	6	US-10-975-692-1	Sequence 1, Appli
c 182	14	2.5	1467	6	US-10-953-349-26032	Sequence 26032, A
c 183	14	2.5	1476	7	US-11-217-529-5188	Sequence 5188, Ap
184	14	2.5	1490	6	US-10-953-349-19469	Sequence 19469, A
185	14	2.5	1491	7	US-11-217-529-1027	Sequence 1027, Ap
c 186	14	2.5	1497	6	US-10-953-349-15738	Sequence 15738, A
c 187	14	2.5	1502	7	US-11-338-399-11	Sequence 11, Appl
188	14	2.5	1545	7	US-11-217-529-79070	Sequence 79070, A
189	14	2.5	1548	7	US-11-217-529-78132	Sequence 78132, A
c 190	14	2.5	1578	6	US-10-953-349-33142	Sequence 33142, A
191	14	2.5	1583	6	US-10-953-349-23893	Sequence 23893, A
192	14	2.5	1584	7	US-11-217-529-75662	Sequence 75662, A
c 193	14	2.5	1589	6	US-10-953-349-23807	Sequence 23807, A
194	14	2.5	1602	7	US-11-217-529-5803	Sequence 5803, Ap
195	14	2.5	1602	7	US-11-217-529-79080	Sequence 79080, A
196	14	2.5	1602	7	US-11-217-529-79081	Sequence 79081, A
c 197	14	2.5	1608	6	US-10-953-349-8942	Sequence 8942, Ap
c 198	14	2.5	1635	7	US-11-217-529-2352	Sequence 2352, Ap
c 199	14	2.5	1652	7	US-11-335-754-2	Sequence 2, Appli
200	14	2.5	1688	6	US-10-953-349-8351	Sequence 8351, Ap

ALIGNMENTS

```
RESULT 1
US-11-266-409-9
; Sequence 9, Application US/11266409
; Publication No. US20060093578A1
; GENERAL INFORMATION:
;  APPLICANT: SUZUMURA, AKIO
;  TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATING MULTIPLE SCLEROSIS
;  FILE REFERENCE: 279847US40
;  CURRENT APPLICATION NUMBER: US/11/266,409
;  CURRENT FILING DATE:  2005-11-04
;  PRIOR APPLICATION NUMBER: US 60/624,851
;  PRIOR FILING DATE: 2004-11-04
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA
US-11-266-409-9

  Query Match             3.2%;  Score 18;  DB 7;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.4;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        292 GACTTGAAGATGTACCAG 309
              ||||||||||||||||||
Db          1 GACTTGAAGATGTACCAG 18


RESULT 2
US-11-293-697-1624
; Sequence 1624, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
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;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1624
;   LENGTH: 2324
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1624

  Query Match             3.2%;  Score 18;  DB 7;  Length 2324;
  Best Local Similarity   100.0%;  Pred. No. 1.7;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        229 AGTTGCCTGGCCTCCAGA 246
              ||||||||||||||||||
Db        170 AGTTGCCTGGCCTCCAGA 187


RESULT 3
US-11-217-529-1610/c
; Sequence 1610, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1610
;   LENGTH: 918
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-1610

  Query Match             3.0%;  Score 17;  DB 7;  Length 918;
  Best Local Similarity   100.0%;  Pred. No. 5.8;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        114 TCATGAAGATATCACAA 130
              |||||||||||||||||
Db        223 TCATGAAGATATCACAA 207


RESULT 4
US-11-293-697-1253/c
; Sequence 1253, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1253
;   LENGTH: 2024
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1253

  Query Match             3.0%;  Score 17;  DB 7;  Length 2024;
  Best Local Similarity   100.0%;  Pred. No. 6.1;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        410 CCCTGAATGTCAACAGT 426
              |||||||||||||||||
Db        191 CCCTGAATGTCAACAGT 175


RESULT 5
US-11-217-529-1583/c
; Sequence 1583, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1583
;   LENGTH: 5298
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-1583

  Query Match             3.0%;  Score 17;  DB 7;  Length 5298;
  Best Local Similarity   100.0%;  Pred. No. 6.4;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        496 CTTCTTCATGCTTTCAG 512
              |||||||||||||||||
Db       1938 CTTCTTCATGCTTTCAG 1922


RESULT 6
US-10-488-619-237
; Sequence 237, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations W
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 237
;   LENGTH: 360
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(444)
;   OTHER INFORMATION: N IS G, C, A OR T
US-10-488-619-237

  Query Match             2.9%;  Score 16;  DB 6;  Length 360;
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Qy        103 GAAGAGATTGATCATG 118
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Db        248 GAAGAGATTGATCATG 263


RESULT 7
US-10-488-619-2250
; Sequence 2250, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2250
;   LENGTH: 569
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-488-619-2250

  Query Match             2.9%;  Score 16;  DB 6;  Length 569;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        445 TCCTCCCTGGAAGAAC 460
              ||||||||||||||||
Db        379 TCCTCCCTGGAAGAAC 394


RESULT 8
US-10-488-619-2249/c
; Sequence 2249, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2249
;   LENGTH: 807
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-488-619-2249

  Query Match             2.9%;  Score 16;  DB 6;  Length 807;
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Qy        445 TCCTCCCTGGAAGAAC 460
              ||||||||||||||||
Db        420 TCCTCCCTGGAAGAAC 405


RESULT 9
US-11-217-529-585
; Sequence 585, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 585
;   LENGTH: 861
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-585

  Query Match             2.9%;  Score 16;  DB 7;  Length 861;
  Best Local Similarity   100.0%;  Pred. No. 21;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        291 GGACTTGAAGATGTAC 306
              ||||||||||||||||
Db        370 GGACTTGAAGATGTAC 385


RESULT 10
US-10-953-349-19286
; Sequence 19286, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19286
;   LENGTH: 1159
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-19286

  Query Match             2.9%;  Score 16;  DB 6;  Length 1159;
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  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        291 GGACTTGAAGATGTAC 306
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Db        561 GGACTTGAAGATGTAC 576


RESULT 11
US-10-953-349-36627/c
; Sequence 36627, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36627
;   LENGTH: 1203
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-36627

  Query Match             2.9%;  Score 16;  DB 6;  Length 1203;
  Best Local Similarity   100.0%;  Pred. No. 21;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        492 CATACTTCTTCATGCT 507
```

```
              ||||||||||||||||
Db        531 CATACTTCTTCATGCT 516


RESULT 12
US-11-183-218-9/c
; Sequence 9, Application US/11183218
; Publication No. US20060088906A1
; GENERAL INFORMATION:
;  APPLICANT: Neose Technologies, Inc.
;  APPLICANT:  DeFrees, Shawn
;  APPLICANT:  Zopf, David
;  APPLICANT:  Bayer, Robert
;  APPLICANT:  Hakes, David
;  APPLICANT:  Chen, Xi
;  APPLICANT:  Bowe, Caryne
;  TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND
;  TITLE OF INVENTION: GLYCOCONJUGATION OF ERYTHROPOIETIN
;  FILE REFERENCE: 040853-01-5083-US02
;  CURRENT APPLICATION NUMBER: US/11/183,218
;  CURRENT FILING DATE:  2005-07-15
;  PRIOR APPLICATION NUMBER: US 10/410,945
;  PRIOR FILING DATE: 2003-04-09
;  PRIOR APPLICATION NUMBER: PCT/US02/32263
;  PRIOR FILING DATE: 2002-10-09
;  PRIOR APPLICATION NUMBER: US 60/407,527
;  PRIOR FILING DATE: 2002-08-28
;  PRIOR APPLICATION NUMBER: US 60/404,249
;  PRIOR FILING DATE: 2002-08-16
;  PRIOR APPLICATION NUMBER: US 60/396,594
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: US 60/391,777
;  PRIOR FILING DATE: 2002-06-25
;  PRIOR APPLICATION NUMBER: US 60/387,292
;  PRIOR FILING DATE: 2002-06-07
;  PRIOR APPLICATION NUMBER: US 60/344,692
;  PRIOR FILING DATE: 2001-11-19
;  PRIOR APPLICATION NUMBER: US 60/334,301
;  PRIOR FILING DATE: 2001-11-28
;  PRIOR APPLICATION NUMBER: US 60/334,233
;  PRIOR FILING DATE: 2001-11-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
;   LENGTH: 1437
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-183-218-9

  Query Match             2.9%;  Score 16;  DB 7;  Length 1437;
  Best Local Similarity   100.0%;  Pred. No. 21;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        347 ATCCTAAAAGGCAGAT 362
              ||||||||||||||||
Db         64 ATCCTAAAAGGCAGAT 49


RESULT 13
US-10-471-571A-2411
; Sequence 2411, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 2411
;   LENGTH: 1536
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-2411

  Query Match             2.9%;  Score 16;  DB 6;  Length 1536;
  Best Local Similarity   100.0%;  Pred. No. 21;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        470 ATAAAACTAAAATCAA 485
              ||||||||||||||||
Db        983 ATAAAACTAAAATCAA 998


RESULT 14
US-10-953-349-16963
; Sequence 16963, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16963
;   LENGTH: 1575
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-16963

  Query Match             2.9%;  Score 16;  DB 6;  Length 1575;
  Best Local Similarity   100.0%;  Pred. No. 21;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        314 AGTTCAAGGCCATGAA 329
              ||||||||||||||||
Db        613 AGTTCAAGGCCATGAA 628


RESULT 15
US-10-953-349-34653
; Sequence 34653, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34653
;   LENGTH: 1676
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-34653

  Query Match             2.9%;  Score 16;  DB 6;  Length 1676;
  Best Local Similarity   100.0%;  Pred. No. 21;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        114 TCATGAAGATATCACA 129
              ||||||||||||||||
Db       1426 TCATGAAGATATCACA 1441


RESULT 16
US-11-293-697-326
```

; Sequence 326, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 326
; LENGTH: 1859
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-326

Query Match 2.9%; Score 16; DB 7; Length 1859;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 304 TACCAGGTGGAGTTCA 319
||||||||||||||||
Db 386 TACCAGGTGGAGTTCA 401

RESULT 17
US-11-217-529-78920/c
; Sequence 78920, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78920
; LENGTH: 1944
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78920

Query Match 2.9%; Score 16; DB 7; Length 1944;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 GAGCCATCAGCAACAC 56
||||||||||||||||
Db 1790 GAGCCATCAGCAACAC 1775

RESULT 18
US-10-511-937-2883/c
; Sequence 2883, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2883
; LENGTH: 2243
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (39)..(39)
; OTHER INFORMATION: n is a, c, g, t or u
US-10-511-937-2883

Query Match 2.9%; Score 16; DB 6; Length 2243;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 178 ATGAATGAGAGTTGCC 193
||||||||||||||||
Db 560 ATGAATGAGAGTTGCC 545

RESULT 19
US-11-293-697-520/c
; Sequence 520, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 520
; LENGTH: 2836
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-520

Query Match 2.9%; Score 16; DB 7; Length 2836;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 357 GCAGATCTTTCTGGAT 372
||||||||||||||||
Db 2681 GCAGATCTTTCTGGAT 2666

RESULT 20
US-11-217-529-76344
; Sequence 76344, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO

```
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76344
;   LENGTH: 4293
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-76344

  Query Match             2.9%;  Score 16;  DB 7;  Length 4293;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        390 TATTGATGAGCTGTTA 405
              ||||||||||||||||
Db       1146 TATTGATGAGCTGTTA 1161


RESULT 21
US-11-248-986-13/c
; Sequence 13, Application US/11248986
; Publication No. US20060112448A1
; GENERAL INFORMATION:
;  APPLICANT: OSBOURN, ANNE E.
;  APPLICANT:  QI, XIAOQUAN
;  TITLE OF INVENTION: ENZYMES INVOLVED IN TRITERPENE SYNTHESIS
;  FILE REFERENCE: BB1550 US NA
;  CURRENT APPLICATION NUMBER: US/11/248,986
;  CURRENT FILING DATE:  2005-10-12
;  PRIOR APPLICATION NUMBER: 60/619,203
;  PRIOR FILING DATE: 2004-10-15
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
;   LENGTH: 5992
;   TYPE: DNA
;   ORGANISM: Avena strigosa
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(5992)
;   OTHER INFORMATION: Genomic sequence for AsCYP51H
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(5992)
;   OTHER INFORMATION: Genomic sequence for AsCYP51H10
US-11-248-986-13

  Query Match             2.9%;  Score 16;  DB 7;  Length 5992;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        472 AAAACTAAAATCAAGC 487
              ||||||||||||||||
Db       2978 AAAACTAAAATCAAGC 2963


RESULT 22
US-10-511-937-2838
; Sequence 2838, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
;  APPLICANT: EXPRESSION DIAGNOSTICS, INC.
;  APPLICANT:  Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  APPLICANT:  Prentice, James
;  APPLICANT:  Morris, MacDonald
;  APPLICANT:  Rosenberg, Steven
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
;  TITLE OF INVENTION:  AND MONITORING TRANSPLANT REJECTION
;  FILE REFERENCE: 506612000104
;  CURRENT APPLICATION NUMBER: US/10/511,937
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: PCT/US2003/012946
;  PRIOR FILING DATE: 2003-04-24
;  PRIOR APPLICATION NUMBER: US 10/131,831
;  PRIOR FILING DATE: 2002-04-24
;  PRIOR APPLICATION NUMBER: US 10/325,899
;  PRIOR FILING DATE: 2002-12-20
;  NUMBER OF SEQ ID NOS: 3117
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2838
;   LENGTH: 6383
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-511-937-2838

  Query Match             2.9%;  Score 16;  DB 6;  Length 6383;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        244 AGAAAGACCTCTTTTA 259
              ||||||||||||||||
Db        438 AGAAAGACCTCTTTTA 453


RESULT 23
US-10-489-730-10
; GENERAL INFORMATION:
;  APPLICANT: Melino, Gennaro
;  APPLICANT:  Hayes, Ian
;  APPLICANT:  de Laurenzi, Vincenzo
;  APPLICANT:  Barcaroli, Daniela
;  APPLICANT:  Candi, Eleonora
;  APPLICANT:  Bernassola, Francesca
;  APPLICANT:  Tobler, Andreas
;  APPLICANT:  Novak, Urban
;  TITLE OF INVENTION: Human Delta-N p73 Molecules and Uses Thereof
;  FILE REFERENCE: 19319.002
;  CURRENT APPLICATION NUMBER: US/10/489,730
;  CURRENT FILING DATE:  2004-03-16
;  PRIOR APPLICATION NUMBER: PCT/GB02/04238
;  PRIOR FILING DATE: 2002-09-17
;  PRIOR APPLICATION NUMBER: US 60/322,436
;  PRIOR FILING DATE: 2001-09-17
;  NUMBER OF SEQ ID NOS: 39
;   OTHER INFORMATION: reverse complement of exons 14 through 1 as reported in GenBank Ac
US-10-489-730-10

  Query Match             2.9%;  Score 16;  DB 6;  Length 138941;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         60 TCAGAAGGCCAGACAA 75
              ||||||||||||||||
Db      28208 TCAGAAGGCCAGACAA 28223


RESULT 24
US-10-489-730-10/c
; GENERAL INFORMATION:
;  APPLICANT: Melino, Gennaro
;  APPLICANT:  Hayes, Ian
;  APPLICANT:  de Laurenzi, Vincenzo
;  APPLICANT:  Barcaroli, Daniela
;  APPLICANT:  Candi, Eleonora
;  APPLICANT:  Bernassola, Francesca
;  APPLICANT:  Tobler, Andreas
;  APPLICANT:  Novak, Urban
;  TITLE OF INVENTION: Human Delta-N p73 Molecules and Uses Thereof
```

```
;  FILE REFERENCE: 19319.002
;  CURRENT APPLICATION NUMBER: US/10/489,730
;  CURRENT FILING DATE:  2004-03-16
;  PRIOR APPLICATION NUMBER: PCT/GB02/04238
;  PRIOR FILING DATE: 2002-09-17
;  PRIOR APPLICATION NUMBER: US 60/322,436
;  PRIOR FILING DATE: 2001-09-17
;  NUMBER OF SEQ ID NOS: 39
;   OTHER INFORMATION: reverse complement of exons 14 through 1 as reported in GenBank A
US-10-489-730-10

  Query Match             2.9%;  Score 16;  DB 6;  Length 138941;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        465 TTTTTATAAAACTAAA 480
              ||||||||||||||||
Db      33604 TTTTTATAAAACTAAA 33589


RESULT 25
US-11-217-529-105697/c
; Sequence 105697, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 105697
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-105697

  Query Match             2.7%;  Score 15;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 61;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        309 GGTGGAGTTCAAGGC 323
              |||||||||||||||
Db         17 GGTGGAGTTCAAGGC 3


RESULT 26
US-11-217-529-155757
; Sequence 155757, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 155757
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-155757

  Query Match             2.7%;  Score 15;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 61;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        488 TCTGCATACTTCTTC 502
              |||||||||||||||
Db          5 TCTGCATACTTCTTC 19


RESULT 27
US-11-217-529-191540/c
; Sequence 191540, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 191540
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-191540

  Query Match             2.7%;  Score 15;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 61;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        117 TGAAGATATCACAAA 131
              |||||||||||||||
Db         19 TGAAGATATCACAAA 5


RESULT 28
US-11-217-529-191845/c
; Sequence 191845, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 191845
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-191845
```

```
  Query Match             2.7%;  Score 15;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 61;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        205 GAGATCTCTCTGATA 219
              |||||||||||||||
Db         17 GAGATCTCTCTGATA 3


RESULT 29
US-10-488-619-2364/c
; Sequence 2364, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2364
;   LENGTH: 400
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-488-619-2364

  Query Match             2.7%;  Score 15;  DB 6;  Length 400;
  Best Local Similarity   100.0%;  Pred. No. 70;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        414 GAATGTCAACAGTGT 428
              |||||||||||||||
Db        285 GAATGTCAACAGTGT 271


RESULT 30
US-10-488-619-857
; Sequence 857, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 857
;   LENGTH: 418
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(418)
;   OTHER INFORMATION: n is g, c, a or t
US-10-488-619-857

  Query Match             2.7%;  Score 15;  DB 6;  Length 418;
  Best Local Similarity   100.0%;  Pred. No. 70;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        177 CATGAATGAGAGTTG 191
              |||||||||||||||
Db         24 CATGAATGAGAGTTG 38


RESULT 31
US-10-473-173-354
; Sequence 354, Application US/10473173
; Publication No. US20060088823A1
; GENERAL INFORMATION:
;  APPLICANT: VAN ANDEL INSTITUTE
;  TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell
;  TITLE OF INVENTION:  Carcinoma: Prognosis and Drug Target Identification
;  FILE REFERENCE: 38345-170094
;  CURRENT APPLICATION NUMBER: US/10/473,173
;  CURRENT FILING DATE:  2003-09-29
;  PRIOR APPLICATION NUMBER: US 60/279,411
;  PRIOR FILING DATE: 2001-03-29
;  NUMBER OF SEQ ID NOS: 498
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 354
;   LENGTH: 425
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: n can be a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (23)..(24)
;   OTHER INFORMATION: n can be a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (425)..(425)
;   OTHER INFORMATION: n can be a, c, g or t
US-10-473-173-354

  Query Match             2.7%;  Score 15;  DB 6;  Length 425;
  Best Local Similarity   100.0%;  Pred. No. 71;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        177 CATGAATGAGAGTTG 191
              |||||||||||||||
Db         26 CATGAATGAGAGTTG 40


RESULT 32
US-10-488-619-858
; Sequence 858, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations W
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 858
;   LENGTH: 425
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(425)
;   OTHER INFORMATION: n is g, a, c or t
US-10-488-619-858

  Query Match             2.7%;  Score 15;  DB 6;  Length 425;
  Best Local Similarity   100.0%;  Pred. No. 71;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        177 CATGAATGAGAGTTG 191
              |||||||||||||||
Db         26 CATGAATGAGAGTTG 40


RESULT 33
US-10-488-619-2365
```

; Sequence 2365, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2365
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(438)
; OTHER INFORMATION: n is g, c, a or t
US-10-488-619-2365

Query Match 2.7%; Score 15; DB 6; Length 438;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 414 GAATGTCAACAGTGT 428
||||||||||||||
Db 105 GAATGTCAACAGTGT 119

RESULT 34
US-10-488-619-1356
; Sequence 1356, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1356
; LENGTH: 441
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1356

Query Match 2.7%; Score 15; DB 6; Length 441;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 128 CAAAAGATAAAACCA 142
||||||||||||||
Db 121 CAAAAGATAAAACCA 135

RESULT 35
US-11-217-529-81573
; Sequence 81573, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81573
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-81573

Query Match 2.7%; Score 15; DB 7; Length 507;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 530 TCAATAGAATGATGA 544
|||||||||||||||
Db 23 TCAATAGAATGATGA 37

RESULT 36
US-11-217-529-79785
; Sequence 79785, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79785
; LENGTH: 510
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79785

Query Match 2.7%; Score 15; DB 7; Length 510;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 CCGAAGAGATTGATC 115
|||||||||||||||
Db 80 CCGAAGAGATTGATC 94

RESULT 37
US-11-217-529-81860
; Sequence 81860, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81860

```
;   LENGTH: 576
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-81860

  Query Match             2.7%;  Score 15;  DB 7;  Length 576;
  Best Local Similarity   100.0%;  Pred. No. 72;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        488 TCTGCATACTTCTTC 502
              |||||||||||||||
Db        328 TCTGCATACTTCTTC 342


RESULT 38
US-10-953-349-39845/c
; Sequence 39845, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39845
;   LENGTH: 608
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-39845

  Query Match             2.7%;  Score 15;  DB 6;  Length 608;
  Best Local Similarity   100.0%;  Pred. No. 72;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        207 GATCTCTCTGATAAC 221
              |||||||||||||||
Db         67 GATCTCTCTGATAAC 53


RESULT 39
US-11-217-529-77395/c
; Sequence 77395, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77395
;   LENGTH: 612
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-77395

  Query Match             2.7%;  Score 15;  DB 7;  Length 612;
  Best Local Similarity   100.0%;  Pred. No. 72;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        309 GGTGGAGTTCAAGGC 323
              |||||||||||||||
Db         24 GGTGGAGTTCAAGGC 10


RESULT 40
US-10-953-349-12334
; Sequence 12334, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12334
;   LENGTH: 630
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (591)..(591)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-12334

  Query Match             2.7%;  Score 15;  DB 6;  Length 630;
  Best Local Similarity   100.0%;  Pred. No. 72;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         21 CCACTCCCAAACCCT 35
              |||||||||||||||
Db         14 CCACTCCCAAACCCT 28


RESULT 41
US-10-953-349-25972
; Sequence 25972, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25972
;   LENGTH: 630
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-10-953-349-25972

  Query Match             2.7%;  Score 15;  DB 6;  Length 630;
  Best Local Similarity   100.0%;  Pred. No. 72;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         21 CCACTCCCAAACCCT 35
              |||||||||||||||
Db         14 CCACTCCCAAACCCT 28


RESULT 42
US-11-217-529-190869/c
; Sequence 190869, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
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;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 190869
;   LENGTH: 768
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-190869

  Query Match             2.7%;  Score 15;  DB 7;  Length 768;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        205 GAGATCTCTCTGATA 219
              |||||||||||||||
Db        163 GAGATCTCTCTGATA 149


RESULT 43
US-10-953-349-355
; Sequence 355, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 355
;   LENGTH: 778
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-355

  Query Match             2.7%;  Score 15;  DB 6;  Length 778;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         98 CTTCCGAAGAGATTG 112
              |||||||||||||||
Db         41 CTTCCGAAGAGATTG 55


RESULT 44
US-10-488-619-1355/c
; Sequence 1355, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1355
;   LENGTH: 782
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(782)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-488-619-1355

  Query Match             2.7%;  Score 15;  DB 6;  Length 782;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        128 CAAAAGATAAAACCA 142
              |||||||||||||||
Db        663 CAAAAGATAAAACCA 649


RESULT 45
US-11-217-529-5224/c
; Sequence 5224, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5224
;   LENGTH: 906
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-5224

  Query Match             2.7%;  Score 15;  DB 7;  Length 906;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        271 TGCCTTAGCAGTATC 285
              |||||||||||||||
Db        852 TGCCTTAGCAGTATC 838


RESULT 46
US-11-217-529-174189
; Sequence 174189, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174189
;   LENGTH: 906
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-174189

  Query Match             2.7%;  Score 15;  DB 7;  Length 906;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy        334 AAGCTGTTAATGGAT 348
              ||||||||||||||
Db        614 AAGCTGTTAATGGAT 628


RESULT 47
US-10-953-349-39221
; Sequence 39221, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39221
;   LENGTH: 1046
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-39221

  Query Match             2.7%;  Score 15;  DB 6;  Length 1046;
  Best Local Similarity   100.0%;  Pred. No. 74;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        376 AACATGCTGACAGCT 390
              ||||||||||||||
Db        383 AACATGCTGACAGCT 397


RESULT 48
US-10-953-349-17993/c
; Sequence 17993, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17993
;   LENGTH: 1124
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-17993

  Query Match             2.7%;  Score 15;  DB 6;  Length 1124;
  Best Local Similarity   100.0%;  Pred. No. 74;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        116 ATGAAGATATCACAA 130
              ||||||||||||||
Db        883 ATGAAGATATCACAA 869


RESULT 49
US-10-953-349-31118/c
; Sequence 31118, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31118
;   LENGTH: 1156
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-10-953-349-31118

  Query Match             2.7%;  Score 15;  DB 6;  Length 1156;
  Best Local Similarity   100.0%;  Pred. No. 74;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        216 GATAACTAATGGGAG 230
              ||||||||||||||
Db       1030 GATAACTAATGGGAG 1016


RESULT 50
US-11-217-529-79991
; Sequence 79991, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79991
;   LENGTH: 1176
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-79991

  Query Match             2.7%;  Score 15;  DB 7;  Length 1176;
  Best Local Similarity   100.0%;  Pred. No. 74;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        176 CCATGAATGAGAGTT 190
              ||||||||||||||
Db        842 CCATGAATGAGAGTT 856


RESULT 51
US-10-953-349-26534
; Sequence 26534, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26534
;   LENGTH: 1190
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-10-953-349-26534

  Query Match             2.7%;  Score 15;  DB 6;  Length 1190;
  Best Local Similarity   100.0%;  Pred. No. 74;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy        384 GACAGCTATTGATGA 398
              ||||||||||||||
Db        884 GACAGCTATTGATGA 898


RESULT 52
US-10-953-349-19889
; Sequence 19889, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19889
;   LENGTH: 1206
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-19889

  Query Match             2.7%;  Score 15;  DB 6;  Length 1206;
  Best Local Similarity   100.0%;  Pred. No. 74;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        479 AAATCAAGCTCTGCA 493
              |||||||||||||||
Db       1008 AAATCAAGCTCTGCA 1022


RESULT 53
US-11-217-529-79181
; Sequence 79181, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79181
;   LENGTH: 1269
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-79181

  Query Match             2.7%;  Score 15;  DB 7;  Length 1269;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        102 CGAAGAGATTGATCA 116
              |||||||||||||||
Db        348 CGAAGAGATTGATCA 362


RESULT 54
US-10-953-349-32614
; Sequence 32614, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32614
;   LENGTH: 1271
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-10-953-349-32614

  Query Match             2.7%;  Score 15;  DB 6;  Length 1271;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        315 GTTCAAGGCCATGAA 329
              |||||||||||||||
Db       1052 GTTCAAGGCCATGAA 1066


RESULT 55
US-10-953-349-9401
; Sequence 9401, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9401
;   LENGTH: 1302
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-9401

  Query Match             2.7%;  Score 15;  DB 6;  Length 1302;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        365 TTCTGGATCAAAACA 379
              |||||||||||||||
Db        546 TTCTGGATCAAAACA 560


RESULT 56
US-11-217-529-79465
; Sequence 79465, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79465
;   LENGTH: 1305
;   TYPE: DNA
```

```
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-79465

  Query Match             2.7%;  Score 15;  DB 7;  Length 1305;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        123 TATCACAAAAGATAA 137
              |||||||||||||||
Db       1291 TATCACAAAAGATAA 1305


RESULT 57
US-11-217-529-190840/c
; Sequence 190840, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 190840
;   LENGTH: 1404
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-190840

  Query Match             2.7%;  Score 15;  DB 7;  Length 1404;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        117 TGAAGATATCACAAA 131
              |||||||||||||||
Db        838 TGAAGATATCACAAA 824


RESULT 58
US-10-953-349-3438
; Sequence 3438, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3438
;   LENGTH: 1406
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-3438

  Query Match             2.7%;  Score 15;  DB 6;  Length 1406;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        336 GCTGTTAATGGATCC 350
              |||||||||||||||
Db        976 GCTGTTAATGGATCC 990


RESULT 59
US-10-953-349-20272/c
; Sequence 20272, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20272
;   LENGTH: 1493
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-20272

  Query Match             2.7%;  Score 15;  DB 6;  Length 1493;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        136 AAAACCAGCACAGTG 150
              |||||||||||||||
Db        184 AAAACCAGCACAGTG 170


RESULT 60
US-10-953-349-10170
; Sequence 10170, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10170
;   LENGTH: 1504
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-10170

  Query Match             2.7%;  Score 15;  DB 6;  Length 1504;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        365 TTCTGGATCAAAACA 379
              |||||||||||||||
Db        583 TTCTGGATCAAAACA 597


RESULT 61
US-10-953-349-13708
; Sequence 13708, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13708
;   LENGTH: 1539
;   TYPE: DNA
```

```
;   ORGANISM: Glycine max
US-10-953-349-13708

  Query Match             2.7%;  Score 15;  DB 6;  Length 1539;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        445 TCCTCCCTGGAAGAA 459
              |||||||||||||||
Db         42 TCCTCCCTGGAAGAA 56


RESULT 62
US-11-217-529-1240/c
; Sequence 1240, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1240
;   LENGTH: 1551
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-1240

  Query Match             2.7%;  Score 15;  DB 7;  Length 1551;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        120 AGATATCACAAAAGA 134
              |||||||||||||||
Db        673 AGATATCACAAAAGA 659


RESULT 63
US-10-953-349-1943
; Sequence 1943, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1943
;   LENGTH: 1821
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-1943

  Query Match             2.7%;  Score 15;  DB 6;  Length 1821;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        387 AGCTATTGATGAGCT 401
              |||||||||||||||
Db        600 AGCTATTGATGAGCT 614


RESULT 64
US-10-953-349-12445
; Sequence 12445, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12445
;   LENGTH: 1869
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (532)..(532)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-12445

  Query Match             2.7%;  Score 15;  DB 6;  Length 1869;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        192 CCTGGCTTCCAGAGA 206
              |||||||||||||||
Db        144 CCTGGCTTCCAGAGA 158


RESULT 65
US-11-293-697-2269
; Sequence 2269, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2269
;   LENGTH: 1902
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-2269

  Query Match             2.7%;  Score 15;  DB 7;  Length 1902;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        421 AACAGTGTGACTGTG 435
              |||||||||||||||
Db        235 AACAGTGTGACTGTG 249


RESULT 66
US-11-293-697-773/c
; Sequence 773, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
```

```
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 773
;   LENGTH: 2043
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-773

  Query Match             2.7%;  Score 15;  DB 7;  Length 2043;
  Best Local Similarity   100.0%;  Pred. No. 77;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        215 TGATAACTAATGGGA 229
              |||||||||||||||
Db        802 TGATAACTAATGGGA 788


RESULT 67
US-11-293-697-153
; Sequence 153, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 153
;   LENGTH: 2151
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-153

  Query Match             2.7%;  Score 15;  DB 7;  Length 2151;
  Best Local Similarity   100.0%;  Pred. No. 77;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         31 ACCCTGCTGCGAGCC 45
              |||||||||||||||
Db       1116 ACCCTGCTGCGAGCC 1130


RESULT 68
US-11-293-697-56
; Sequence 56, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
;   LENGTH: 2205
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-56

  Query Match             2.7%;  Score 15;  DB 7;  Length 2205;
  Best Local Similarity   100.0%;  Pred. No. 77;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        536 GAATGATGAGCTATC 550
              |||||||||||||||
Db       1538 GAATGATGAGCTATC 1552


RESULT 69
US-11-217-529-2489
; Sequence 2489, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2489
;   LENGTH: 2241
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-2489

  Query Match             2.7%;  Score 15;  DB 7;  Length 2241;
  Best Local Similarity   100.0%;  Pred. No. 77;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        292 GACTTGAAGATGTAC 306
              |||||||||||||||
Db       1711 GACTTGAAGATGTAC 1725


RESULT 70
US-11-217-529-80988/c
; Sequence 80988, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80988
;   LENGTH: 2400
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-80988

  Query Match             2.7%;  Score 15;  DB 7;  Length 2400;
  Best Local Similarity   100.0%;  Pred. No. 77;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        364 TTTCTGGATCAAAAC 378
              |||||||||||||||
Db        472 TTTCTGGATCAAAAC 458


RESULT 71
US-11-293-697-2092/c
```

; Sequence 2092, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2092
; LENGTH: 2537
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-2092

Query Match 2.7%; Score 15; DB 7; Length 2537;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 GCCTCAACCACTCCC 28
||||||||||||||||
Db 1344 GCCTCAACCACTCCC 1330

RESULT 72
US-11-293-697-749/c
; Sequence 749, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 749
; LENGTH: 2650
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-749

Query Match 2.7%; Score 15; DB 7; Length 2650;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 362 TCTTTCTGGATCAAA 376
||||||||||||||||
Db 1786 TCTTTCTGGATCAAA 1772

RESULT 73
US-11-217-529-1172
; Sequence 1172, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1172
; LENGTH: 4533
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1172

Query Match 2.7%; Score 15; DB 7; Length 4533;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 GATTGATCATGAAGA 122
||||||||||||||||
Db 2550 GATTGATCATGAAGA 2564

RESULT 74
US-10-501-834-216
; Sequence 216, Application US/10501834
; Publication No. US20060088828A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Peter C., Ward, Christopher J., Rossetti, Sandro, and Torres,
; APPLICANT: Vicente E.
; TITLE OF INVENTION: Polycystic Kidney Disease Nucleic Acids
; TITLE OF INVENTION: and Proteins
; FILE REFERENCE: 07039/386US1
; CURRENT APPLICATION NUMBER: US/10/501,834
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: PCT/US03/02038
; PRIOR FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: 60/351,110
; PRIOR FILING DATE: 2002-01-23
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 216
; LENGTH: 5171
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-501-834-216

Query Match 2.7%; Score 15; DB 6; Length 5171;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 431 CTGTGCCACAGAACT 445
||||||||||||||||
Db 2813 CTGTGCCACAGAACT 2827

RESULT 75
US-11-217-529-191092
; Sequence 191092, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 191092
; LENGTH: 5703
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus

```
US-11-217-529-191092

  Query Match             2.7%;  Score 15;  DB 7;  Length 5703;
  Best Local Similarity   100.0%;  Pred. No. 81;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        334 AAGCTGTTAATGGAT 348
              |||||||||||||||
Db       5123 AAGCTGTTAATGGAT 5137


RESULT 76
US-10-505-928-28/c
; Sequence 28, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
;  APPLICANT: Ludwig Institute for Cancer Research et al.
;  TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
;  FILE REFERENCE: 28967/39178
;  CURRENT APPLICATION NUMBER: US/10/505,928
;  CURRENT FILING DATE:  2004-08-27
;  PRIOR APPLICATION NUMBER: US 60/363,019
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: PatentIn 3.2
; SEQ ID NO 28
;   LENGTH: 5734
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-505-928-28

  Query Match             2.7%;  Score 15;  DB 6;  Length 5734;
  Best Local Similarity   100.0%;  Pred. No. 81;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        428 TGACTGTGCCACAGA 442
              |||||||||||||||
Db       5362 TGACTGTGCCACAGA 5348


RESULT 77
US-11-313-450-15/c
; Sequence 15, Application US/11313450
; Publication No. US20060110778A1
; GENERAL INFORMATION:
;  APPLICANT: Adorante, Joeseph S.
;  APPLICANT:  Ehring, George R.
;  TITLE OF INVENTION: High-Throughput Screens For Identifying
;  TITLE OF INVENTION:  Selective Persistent Sodium Channels Channel Blockers
;  FILE REFERENCE: 17407 CIP (AP)
;  CURRENT APPLICATION NUMBER: US/11/313,450
;  CURRENT FILING DATE:  2005-12-19
;  PRIOR APPLICATION NUMBER: 09/989797
;  PRIOR FILING DATE: 2001-11-20
;  PRIOR APPLICATION NUMBER: 60/252771
;  PRIOR FILING DATE: 2000-11-22
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 5874
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-313-450-15

  Query Match             2.7%;  Score 15;  DB 7;  Length 5874;
  Best Local Similarity   100.0%;  Pred. No. 81;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GATGTTCCAGTGCCT 17
              |||||||||||||||
Db       3158 GATGTTCCAGTGCCT 3144


RESULT 78
US-10-505-928-330/c
; Sequence 330, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
;  APPLICANT: Ludwig Institute for Cancer Research et al.
;  TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
;  FILE REFERENCE: 28967/39178
;  CURRENT APPLICATION NUMBER: US/10/505,928
;  CURRENT FILING DATE:  2004-08-27
;  PRIOR APPLICATION NUMBER: US 60/363,019
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: PatentIn 3.2
; SEQ ID NO 330
;   LENGTH: 6826
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-505-928-330

  Query Match             2.7%;  Score 15;  DB 6;  Length 6826;
  Best Local Similarity   100.0%;  Pred. No. 81;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         21 CCACTCCCAAACCCT 35
              |||||||||||||||
Db       5759 CCACTCCCAAACCCT 5745


RESULT 79
US-10-505-928-151
; Sequence 151, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
;  APPLICANT: Ludwig Institute for Cancer Research et al.
;  TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
;  FILE REFERENCE: 28967/39178
;  CURRENT APPLICATION NUMBER: US/10/505,928
;  CURRENT FILING DATE:  2004-08-27
;  PRIOR APPLICATION NUMBER: US 60/363,019
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: PatentIn 3.2
; SEQ ID NO 151
;   LENGTH: 128361
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-505-928-151

  Query Match             2.7%;  Score 15;  DB 6;  Length 128361;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        315 GTTCAAGGCCATGAA 329
              |||||||||||||||
Db     117581 GTTCAAGGCCATGAA 117595


RESULT 80
US-11-260-842-1/c
; Sequence 1, Application US/11260842
; Publication No. US20060115845A1
; GENERAL INFORMATION:
;  APPLICANT: Vance, Jeffrey M.
;  APPLICANT:  Kraus, William E.
;  APPLICANT:  Goldschmidt, Pascal J.
;  APPLICANT:  Gregory, Simon G.
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING GENETIC MARKERS WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISEASE
;  FILE REFERENCE: 5405-347
;  CURRENT APPLICATION NUMBER: US/11/260,842
;  CURRENT FILING DATE:  2005-10-27
;  PRIOR APPLICATION NUMBER: US 60/662,447
```

```
;  PRIOR FILING DATE: 2004-10-27
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
;   LENGTH: 261789
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-260-842-1

  Query Match             2.7%;  Score 15;  DB 7;  Length 261789;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        528 CATCAATAGAATGAT 542
              |||||||||||||||
Db      29696 CATCAATAGAATGAT 29682


RESULT 81
US-11-217-529-26117
; Sequence 26117, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26117
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-26117

  Query Match             2.5%;  Score 14;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        414 GAATGTCAACAGTG 427
              ||||||||||||||
Db          1 GAATGTCAACAGTG 14


RESULT 82
US-11-217-529-40959
; Sequence 40959, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 40959
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-40959

  Query Match             2.5%;  Score 14;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GTGCCTCAACCACT 25
              ||||||||||||||
Db         11 GTGCCTCAACCACT 24


RESULT 83
US-11-217-529-124406
; Sequence 124406, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 124406
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-124406

  Query Match             2.5%;  Score 14;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        159 CTTACCACTGGAAT 172
              ||||||||||||||
Db          2 CTTACCACTGGAAT 15


RESULT 84
US-11-217-529-136455/c
; Sequence 136455, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 136455
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-136455

  Query Match             2.5%;  Score 14;  DB 7;  Length 25;
```

Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        264 GACCCTGTGCCTTA 277
              ||||||||||||||
Db         23 GACCCTGTGCCTTA 10
```

RESULT 85
US-11-217-529-148494/c
; Sequence 148494, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 148494
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-148494

Query Match 2.5%; Score 14; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        296 TGAAGATGTACCAG 309
              ||||||||||||||
Db         16 TGAAGATGTACCAG 3
```

RESULT 86
US-10-511-937-3058/c
; Sequence 3058, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3058
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-3058

Query Match 2.5%; Score 14; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        132 AGATAAAACCAGCA 145
              ||||||||||||||
Db         41 AGATAAAACCAGCA 28
```

RESULT 87
US-10-471-571A-1747/c
; Sequence 1747, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 1747
; LENGTH: 258
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-471-571A-1747

Query Match 2.5%; Score 14; DB 6; Length 258;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        469 TATAAAACTAAAAT 482
              ||||||||||||||
Db         92 TATAAAACTAAAAT 79
```

RESULT 88
US-11-217-529-5872/c
; Sequence 5872, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5872
; LENGTH: 312
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5872

Query Match 2.5%; Score 14; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         43 GCCATCAGCAACAC 56
              ||||||||||||||
Db         41 GCCATCAGCAACAC 28
```

```
RESULT 89
US-11-217-529-76063/c
; Sequence 76063, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76063
;   LENGTH: 330
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-76063

  Query Match             2.5%;  Score 14;  DB 7;  Length 330;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 TTCCAGTGCCTCAA 20
              ||||||||||||||
Db         75 TTCCAGTGCCTCAA 62


RESULT 90
US-10-471-571A-127
; Sequence 127, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 127
;   LENGTH: 360
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-127

  Query Match             2.5%;  Score 14;  DB 6;  Length 360;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        292 GACTTGAAGATGTA 305
              ||||||||||||||
Db         95 GACTTGAAGATGTA 108


RESULT 91
US-11-217-529-166773
; Sequence 166773, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 166773
;   LENGTH: 381
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-166773

  Query Match             2.5%;  Score 14;  DB 7;  Length 381;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        474 AACTAAAATCAAGC 487
              ||||||||||||||
Db        168 AACTAAAATCAAGC 181


RESULT 92
US-10-473-173-293/c
; Sequence 293, Application US/10473173
; Publication No. US20060088823A1
; GENERAL INFORMATION:
;  APPLICANT: VAN ANDEL INSTITUTE
;  TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell
;  TITLE OF INVENTION:  Carcinoma: Prognosis and Drug Target Identification
;  FILE REFERENCE: 38345-170094
;  CURRENT APPLICATION NUMBER: US/10/473,173
;  CURRENT FILING DATE:  2003-09-29
;  PRIOR APPLICATION NUMBER: US 60/279,411
;  PRIOR FILING DATE: 2001-03-29
;  NUMBER OF SEQ ID NOS: 498
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 293
;   LENGTH: 410
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-473-173-293

  Query Match             2.5%;  Score 14;  DB 6;  Length 410;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        154 GCCTGCTTACCACT 167
              ||||||||||||||
Db        322 GCCTGCTTACCACT 309


RESULT 93
US-10-488-619-2658
; Sequence 2658, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations W
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2658
;   LENGTH: 426
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-488-619-2658
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  Query Match             2.5%;  Score 14;  DB 6;  Length 426;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        182 ATGAGAGTTGCCTG 195
              ||||||||||||||
Db        283 ATGAGAGTTGCCTG 296


RESULT 94
US-10-473-173-445
; Sequence 445, Application US/10473173
; Publication No. US20060088823A1
; GENERAL INFORMATION:
;  APPLICANT: VAN ANDEL INSTITUTE
;  TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell
;  TITLE OF INVENTION:  Carcinoma: Prognosis and Drug Target Identification
;  FILE REFERENCE: 38345-170094
;  CURRENT APPLICATION NUMBER: US/10/473,173
;  CURRENT FILING DATE:  2003-09-29
;  PRIOR APPLICATION NUMBER: US 60/279,411
;  PRIOR FILING DATE: 2001-03-29
;  NUMBER OF SEQ ID NOS: 498
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 445
;   LENGTH: 449
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (289)..(289)
;   OTHER INFORMATION: n can be a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (408)..(408)
;   OTHER INFORMATION: n can be a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (431)..(431)
;   OTHER INFORMATION: n can be a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (431)..(431)
;   OTHER INFORMATION: n can be a, c, g or t
US-10-473-173-445

  Query Match             2.5%;  Score 14;  DB 6;  Length 449;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        473 AAACTAAAATCAAG 486
              ||||||||||||||
Db         99 AAACTAAAATCAAG 112


RESULT 95
US-11-217-529-82632
; Sequence 82632, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82632
;   LENGTH: 453
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-82632

  Query Match             2.5%;  Score 14;  DB 7;  Length 453;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        358 CAGATCTTTCTGGA 371
              ||||||||||||||
Db        272 CAGATCTTTCTGGA 285


RESULT 96
US-10-488-619-943
; Sequence 943, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations W
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 943
;   LENGTH: 467
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-488-619-943

  Query Match             2.5%;  Score 14;  DB 6;  Length 467;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        149 TGGAGGCCTGCTTA 162
              ||||||||||||||
Db         91 TGGAGGCCTGCTTA 104


RESULT 97
US-10-473-173-454/c
; Sequence 454, Application US/10473173
; Publication No. US20060088823A1
; GENERAL INFORMATION:
;  APPLICANT: VAN ANDEL INSTITUTE
;  TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell
;  TITLE OF INVENTION:  Carcinoma: Prognosis and Drug Target Identification
;  FILE REFERENCE: 38345-170094
;  CURRENT APPLICATION NUMBER: US/10/473,173
;  CURRENT FILING DATE:  2003-09-29
;  PRIOR APPLICATION NUMBER: US 60/279,411
;  PRIOR FILING DATE: 2001-03-29
;  NUMBER OF SEQ ID NOS: 498
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 454
;   LENGTH: 470
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (55)..(55)
;   OTHER INFORMATION: n can be a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (70)..(70)
;   OTHER INFORMATION: n can be a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
```

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;   LOCATION: (178)..(178)
;   OTHER INFORMATION: n can be a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (464)..(464)
;   OTHER INFORMATION: n can be a, c, g or t
US-10-473-173-454

  Query Match             2.5%;  Score 14;  DB 6;  Length 470;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        355 AGGCAGATCTTTCT 368
              ||||||||||||||
Db        393 AGGCAGATCTTTCT 380


RESULT 98
US-11-217-529-3168
; Sequence 3168, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3168
;   LENGTH: 510
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-3168

  Query Match             2.5%;  Score 14;  DB 7;  Length 510;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GTGCCTCAACCACT 25
              ||||||||||||||
Db         73 GTGCCTCAACCACT 86


RESULT 99
US-10-488-619-949
; Sequence 949, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 949
;   LENGTH: 541
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-488-619-949

  Query Match             2.5%;  Score 14;  DB 6;  Length 541;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        362 TCTTTCTGGATCAA 375
              ||||||||||||||
Db        283 TCTTTCTGGATCAA 296


RESULT 100
US-11-301-554-137
; Sequence 137, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
;  APPLICANT: Henderson, Robert A.
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Watanabe, Yoshihiro
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Sleath, Paul R.
;  APPLICANT:  Johnson, Jeffrey C.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Durham, Margarita
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  McNabb, Andria
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.478C21
;  CURRENT APPLICATION NUMBER: US/11/301,554
;  CURRENT FILING DATE:  2005-12-13
;  PRIOR APPLICATION NUMBER: US 10/283,017
;  PRIOR FILING DATE: 2002-10-28
;  PRIOR APPLICATION NUMBER: US 10/113,872
;  PRIOR FILING DATE: 2002-03-28
;  PRIOR APPLICATION NUMBER: US 10/017,754
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: US 09/902,941
;  PRIOR FILING DATE: 2001-07-10
;  PRIOR APPLICATION NUMBER: US 09/849,626
;  PRIOR FILING DATE: 2001-05-03
;  PRIOR APPLICATION NUMBER: US 09/736,457
;  PRIOR FILING DATE: 2000-12-13
;  PRIOR APPLICATION NUMBER: US 09/702,705
;  PRIOR FILING DATE: 2000-10-30
;  PRIOR APPLICATION NUMBER: US 09/677,419
;  PRIOR FILING DATE: 2000-10-06
;  PRIOR APPLICATION NUMBER: US 09/671,325
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US 09/658,824
;  PRIOR FILING DATE: 2000-09-08
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2157
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 137
;   LENGTH: 552
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 310
;   OTHER INFORMATION: n = A,T,C or G
US-11-301-554-137

  Query Match             2.5%;  Score 14;  DB 7;  Length 552;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        465 TTTTTATAAAACTA 478
              ||||||||||||||
Db        518 TTTTTATAAAACTA 531


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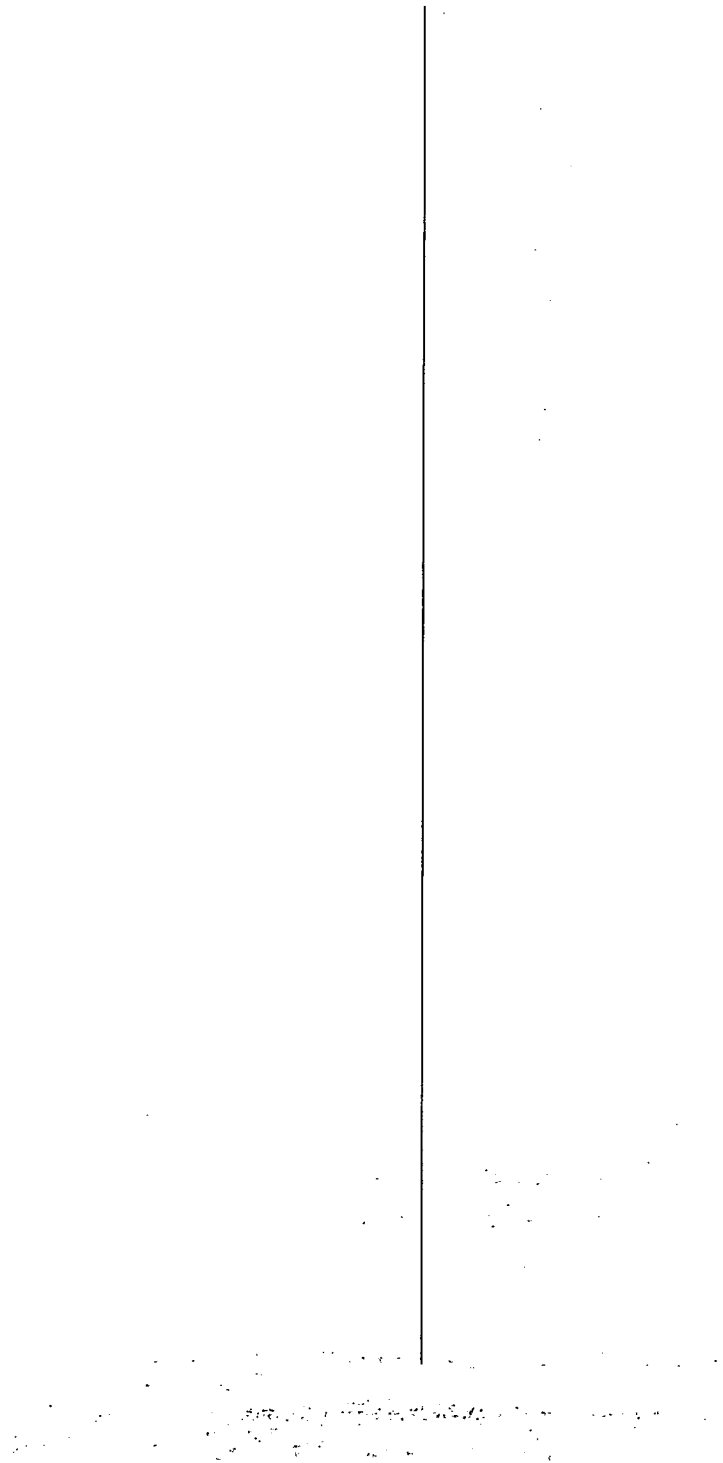

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 12, 2006, 15:14:42 ; Search time 2535.66 Seconds
(without alignments)
7073.997 Million cell updates/sec

Title: US-10-821-670A-102
Perfect score: 944
Sequence: 1 GMFQCLNHSQTLLRAISNTL.....HAFRIRAVTINRMMSYLNAS 187

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss06h
-USER=US10821670_@CGN_1_1_5308_@runat_07062006_110102_26152 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
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2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	944	100.0	561	2	AR596007	AR596007 Sequence
c	2	944	100.0	561	2	AR596008	AR596008 Sequence
	3	944	100.0	591	2	AR595954	AR595954 Sequence
c	4	944	100.0	591	2	AR595955	AR595955 Sequence
	5	944	100.0	666	2	AR595952	AR595952 Sequence
c	6	944	100.0	666	2	AR595953	AR595953 Sequence
	7	944	100.0	669	14	FCIL12P35	Y07761 Felis catus
	8	944	100.0	1533	2	AR595959	AR595959 Sequence
c	9	944	100.0	1533	2	AR595960	AR595960 Sequence
	10	944	100.0	1599	2	AR595956	AR595956 Sequence
c	11	944	100.0	1599	2	AR595957	AR595957 Sequence
	12	941	99.7	591	2	AR242439	AR242439 Sequence
	13	941	99.7	591	2	AR280207	AR280207 Sequence
	14	941	99.7	591	2	AR322422	AR322422 Sequence
	15	941	99.7	689	2	AR242451	AR242451 Sequence
	16	941	99.7	689	2	AR280219	AR280219 Sequence
	17	941	99.7	689	2	AR322434	AR322434 Sequence
	18	941	99.7	1441	2	AR242438	AR242438 Sequence
	19	941	99.7	1441	2	AR280206	AR280206 Sequence
	20	941	99.7	1441	2	AR322421	AR322421 Sequence
	21	936	99.2	669	14	FCU83185	U83185 Felis catus
	22	923	97.8	669	2	AX076201	AX076201 Sequence
	23	923	97.8	669	2	AX076483	AX076483 Sequence
	24	923	97.8	4201	2	AX076477	AX076477 Sequence
	25	903	95.7	1533	2	AR595973	AR595973 Sequence
c	26	903	95.7	1533	2	AR595974	AR595974 Sequence
	27	903	95.7	1599	2	AR595971	AR595971 Sequence
c	28	903	95.7	1599	2	AR595972	AR595972 Sequence
	29	889	94.2	591	2	BD171284	BD171284 Novel can
	30	889	94.2	591	2	AR595963	AR595963 Sequence
c	31	889	94.2	591	2	AR595964	AR595964 Sequence
	32	889	94.2	666	2	AR595961	AR595961 Sequence
c	33	889	94.2	666	2	AR595962	AR595962 Sequence
	34	889	94.2	669	2	AR151072	AR151072 Sequence
	35	889	94.2	669	2	BD014664	BD014664 Process f
	36	889	94.2	669	2	E15018	E15018 Canine mRNA
	37	889	94.2	669	2	AR316471	AR316471 Sequence
	38	889	94.2	1282	2	BD171283	BD171283 Novel can
	39	889	94.2	1455	2	AR596009	AR596009 Sequence
c	40	889	94.2	1455	2	AR596010	AR596010 Sequence
	41	884	93.6	669	2	AR151062	AR151062 Sequence
	42	884	93.6	669	2	BD014654	BD014654 Process f
	43	884	93.6	669	2	AR316461	AR316461 Sequence
	44	876	92.8	669	14	CFU49085	U49085 Canis famil
	45	870	92.2	657	8	AY191828	AY191828 Synthetic

ALIGNMENTS

RESULT 1
AR596007
LOCUS AR596007 561 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 101 from patent US 6818444.
ACCESSION AR596007
VERSION AR596007.1 GI:56646988
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 561)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 101 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .561
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.: 8.23e-102 Length: 561
Score: 944.00 Matches: 187
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0

```
DB:                    2             Gaps:          0

US-10-821-670A-102 (1-187) x AR596007 (1-561)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db        541 ATGAGCTATCTGAATGCTTCC 561

RESULT 2
AR596008/c
LOCUS       AR596008                561 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 103 from patent US 6818444.
ACCESSION   AR596008
VERSION     AR596008.1  GI:56646989
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 561)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 103 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .561
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              8.23e-102      Length:         561
Score:                  944.00         Matches:        187
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-102 (1-187) x AR596008 (1-561)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1

RESULT 3
AR595954
LOCUS       AR595954                591 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 35 from patent US 6818444.
ACCESSION   AR595954
VERSION     AR595954.1  GI:56646935
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 35 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              8.68e-102      Length:         591
Score:                  944.00         Matches:        187
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-102 (1-187) x AR595954 (1-591)
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Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 90

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 210

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 390

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 450

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 510

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 570

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db        571 ATGAGCTATCTGAATGCTTCC 591
```

RESULT 4
AR595955/c
LOCUS AR595955 591 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 37 from patent US 6818444.
ACCESSION AR595955
VERSION AR595955.1 GI:56646936
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 591)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 37 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .591
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Alignment Scores:

Pred. No.:	8.68e-102	Length:	591
Score:	944.00	Matches:	187
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-102 (1-187) x AR595955 (1-591)

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Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1
```

RESULT 5
AR595952
LOCUS AR595952 666 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 32 from patent US 6818444.
ACCESSION AR595952
VERSION AR595952.1 GI:56646933
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 666)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 32 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .666
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Alignment Scores:

Pred. No.:	9.82e-102	Length:	666
Score:	944.00	Matches:	187
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-102 (1-187) x AR595952 (1-666)

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Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 165
```

```
Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 225

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 285

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 345

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 405

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 465

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 525

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 585

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
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Db        586 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 645

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db        646 ATGAGCTATCTGAATGCTTCC 666
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RESULT 6
AR595953/c
LOCUS AR595953 666 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 34 from patent US 6818444.
ACCESSION AR595953
VERSION AR595953.1 GI:56646934
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 666)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 34 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .666
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Alignment Scores:

Pred. No.:	9.82e-102	Length:	666
Score:	944.00	Matches:	187
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-102 (1-187) x AR595953 (1-666)

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Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1
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RESULT 7
FCIL12P35
LOCUS FCIL12P35 669 bp mRNA linear MAM 18-APR-2005
DEFINITION Felis catus mRNA for interleukin-12 p35 chain.
ACCESSION Y07761
VERSION Y07761.1 GI:2102662
KEYWORDS interleukin-12 subunit p35.
SOURCE Felis catus (cat)
ORGANISM Felis catus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
Felinae; Felis.
REFERENCE 1
AUTHORS Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
TITLE Molecular cloning of cat interleukin-12
JOURNAL Immunogenetics 45 (6), 462-463 (1997)
PUBMED 9089110
REFERENCE 2 (bases 1 to 669)
AUTHORS Schijns,V.E.C.J.
TITLE Direct Submission
JOURNAL Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
Utrecht, NETHERLANDS
FEATURES Location/Qualifiers
source 1. .669
/organism="Felis catus"
/mol_type="mRNA"
/db_xref="taxon:9685"
/cell_type="lymphocyte"
/tissue_type="peripheral blood"
gene 1. .669
/gene="IL-12.p35"
CDS 1. .669
/gene="IL-12.p35"
/function="heterodimer with IL-12 p40 chain"
/codon_start=1
/product="interleukin-12 p35 chain"
/protein_id="CAA69067.1"
/db_xref="GI:2102663"

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                     LNAS"
ORIGIN

Alignment Scores:
Pred. No.:                9.86e-102      Length:          669
Score:                    944.00         Matches:         187
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       14             Gaps:            0

US-10-821-670A-102 (1-187) x FCIL12P35 (1-669)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 165

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 225

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 285

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 345

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 405

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 465

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 525

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 585

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 645

Qy        181 MetSerTyrLeuAsnAlaSer 187
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Db        646 ATGAGCTATCTGAATGCTTCC 666

RESULT 8
AR595959
LOCUS       AR595959               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 43 from patent US 6818444.
ACCESSION   AR595959
VERSION     AR595959.1  GI:56646940
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 43 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                2.31e-101      Length:          1533
Score:                    944.00         Matches:         187
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-102 (1-187) x AR595959 (1-1533)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1032

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1092

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1093 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1152

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1153 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1212

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1213 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1272

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1273 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1332

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1333 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1392

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1393 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1452

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1453 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1512

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db       1513 ATGAGCTATCTGAATGCTTCC 1533

RESULT 9
AR595960/c
LOCUS       AR595960               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 45 from patent US 6818444.
ACCESSION   AR595960
VERSION     AR595960.1  GI:56646941
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 45 16-NOV-2004;
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          Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.31e-101      Length:         1533
Score:                  944.00         Matches:        187
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-102 (1-187) x AR595960 (1-1533)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
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Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1

RESULT 10
AR595956
LOCUS       AR595956               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 38 from patent US 6818444.
ACCESSION   AR595956
VERSION     AR595956.1  GI:56646937
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 38 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.41e-101      Length:         1599
Score:                  944.00         Matches:        187
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-102 (1-187) x AR595956 (1-1599)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1098

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1158

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1218

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1219 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1278

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1338

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1398

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1458

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1459 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1518

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1519 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1578

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db       1579 ATGAGCTATCTGAATGCTTCC 1599

RESULT 11
AR595957/c
LOCUS       AR595957               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 40 from patent US 6818444.
ACCESSION   AR595957
VERSION     AR595957.1  GI:56646938
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 40 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
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/mol_type="genomic DNA"
ORIGIN

Alignment Scores:

Pred. No.:	2.41e-101	Length:	1599
Score:	944.00	Matches:	187
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-102 (1-187) x AR595957 (1-1599)

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Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1
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RESULT 12
AR242439
LOCUS AR242439 591 bp mRNA linear PAT 20-DEC-2002
DEFINITION Sequence 9 from patent US 6472509.
ACCESSION AR242439
VERSION AR242439.1 GI:27288856
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 591)
AUTHORS Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
TITLE Feline cytokine protein
JOURNAL Patent: US 6472509-A 9 29-OCT-2002;
Juridical Foundation: The Chemo-Seso-Therapeutic Research
Institute; Kumamoto;
EPX;
FEATURES Location/Qualifiers
source 1. .591
/organism="unknown"

/mol_type="mRNA"
ORIGIN

Alignment Scores:

Pred. No.:	1.96e-101	Length:	591
Score:	941.00	Matches:	186
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	99.5%	Mismatches:	0
Query Match:	99.7%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-102 (1-187) x AR242439 (1-591)

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Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 90

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 210

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 390

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 450

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 510

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 570

Qy        181 MetSerTyrLeuAsnAlaSer 187
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Db        571 ATGAGCTACCTGAATTCTTCC 591
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RESULT 13
AR280207
LOCUS AR280207 591 bp mRNA linear PAT 10-APR-2003
DEFINITION Sequence 9 from patent US 6518045.
ACCESSION AR280207
VERSION AR280207.1 GI:29715597
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 591)
AUTHORS Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
TITLE Feline cytokine protein
JOURNAL Patent: US 6518045-A 9 11-FEB-2003;
Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
Kumamoto-ken;
EPX;
FEATURES Location/Qualifiers
source 1. .591
/organism="unknown"

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                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:                1.96e-101      Length:          591
Score:                    941.00         Matches:         186
Percent Similarity:       100.0%         Conservative:    1
Best Local Similarity:    99.5%          Mismatches:      0
Query Match:              99.7%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-102 (1-187) x AR280207 (1-591)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 90

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 210

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 390

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 450

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 510

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
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Db        511 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 570

Qy        181 MetSerTyrLeuAsnAlaSer 187
              ||||||||||||||:::|||
Db        571 ATGAGCTACCTGAATTCTTCC 591

RESULT 14
AR322422
LOCUS       AR322422                591 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 9 from patent US 6566097.
ACCESSION   AR322422
VERSION     AR322422.1  GI:33708175
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 9 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
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                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:                1.96e-101      Length:          591
Score:                    941.00         Matches:         186
Percent Similarity:       100.0%         Conservative:    1
Best Local Similarity:    99.5%          Mismatches:      0
Query Match:              99.7%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-102 (1-187) x AR322422 (1-591)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
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Db         31 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 90

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 210

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 450

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 510

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 570

Qy        181 MetSerTyrLeuAsnAlaSer 187
              ||||||||||||||:::|||
Db        571 ATGAGCTACCTGAATTCTTCC 591

RESULT 15
AR242451
LOCUS       AR242451                689 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 26 from patent US 6472509.
ACCESSION   AR242451
VERSION     AR242451.1  GI:27288868
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 26 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .689
                     /organism="unknown"
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/mol_type="mRNA"
ORIGIN

Alignment Scores:

Pred. No.:	2.3e-101	Length:	689
Score:	941.00	Matches:	186
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	99.5%	Mismatches:	0
Query Match:	99.7%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-102 (1-187) x AR242451 (1-689)

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Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 171

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 231

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATG 291

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
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Db        292 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 351

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 411

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAG 471

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 531

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 591

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 651

Qy        181 MetSerTyrLeuAsnAlaSer 187
              ||||||||||||||:::|||
Db        652 ATGAGCTACCTGAATTCTTCC 672
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 9, 2006, 23:43:41 ; Search time 399.181 Seconds
(without alignments)
4899.317 Million cell updates/sec

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Perfect score: 944
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Searched: 5244920 seqs, 3486124231 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	3	944	100.0	561	14	ADV34751	Adv34751 Feline N-
c	4	944	100.0	561	14	ADV34753	Adv34753 Feline N-
	5	944	100.0	591	6	ABK98948	Abk98948 Feline in
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	11	944	100.0	666	14	ADV34685	Adv34685 Feline si
c	12	944	100.0	666	14	ADV34687	Adv34687 Feline si
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	17	944	100.0	1599	6	ABK98950	Abk98950 Feline in
c	18	944	100.0	1599	6	ABK98951	Abk98951 Feline in
	19	944	100.0	1599	14	ADV34691	Adv34691 Feline si
c	20	944	100.0	1599	14	ADV34693	Adv34693 Feline si
	21	941	99.7	591	2	AAV56629	Aav56629 Feline FL
	22	941	99.7	689	2	AAV56641	Aav56641 Feline FL
	23	941	99.7	1441	2	AAV56628	Aav56628 Feline FL
	24	923	97.8	669	4	AAF26083	Aaf26083 Feline IL
	25	923	97.8	669	4	AAF26086	Aaf26086 Feline IL
	26	923	97.8	4201	4	AAF26077	Aaf26077 Feline IL
	27	912	96.6	639	4	AAF26098	Aaf26098 Plasmid p
	28	907	96.1	679	4	AAF26097	Aaf26097 Feline fi
	29	903	95.7	1533	6	ABK98967	Abk98967 Canine in
c	30	903	95.7	1533	6	ABK98968	Abk98968 Canine in
c	31	903	95.7	1533	14	ADV34718	Adv34718 Canine si
	32	903	95.7	1533	14	ADV34716	Adv34716 Canine si
	33	903	95.7	1599	6	ABK98965	Abk98965 Canine in
c	34	903	95.7	1599	6	ABK98966	Abk98966 Canine in
c	35	903	95.7	1599	14	ADV34715	Adv34715 Canine si
	36	903	95.7	1599	14	ADV34713	Adv34713 Canine si
	37	889	94.2	591	2	AAX18179	Aax18179 Canine ma
c	38	889	94.2	591	6	ABK98958	Abk98958 Canine in
	39	889	94.2	591	6	ABK98957	Abk98957 Canine in
	40	889	94.2	591	14	ADV34701	Adv34701 Canine si
c	41	889	94.2	591	14	ADV34703	Adv34703 Canine si
	42	889	94.2	666	6	ABK98955	Abk98955 Canine in
c	43	889	94.2	666	6	ABK98956	Abk98956 Canine in
c	44	889	94.2	666	14	ADV34700	Adv34700 Canine si
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ALIGNMENTS

RESULT 1
ABK99001
ID ABK99001 standard; cDNA; 561 BP.
XX
AC ABK99001;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p35-N561 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX

```
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69315.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Disclosure; Page 92-93; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 561 BP; 167 A; 134 C; 120 G; 140 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              7.56e-98        Length:         561
Score:                  944.00          Matches:        187
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-102 (1-187) x ABK99001 (1-561)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
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Db          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
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Db        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
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Db        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
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Db        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db        541 ATGAGCTATCTGAATGCTTCC 561

RESULT 2
ABK99002/c
ID   ABK99002 standard; cDNA; 561 BP.
XX
AC   ABK99002;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12nFeIL-12p35-N561 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Disclosure; Page 94; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 561 BP; 140 A; 120 C; 134 G; 167 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              7.56e-98        Length:         561
Score:                  944.00          Matches:        187
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-102 (1-187) x ABK99002 (1-561)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1
```

RESULT 3
ADV34751
ID ADV34751 standard; cDNA; 561 BP.
XX
AC ADV34751;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline N-terminal single chain IL-12p35 cDNA, nFeIL-12p35-N561.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; gene; ss.
XX
OS Felis catus.
XX

```
FH  Key             Location/Qualifiers
FT  CDS             1. .561
FT                  /*tag= a
FT                  /product= "PFeIL-12p35-N187 protein"
FT                  /partial
FT                  /note= "No start and stop codon"
```

XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
DR P-PSDB; ADV34752.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Claim 23; SEQ ID NO 101; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline N-terminal single chain IL-12p35 subunit
CC protein encoding cDNA.
XX
SQ Sequence 561 BP; 167 A; 134 C; 120 G; 140 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	7.56e-98	Length:	561
Score:	944.00	Matches:	187
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-102 (1-187) x ADV34751 (1-561)

```
Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db        541 ATGAGCTATCTGAATGCTTCC 561
```

RESULT 4
ADV34753/c
ID ADV34753 standard; cDNA; 561 BP.
XX
AC ADV34753;
XX

```
DT   24-FEB-2005  (first entry)
XX
DE   Feline N-terminal IL-12p35 complementary DNA, nFeIL-12p35-N561.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Disclosure; SEQ ID NO 103; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline N-terminal single chain IL-12p35 subunit
CC   protein complementary DNA.
XX
SQ   Sequence 561 BP; 140 A; 120 C; 134 G; 167 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              7.56e-98        Length:         561
Score:                  944.00          Matches:        187
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-102 (1-187) x ADV34753 (1-561)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1

RESULT 5
ABK98948
ID   ABK98948 standard; cDNA; 591 BP.
XX
AC   ABK98948;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p35-591 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69305.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 56-57; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 591 BP; 178 A; 149 C; 122 G; 142 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.:              8.13e-98        Length:         591
Score:                  944.00          Matches:        187
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-102 (1-187) x ABK98948 (1-591)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 90

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 210

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 390

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 450

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 510

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 570

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db        571 ATGAGCTATCTGAATGCTTCC 591

RESULT 6
ABK98949/c
ID   ABK98949 standard; cDNA; 591 BP.
XX
AC   ABK98949;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p35-591 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Disclosure; Page 58; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 591 BP; 142 A; 122 C; 149 G; 178 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              8.13e-98        Length:         591
Score:                  944.00          Matches:        187
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-102 (1-187) x ABK98949 (1-591)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
```

```
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1
```

RESULT 7
ADV34688
ID ADV34688 standard; cDNA; 591 BP.
XX
AC ADV34688;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain mature IL-12p35 protein cDNA, nFeIL-12p35 591.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; gene; ss.
XX
OS Felis catus.
XX
FH Key   Location/Qualifiers
FT CDS   1. .591
FT   /*tag= a
FT   /product= "PFeIL-12p35 197 protein"
FT   /partial
FT   /note= "No start and stop codon"
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
DR P-PSDB; ADV34689.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Claim 23; SEQ ID NO 35; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain mature IL-12p35 subunit
CC protein encoding cDNA.
XX
SQ Sequence 591 BP; 178 A; 149 C; 122 G; 142 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	8.13e-98	Length:	591
Score:	944.00	Matches:	187
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-102 (1-187) x ADV34688 (1-591)

```
Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 90

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 210

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 390

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 450

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 510

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 570

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||
Db        571 ATGAGCTATCTGAATGCTTCC 591
```

RESULT 8
ADV34690/c
ID ADV34690 standard; DNA; 591 BP.
XX
AC ADV34690;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain mature IL-12p35 complementary DNA, nFeIL-12p35 591.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Felis catus.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a

```
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 37; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain mature IL-12p35 subunit
CC   complementary DNA.
XX
SQ   Sequence 591 BP; 142 A; 122 C; 149 G; 178 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              8.13e-98        Length:         591
Score:                  944.00          Matches:        187
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-102 (1-187) x ADV34690 (1-591)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1

RESULT 9
ABK98947/c
ID   ABK98947 standard; cDNA; 666 BP.
XX
AC   ABK98947;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p35-666 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 3; Page 56; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 666 BP; 160 A; 138 C; 179 G; 189 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              9.58e-98        Length:         666
Score:                  944.00          Matches:        187
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-102 (1-187) x ABK98947 (1-666)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1

RESULT 10
ABK98946
ID   ABK98946 standard; cDNA; 666 BP.
XX
AC   ABK98946;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p35-666 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69304.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 54-55; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 666 BP; 189 A; 179 C; 138 G; 160 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:               9.58e-98        Length:          666
Score:                   944.00          Matches:         187
Percent Similarity:      100.0%          Conservative:    0
Best Local Similarity:   100.0%          Mismatches:      0
Query Match:             100.0%          Indels:          0
DB:                      6               Gaps:            0

US-10-821-670A-102 (1-187) x ABK98946 (1-666)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 165

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 225

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 285

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 345

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 405

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 465

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 525

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 585

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 645

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||
Db        646 ATGAGCTATCTGAATGCTTCC 666

RESULT 11
ADV34685
ID   ADV34685 standard; cDNA; 666 BP.
XX
AC   ADV34685;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12p35 full-length cDNA, nFeIL-12p35 666.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .666
FT                   /*tag=  a
FT                   /product= "PFeIL-12p35 222 protein "
FT                   /partial
```

```
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34686.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 23; SEQ ID NO 32; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12p35 subunit protein
CC   encoding full-length cDNA.
XX
SQ   Sequence 666 BP; 189 A; 179 C; 138 G; 160 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              9.58e-98        Length:         666
Score:                  944.00          Matches:        187
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-102 (1-187) x ADV34685 (1-666)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 165

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 225

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 285

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 345

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 405

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 465

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 525

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 585

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 645

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||
Db        646 ATGAGCTATCTGAATGCTTCC 666

RESULT 12
ADV34687/c
ID   ADV34687 standard; DNA; 666 BP.
XX
AC   ADV34687;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12p35 complementary DNA, nFeIL-12p35 666.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 34; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12p35 subunit full-length
CC   complementary DNA.
XX
SQ   Sequence 666 BP; 160 A; 138 C; 179 G; 189 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              9.58e-98        Length:         666
Score:                  944.00          Matches:        187
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-102 (1-187) x ADV34687 (1-666)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        561 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              ||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1
```

```
RESULT 13
ABK98954/c
ID   ABK98954 standard; cDNA; 1533 BP.
XX
AC   ABK98954;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1533 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 66-67; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.:                3.02e-97        Length:          1533
Score:                    944.00          Matches:         187
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              100.0%          Indels:          0
DB:                       6               Gaps:            0

US-10-821-670A-102 (1-187) x ABK98954 (1-1533)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              ||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1
```

```
RESULT 14
ABK98953
ID   ABK98953 standard; cDNA; 1533 BP.
XX
AC   ABK98953;
```

```
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1533 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69307.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 63-64; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              3.02e-97      Length:          1533
Score:                  944.00        Matches:         187
Percent Similarity:     100.0%        Conservative:    0
Best Local Similarity:  100.0%        Mismatches:      0
Query Match:            100.0%        Indels:          0
DB:                     6             Gaps:            0

US-10-821-670A-102 (1-187) x ABK98953 (1-1533)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1032

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1092

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1093 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1152

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1153 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1212

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1213 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1272

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1273 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1332

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1333 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1392

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1393 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1452

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1453 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1512

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||
Db       1513 ATGAGCTATCTGAATGCTTCC 1533

RESULT 15
ADV34697/c
ID   ADV34697 standard; DNA; 1533 BP.
XX
AC   ADV34697;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 complementary DNA, nFeIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 45; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 complementary DNA.
XX
SQ   Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;
```

Alignment Scores:

Pred. No.:	3.02e-97	Length:	1533
Score:	944.00	Matches:	187
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-102 (1-187) x ADV34697 (1-1533)

```
Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1
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Search completed: June 10, 2006, 01:18:09
Job time : 402.181 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 10, 2006, 00:20:47 ; Search time 2292 Seconds
(without alignments)
6843.525 Million cell updates/sec

Title: US-10-821-670A-102
Perfect score: 944
Sequence: 1 GMFQCLNHSQTLLRAISNTL.....HAFRIRAVTINRMMSYLNAS 187

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10821670/runat_07062006_110104_26172/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
-USER=US10821670_@CGN_1_1_27300_@runat_07062006_110104_26172 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	843	89.3	762	14	DQ033872	DQ033872 Homo sapi
2	833	88.2	762	14	DQ033873	DQ033873 Pan trogl
3	820.5	86.9	1136	4	CD013915	CD013915 90138132
4	774	82.0	935	4	CD013914	CD013914 90138124
5	708.5	75.1	1938	6	BC035571	BC035571 Homo sapi
6	628	66.5	863	4	CD013916	CD013916 90138296
7	460	48.7	1299	6	AK153729	AK153729 Mus muscu
8	418.5	44.3	563	3	BU698113	BU698113 LL2in1206
9	404	42.8	589	1	AI050362	AI050362 ub30a07.r
c 10	374.5	39.7	1099	2	BI523344	BI523344 603175938
11	372.5	39.5	812	2	BG702253	BG702253 602683459
c 12	355	37.6	778	1	AJ820622	AJ820622 AJ820622
13	349.5	37.0	561	3	BU699383	BU699383 LL2in1157
14	345	36.5	373	7	BF552757	BF552757 UI-R-C0-i
15	344	36.4	692	5	CJ137697	CJ137697 CJ137697
16	321	34.0	456	10	DT913216	DT913216 S13.1426
17	320	33.9	427	10	DT930939	DT930939 S13.1784
18	300	31.8	371	3	BU699957	BU699957 B4-79 Hem
19	295	31.2	412	4	CB801533	CB801533 AMGNNUC:S
c 20	295	31.2	777	4	CB168830	CB168830 CWI602769
21	287	30.4	354	4	BY230958	BY230958 BY230958
22	277	29.3	832	2	BI523569	BI523569 603175938
23	265	28.1	777	14	CT080894	CT080894 Sus scrof
24	259	27.4	581	3	BP260963	BP260963 BP260963
25	221	23.4	551	10	DT919655	DT919655 PCRS30821
26	215.5	22.8	373	3	BU695376	BU695376 B1-30 Hem
27	193.5	20.5	571	9	DN829917	DN829917 pat.pk005
28	191	20.2	571	3	BP261459	BP261459 BP261459
c 29	156.5	16.6	940	14	BX963061	BX963061 Forward s
30	150	15.9	840	11	BZ261813	BZ261813 CH230-420
31	147	15.6	342	2	BM257856	BM257856 521721 MA
32	137	14.5	592	12	CE159257	CE159257 tigr-gss-
33	133.5	14.1	817	3	BU474924	BU474924 603761859
34	129	13.7	447	2	BI824638	BI824638 603033580
35	126	13.3	558	9	CX570753	CX570753 RVL1941 W
36	122	12.9	382	4	CB809298	CB809298 AMGNNUC:T
37	114.5	12.1	361	3	BU694675	BU694675 B2-56 Hem
38	114	12.1	344	14	BX537236	BX537236 INRA porc
39	114	12.1	451	4	BX258840	BX258840 BX258840
c 40	102	10.8	528	1	AI332701	AI332701 qg19a07.x
41	101	10.7	477	4	BX258839	BX258839 BX258839
42	100	10.6	905	3	BU540821	BU540821 AGENCOURT
43	97.5	10.3	994	3	BQ222548	BQ222548 AGENCOURT
44	96.5	10.2	880	3	BQ420717	BQ420717 AGENCOURT
c 45	96.5	10.2	995	11	BZ469395	BZ469395 BONKE63TF

ALIGNMENTS

RESULT 1
DQ033872
LOCUS DQ033872 762 bp DNA linear GSS 02-JUN-2005
DEFINITION Homo sapiens IL12A gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION DQ033872
VERSION DQ033872.1 GI:66885081
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 762)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 762)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

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COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.  Translation starts at the beginning of
            alignment.
FEATURES             Location/Qualifiers
     source          1. .762
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="3"
     gene            <1. .>762
                     /gene="IL12A"
                     /locus_tag="HC3464"
ORIGIN

Alignment Scores:
Pred. No.:              7e-90          Length:         762
Score:                  843.00         Matches:        166
Percent Similarity:     91.4%          Conservative:   5
Best Local Similarity:  88.8%          Mismatches:     16
Query Match:            89.3%          Indels:         0
DB:                     14             Gaps:           0

US-10-821-670A-102 (1-187) x DQ033872 (1-762)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||  ||||||:::|||||||||  ||||||||||||:::||||||  |||
Db        199 GGAATGTTCCCATGCCTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTC 258

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        259 CAGAAGGCCAGACAAACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAA 318

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAG 378

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||  |||||||||  |||  ||||||||||||||||||||||||||||
Db        379 AATGAGAGTTGCCTAAATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCC 438

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||      ||||||||||||||||||||||||||||||||||
Db        439 TCCAGAAAGACCTCTTTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAG 498

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        499 ATGTACCAGGTGGAGTTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAG 558

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||      ||||||||||:::|||||||||||||||||||
Db        559 ATCTTTCTAGATCAAAACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTC 618

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||  ||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        619 AACAGTGAGACTGTGCCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAA 678

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||:::|||:::
Db        679 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTG 738

Qy        181 MetSerTyrLeuAsnAlaSer 187
              ||||||||||||||||||||
Db        739 ATGAGCTATCTGAATGCTTCC 759

RESULT 2
DQ033873
LOCUS       DQ033873                762 bp    DNA     linear   GSS 02-JUN-2005
DEFINITION  Pan troglodytes IL12A gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   DQ033873
VERSION     DQ033873.1  GI:66885082
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     A Scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
  JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
   PUBMED   15869325
REFERENCE   2  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.  Translation starts at the beginning of
            alignment.
FEATURES             Location/Qualifiers
     source          1. .762
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     gene            <1. .>762
                     /gene="IL12A"
                     /locus_tag="HC3464"
ORIGIN

Alignment Scores:
Pred. No.:              1.1e-88        Length:         762
Score:                  833.00         Matches:        165
Percent Similarity:     90.9%          Conservative:   5
Best Local Similarity:  88.2%          Mismatches:     17
Query Match:            88.2%          Indels:         0
DB:                     14             Gaps:           0

US-10-821-670A-102 (1-187) x DQ033873 (1-762)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||  ||||||:::|||||||||  ||||||||||||:::||||||  |||
Db        199 GGAATGTTCCCATGCCTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTC 258

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        259 CAGAAGGCCAGACAAACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAA 318

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAG 378

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||  |||||||||  |||  ||||||||||||||||||||||||||||
Db        379 AATGAGAGTTGCCTAAATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCC 438

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||      ||||||||||||||||||||||||||||||||||
Db        439 TCCAGAAAGACCTCTTTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAG 498

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        499 ATGTACCAGGTGGAGTTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAG 558

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||      ||||||||||:::|||||||||||||||||||
Db        559 ATCTTTCTAGATCAAAACATGCTGGCAGTTATTGACGAGCTGATGCAGGCCCTGAATTTC 618

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||  ||||||||||||  ||||||||||||||||  ||||||||||||||||||||
Db        619 AACAGTGAGACTGTGCCACAAAAATCCTCCCTTGAAGAACTGGATTTTTATAAAACTAAA 678
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Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::|||:::
Db        679 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTG 738

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||
Db        739 ATGAGCTATCTGAATGCTTCC 759

RESULT 3
CD013915
LOCUS       CD013915               1136 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION  90138132 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD013915
VERSION     CD013915.1  GI:37777445
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1136)
  AUTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
            Au-Young,J. and Stuve,L.L.
  TITLE     PCR isolation and cloning of novel splice variant mRNAs from known
            drug target genes
  JOURNAL   Genomics 83 (4), 566-571 (2004)
   PUBMED   15028279
COMMENT     Contact: Jin, P.
            Incyte Corporation
            3160 Porter Drive, Palo Alto, CA 94304, USA
            Tel: 650 621 8639
            Fax: 650 621 8965
            Email: pjin@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .1136
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Single gene library"
                     /note="Vector: pDrive Cloning Vector; RT-PCR was performed
                     using gene-specific primers flanking the open-reading
                     frame. PCR products were subcloned into pDrive Cloning
                     Vector and sequenced completely using M13 forward and
                     reverse primers. Sequencing gaps were closed by
                     re-sequencig using primers flanking the gapped areas."
ORIGIN

Alignment Scores:
Pred. No.:              6.11e-87       Length:         1136
Score:                  820.50         Matches:        166
Percent Similarity:     80.7%          Conservative:   5
Best Local Similarity:  78.3%          Mismatches:     16
Query Match:            86.9%          Indels:         25
DB:                     4              Gaps:           1

US-10-821-670A-102 (1-187) x CD013915 (1-1136)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              |||||||||   ||||||:::|||||||||   ||||||||||||:::||||||   |||
Db        386 GGAATGTTCCCATGCCTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTC 445

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        446 CAGAAGGCCAGACAAACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAA 505

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        506 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAG 565

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThr---------------- 74
              ||||||||||||||   |||||||||   |||   ||||||
Db        566 AATGAGAGTTGCCTAAATTCCAGAGAGACCTCTTTCATAACTGTAAGTCAAAAAATGAAA 625

Qy         75 ----------------------------------------------------------Asn 75
                                                                         |||
Db        626 AGTTTCAGCCTGTATGATGAATTCATATCACTGATGTCTGATTATTTTTTCCTCTAGAAT 685

Qy         76 GlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIle 95
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        686 GGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATGGCCCTGTGCCTTAGTAGTATT 745

Qy         96 TyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMet 115
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        746 TATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAATGCAAAGCTTCTGATG 805

Qy        116 AspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeu 135
              ||||||||||||||||||||||||||||||||||||   ||||||||||||:::
Db        806 GATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCAGTTATTGATGAGCTGATG 865

Qy        136 GlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAsp 155
              ||||||||||||   ||||||   ||||||||||||   ||||||||||||||||||||
Db        866 CAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCCCTTGAAGAACCGGAT 925

Qy        156 PheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaVal 175
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Db        926 TTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGGGCAGTG 985

Qy        176 ThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 187
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Db        986 ACTATTGATAGAGTGATGAGCTATCTGAATGCTTCC 1021

RESULT 4
CD013914
LOCUS       CD013914                935 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION  90138124 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD013914
VERSION     CD013914.1  GI:37777444
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 935)
  AUTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
            Au-Young,J. and Stuve,L.L.
  TITLE     PCR isolation and cloning of novel splice variant mRNAs from known
            drug target genes
  JOURNAL   Genomics 83 (4), 566-571 (2004)
   PUBMED   15028279
COMMENT     Contact: Jin, P.
            Incyte Corporation
            3160 Porter Drive, Palo Alto, CA 94304, USA
            Tel: 650 621 8639
            Fax: 650 621 8965
            Email: pjin@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .935
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Single gene library"
                     /note="Vector: pDrive Cloning Vector; RT-PCR was performed
                     using gene-specific primers flanking the open-reading
                     frame. PCR products were subcloned into pDrive Cloning
                     Vector and sequenced completely using M13 forward and
                     reverse primers. Sequencing gaps were closed by
                     re-sequencig using primers flanking the gapped areas."
ORIGIN

Alignment Scores:
Pred. No.:              1.67e-81       Length:         935
Score:                  774.00         Matches:        155
Percent Similarity:     85.6%          Conservative:   5
Best Local Similarity:  82.9%          Mismatches:     13
```

```
Query Match:            82.0%          Indels:        14
DB:                     4              Gaps:          1

US-10-821-670A-102 (1-187) x CD013914 (1-935)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              |||||||||   ||||||:::|||||||||   ||||||||||:::||||||   |||
Db        302 GGAATGTTCCCATGCCTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTC 361

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        362 CAGAAGGCCAGACAAACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAA 421

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACC--- 478

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
                                                   ||||||||||||||||||
Db        479 ------------------------------------AAGAATGGGAGTTGCCTGGCC 499

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||      ||||||||||||||||||||||||||||||||
Db        500 TCCAGAAAGACCTCTTTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAG 559

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        560 ATGTACCAGGTGGAGTTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAG 619

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||      ||||||||||:::||||||||||||
Db        620 ATCTTTCTAGATCAAAACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTC 679

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||   ||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        680 AACAGTGAGACTGTGCCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAA 739

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||:::|||:::
Db        740 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTG 799

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||
Db        800 ATGAGCTATCTGAATGCTTCC 820

RESULT 5
BC035571
LOCUS       BC035571               1938 bp    mRNA    linear   HTC 04-MAR-2003
DEFINITION  Homo sapiens, clone IMAGE:5240216, mRNA.
ACCESSION   BC035571
VERSION     BC035571.1  GI:23958681
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1938)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 69 Row: b Column: 15
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 4504638
            This clone has the following problem: retained intron.
FEATURES             Location/Qualifiers
     source          1. .1938
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240216"
                     /tissue_type="Brain, fetal, whole pooled"
                     /clone_lib="NIH_MGC_121"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
ORIGIN

Alignment Scores:
Pred. No.:              3.26e-73       Length:        1938
Score:                  708.50         Matches:       166
Percent Similarity:     48.9%          Conservative:  6
Best Local Similarity:  47.2%          Mismatches:    15
Query Match:            75.1%          Indels:        165
DB:                     6              Gaps:          3

US-10-821-670A-102 (1-187) x BC035571 (1-1938)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              |||||||||   ||||||:::|||||||||   ||||||||||:::||||||   |||
Db        391 GGAATGTTCCCATGCCTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTC 450

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        451 CAGAAGGCCAGACAAACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAA 510

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThr--- 59
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAG 570

Qy         59 ---------------------------------------------------------- 59

Db        571 GTATAAAGGATTTTCCTCCCAGAGCATGCAGTGTGGTTAAAAACTGTGCATCAAATCTCA 630

Qy         59 ---------------------------------------------------------- 59

Db        631 CCTGCTTCTAAAAATTCACGTTTCTGGTATCCATCATTATGGGATTTTAACTGGTCCTAC 690

Qy         59 ---------------------------------------------------------- 59

Db        691 TTCAGAAGTTAGATTTGGGAGAAAAATTATTTTTAAAAAATGGTTTTTTTTGCAACAATG 750

Qy         59 ---------------------------------------------------------- 59

Db        751 TGAATACACTTAACACTTAAAAATAGTTCAGATGCTAAATATTATGATATGTGTTTTTAC 810

Qy         59 ---------------------------------------------------------- 59

Db        811 CATAATAAAAAAAATTTGAGACCTGAAGAGTCAGAAAGATTTATACTAAGAATTAATACT 870

Qy         60 --------------------Met-AsnGluSerCysLeuAlaSerArgGluIleSerLe 72
                                  ::: ||||||||||||||   |||||||||   |||
```

```
Db        871 TTGATATATGATTTTTTCCCTCTAGAATGAGAGTTGCCTAAATTCCAGAGAGACCTCTTT 930

Qy         72 uIleThr---------------------------------------------------- 74
              ||||||
Db        931 CATAACTGTAAGTCAAAAAATGAAAAGTTTCAGCCTGTATGATGAATTCATATCACTGAT 990

Qy         75 ----------------------AsnGlySerCysLeuAlaSerArgLysThrSerPheMe 87
                                    ||||||||||||||||||||||||||||||||||||
Db        991 GTCTGATTATTTTTTCCTCTAGAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTAT 1050

Qy         87 t---------------------------------------------------------- 87
              |
Db       1051 GATGGTAAGACACACAGCTCTTTCCTCAAATGCAATGGGGGAAATGTTTTTAGCCCATCT 1110

Qy         88 --------------------------------ThrThrLeuCysLeuSerSerIleTyrG 97
                                              |||||||||||||||||||||||||
Db       1111 CAATGGATACTTCCCCATCTTGTCATGTCACCCAGGCCCTGTGCCTTAGTAGTATTTATG 1170

Qy         97 luAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspP 117
              |||||||||||||||||||||||||||||||   |||||||||||||||||||||||||
Db       1171 AAGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAATGCAAAGCTTCTGATGGATC 1230

Qy        117 roLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnA 137
              |||||||||||||||||||||||||||||||||||||       |||||||||||:::||||
Db       1231 CTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCAGTTATTGATGAGCTGATGCAGG 1290

Qy        137 laLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheT 157
              ||||||||   ||||||   ||||||||||||   |||||||||||||||||||||||||
Db       1291 CCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCCCTTGAAGAACCGGATTTTT 1350

Qy        157 yrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrI 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1351 ATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGGGCAGTGACTA 1410

Qy        177 leAsnArgMetMetSerTyrLeuAsnAlaSer 187
              ||:::|||:::|||||||||||||||||||||
Db       1411 TTGATAGAGTGATGAGCTATCTGAATGCTTCC 1442
```

```
RESULT 6
CD013916
LOCUS       CD013916                863 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION  90138296 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD013916
VERSION     CD013916.1  GI:37777446
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 863)
  AUTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
            Au-Young,J. and Stuve,L.L.
  TITLE     PCR isolation and cloning of novel splice variant mRNAs from known
            drug target genes
  JOURNAL   Genomics 83 (4), 566-571 (2004)
   PUBMED   15028279
COMMENT     Contact: Jin, P.
            Incyte Corporation
            3160 Porter Drive, Palo Alto, CA 94304, USA
            Tel: 650 621 8639
            Fax: 650 621 8965
            Email: pjin@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .863
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Single gene library"
                     /note="Vector: pDrive Cloning Vector; RT-PCR was performed
                     using gene-specific primers flanking the open-reading
                     frame. PCR products were subcloned into pDrive Cloning
                     Vector and sequenced completely using M13 forward and
                     reverse primers. Sequencing gaps were closed by
                     re-sequencig using primers flanking the gapped areas."
ORIGIN
```

```
Alignment Scores:
Pred. No.:              4.27e-64        Length:         863
Score:                  628.00          Matches:        130
Percent Similarity:     72.2%           Conservative:   5
Best Local Similarity:  69.5%           Mismatches:     14
Query Match:            66.5%           Indels:         38
DB:                     4               Gaps:           1

US-10-821-670A-102 (1-187) x CD013916 (1-863)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              |||||||||   ||||||:::|||||||||   ||||||||||||:::|||||||   |||
Db        302 GGAATGTTCCCATGCCTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTC 361

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||
Db        362 CAGAAG---------------------------------------------------- 367

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60

Db        367 ---------------------------------------------------------- 367

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||   |||||||||   |||   ||||||||||||||||||||||||
Db        368 AATGAGAGTTGCCTAAATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCC 427

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||      ||||||||||||||||||||||||||||||||
Db        428 TCCAGAAAGACCTCTTTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAG 487

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        488 ATGTACCAGGTGGAGTTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAG 547

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||      |||||||||||:::||||||||||||
Db        548 ATCTTTCTAGATCAAAACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTC 607

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||   ||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        608 AACAGTGAGACTGTGCCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAA 667

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::|||:::
Db        668 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTG 727

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||
Db        728 ATGAGCTATCTGAATGCTTCC 748
```

```
RESULT 7
AK153729
LOCUS       AK153729                1299 bp    mRNA    linear   HTC 21-SEP-2005
DEFINITION  Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
            library, clone:A630064E02 product:interleukin 12a, full insert
            sequence.
ACCESSION   AK153729
VERSION     AK153729.1  GI:74148962
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   PUBMED   10349636
```

REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
CONSRTM RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
PUBMED 11217851
REFERENCE 5
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
CONSRTM FANTOM Consortium
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420 (6915), 563-573 (2002)
PUBMED 12466851
REFERENCE 6
AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.
CONSRTM FANTOM Consortium
TITLE The transcriptional landscape of the mammalian genome
JOURNAL Science 309 (5740), 1559-1563 (2005)
PUBMED 16141072
REFERENCE 7
AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.
CONSRTM RIKEN Genome Exploration Research Group
TITLE Antisense transcription in the mammalian transcriptome
JOURNAL Science 309 (5740), 1564-1566 (2005)
PUBMED 16141073
REFERENCE 8 (bases 1 to 1299)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

```
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
     source          1. .1299
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM_DB:A630064E02"
                     /db_xref="taxon:10090"
                     /clone="A630064E02"
                     /tissue_type="thymus"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="3 days neonate"
     misc_feature    1. .1299
                     /note="interleukin 12a (MGD|MGI:96539 GB|NM_008351,
                     evidence: BLASTN, 100%, match=776)
                     putative"
ORIGIN

Alignment Scores:
Pred. No.:              9.42e-44        Length:         1299
Score:                  460.00          Matches:        103
Percent Similarity:     57.0%           Conservative:   27
Best Local Similarity:  45.2%           Mismatches:     43
Query Match:            48.7%           Indels:         55
DB:                     6               Gaps:           2

US-10-821-670A-102 (1-187) x AK153729 (1-1299)

Qy          15 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 34
               :::   |||           :::||||||:::   |||:::   ||||||||||||:::
Db         118 AGCTTCTCCTTATGTTTTTCCCAGGCCAGAGAAAAACTGAAACATTATTCCTGCACTGCT 177

Qy          35 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeu 54
               |||:::||||||||||||||||||:::|||:::|||||||||::::::   ||||||
Db         178 GAAGACATCGATCATGAAGACATCACACGGGACCAAACCAGCACATTGAAGACCTGTTTA 237

Qy          55 ProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSer--------- 71
               ||||||||||||      ||||||||||||||||||:::||||||   |||
Db         238 CCACTGGAACTACACAAGAACGAGAGTTGCCTGGCTACTAGAGAGACTTCTTCCACAACA 297

Qy          71 ------------------------------------------------------------ 71

Db         298 GTAAGTAAGCACTCTAAGGGTTCCTTCCCCATGACGGATTCATAACACTGATGCCTGGTC 357

Qy          72 ---Leu-IleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThr----- 88
                  ||| :::      ||||||||||||      :::|||||||||   |||
Db         358 ATTCTTTCTCTAGAGAGGGAGCTGCCTGCCCCCACAGAAGACGTCTTTGATGATGGTAAG 417

Qy          88 ------------------------------------------------------------ 88

Db         418 CCACATCACTTTTCTGAAATGCAGCAGGGTCCTGTAGTTCCAGCCCATCTCAATGATTCC 477

Qy          89 ------------------------ThrLeuCysLeuSerSerIleTyrGluAspLeuLy 100
                                       ||||||||||||   ||||||||||||||||||
Db         478 TTGCCCATTGTGTCCTGCGCTCTAGACCCTGTGCCTTGGTAGCATCTATGAGGACTTGAA 537

Qy         100 sMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGl 120
               ||||||||||   ||||||:::|||:::||||||   |||                :::||
Db         538 GATGTACCAGACAGAGTTCCAGGCCATCAACGCAGCACTTCAGAATCACAACCATCAGCA 597

Qy         120 nIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVa 140
               ||||   ||||||:::   ||||||   ||||||||||||||:::|||:::||||||
Db         598 GATCATTCTAGACAAGGGCATGCTGGTGGCCATCGATGAGCTGATGCAGTCTCTGAATCA 657

Qy         140 lAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLy 160
                |||      |||:::   |||         :::   |||   |||   |||:::   ||

Db         658 TAATGGCGAGACTCTGCGCCAGAAACCTCCTGTGGGAGAAGCAGACCCTTACAGAGTGAA 717

Qy         160 sIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMe 180
               |:::|||||||||||||||||||||||||||      |||   ||||||||||||||::
Db         718 AATGAAGCTCTGCATCCTGCTTCACGCCTTCAGCACCCGCGTCGTGACCATCAACAGGGT 777

Qy         180 tMetSerTyrLeuAsnAlaSer 187
               :|||   ||||||:::::::::
Db         778 GATGGGCTATCTGAGCTCCGCC 799

RESULT 8
BU698113
LOCUS       BU698113                563 bp    mRNA    linear   EST 09-OCT-2002
DEFINITION  LL2in12067T7 Hematopoietic Stem Cell Subtracted Library Mus
            musculus cDNA 5' similar to interleukin 12 p35 subunit, mRNA
            sequence.
ACCESSION   BU698113
VERSION     BU698113.1  GI:23610620
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 563)
  AUTHORS   Phillips,R.L., Ernst,R.E., Brunk,B.P., Ivanova,N., Mahan,M.A.,
            Deanehan,J.K., Moore,K.A., Overton,G.C. and Lemischka,I.R.
  TITLE     The genetic program of hematopoietic stem cells
  JOURNAL   Science 288 (5471), 1635-1640 (2000)
   PUBMED   10834841
COMMENT     Contact: Lemischka, Ihor R.
            Department of Molecular Biology
            Princeton University
            Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544, USA
            Tel: 609 258 2838
            Fax: 609 258 2759
            Email: ilemischka@molbio.princeton.edu
            These ESTs are derived from a subtracted cDNA library enriched for
            gene products expressed in day 14-14.5 fetal liver hematopoietic
            stem cells defined as Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E
            (Sca-1)pos
            Seq primer: M13Reverse or T7.
FEATURES             Location/Qualifiers
     source          1. .563
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /tissue_type="Hematopoietic"
                     /cell_type="Stem Cells; Lineageneg/lo, AA4.1pos, cKitpos,
                     Ly6A/E (Sca-1)pos"
                     /dev_stage="Embryonic day 14-14.5"
                     /lab_host="DH10B"
                     /clone_lib="Hematopoietic Stem Cell Subtracted Library"
                     /note="Organ: Fetal Liver; Vector: Sport 1; Site_1: Sal I;
                     Site_2: Not I; Two directionally cloned cDNA libraries
                     were made from fetal liver  hematopoietic stem cells
                     enriched to be Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E
                     (Sca-1)pos called Scapos and from AA4.1neg fetal liver
                     cells. Subtractive hybridization was  performed by
                     hybridization of the target, Scapos, single stranded cDNA
                     library in pSport1 to  biotinylated RNA transcribed from
                     the driver, AA4.1neg cDNA library in pSport2 with  inserts
                     cloned in the complementary orientation. For detailed
                     protocols and additional  information please see our
                     website at http://stemcell.princeton.edu."
ORIGIN

Alignment Scores:
Pred. No.:              2.58e-39        Length:         563
Score:                  418.50          Matches:        88
Percent Similarity:     72.5%           Conservative:   23
Best Local Similarity:  57.5%           Mismatches:     40
```

```
Query Match:            44.3%          Indels:        2
DB:                     3              Gaps:          1

US-10-821-670A-102 (1-187) x BU698113 (1-563)

Qy         15 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 34
              :::   |||            :::||||||:::   |||:::   |||||||||||:::
Db         78 AGCTTCTCCTTATGTTTTTCCCAGGCCAGAGAAAAACTGAAACATTATTCCTGCACTGCT 137

Qy         35 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeu 54
              |||:::|||||||||||||||||||:::|||:::||||||||||::::::   ||||||
Db        138 GAAGACATCGATCATGAAGACATCACACGGGACCAAACCAGCACATTGAAGACCTGTTTA 197

Qy         55 ProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThr 74
              ||||||||||||      ||||||||||||||||||:::||||||   |||      |||
Db        198 CCACTGGAACTACACAAGAACGAGAGTTGCCTGGCTACTAGAGAGACTTCTTCCACAACA 257

Qy         75 AsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSer 94
                 ||||||||||||      :::||||||||||   |||   ||||||||||||   |||
Db        258 AGAGGGAGCTGCCTGCCCCCACAGAAGACGTCTTTGATGATGACCCTGTGCCTTGGTAGC 317

Qy         95 IleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeu 114
              ||||||||||||||||||||||||||   ||||||:::|||:::||||||   |||
Db        318 ATCTATGAGGACTTGAAGATGTACCAGACAGAGTTCCAGGCCATCAACGCAGCACTTCAG 377

Qy        115 MetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 134
                     :::||||||   ||||||:::   ||||||   ||||||||||||||||
Db        378 AATCACAACCATCAGCAGATCATTCTAGACAAGGGCATGCTGGTGGCCATCGATGAGCTG 437

Qy        135 LeuGlnAlaLeuAsnValAsnSerVal-ThrVal---ProGlnAsnSerSerLeuGluGl 153
              :::|||:::||||||   |||       |||:::   |||:::            |||::
Db        438 ATGCAGTCTCTGAATCATAATGGGNGAGACTCTTGCGCCAGAAACCTTCCTGTGGGAGAA 497

Qy        153 uProAspPheTyrLysThrLysIleLysLeuCysIle 165
              :   |||   |||:::   |||:::||||||   |||
Db        498 GCAGGACCCTTACAGAGTGAAAATGAAGCTCTTGATT 534


RESULT 9
AI050362
LOCUS       AI050362                589 bp    mRNA    linear   EST 09-JUL-1998
DEFINITION  ub30a07.r1 Soares_thymus_2NbMT Mus musculus cDNA clone
            IMAGE:1379220 5' similar to gb:M65291 INTERLEUKIN-12 ALPHA CHAIN
            PRECURSOR (HUMAN); gb:M86672 Mus musculus interleukin 12 p35
            subunit, complete cds (MOUSE);, mRNA sequence.
ACCESSION   AI050362
VERSION     AI050362.1  GI:3299479
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 589)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:901688
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 60.
FEATURES             Location/Qualifiers
     source          1. .589
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1379220"
                     /sex="male"
                     /tissue_type="Thymus"
                     /dev_stage="4 weeks"
                     /lab_host="DH10B"
                     /clone_lib="Soares_thymus_2NbMT"
                     /note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI;
                     1st strand cDNA was primed with a Not I - oligo(dT) primer
                     [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGTTTTTTTTTTTTTTTTTTTTTTTT
                     3']; double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. RNA
                     provided by Dr. Bertrand Jordan. Library went through two
                     rounds of normalization, and was constructed by Bento
                     Soares and M.Fatima Bonaldo."
ORIGIN

Alignment Scores:
Pred. No.:              1.49e-37        Length:         589
Score:                  404.00          Matches:        94
Percent Similarity:     68.8%           Conservative:   23
Best Local Similarity:  55.3%           Mismatches:     46
Query Match:            42.8%           Indels:         8
DB:                     1               Gaps:           3

US-10-821-670A-102 (1-187) x AI050362 (1-589)

Qy         15 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 34
              :::   |||            :::||||||:::   |||:::   |||||||||||:::
Db         87 AGCTTCTCCTTATGTTTTTCCCAGGCCAGAGAAAAACTGAAACATTATTCCTGCACTGCT 146

Qy         35 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeu 54
              |||:::|||||||||||||||||||:::|||:::||||||||||::::::   ||||||
Db        147 GAAGACATCGATCATGAAGACATCACACGGGACCAAACCAGCACATTGAAGACCTGTTTA 206

Qy         55 ProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThr 74
              ||||||||||||      ||||||||||||||||||:::||||||   |||      |||
Db        207 CCACTGGAACTACACAAGAACGAGAGTTGCCTGGCTACTAGAGAGACTTCTTCCACAACA 266

Qy         75 AsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSer 94
                 ||||||||||||      :::||||||||||   |||   ||||||||||||   |||
Db        267 AGAGGGAGCTGCCTGCCCCCACAGAAGACGTCTTTGATGATGACCCTGTGCCTTGGTAGC 326

Qy         95 IleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeu 114
              ||||||||||||||||||||||||||   ||||||:::|||:::||||||   |||
Db        327 ATCTATGAGGACTTGAAGATGTACCAGACAGAGTTCCAGGCCATCAACGCAGCACTTCAG 386

Qy        115 MetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 134
                        :::||||||   ||||||:::   ||||||      ||||||||||||
Db        387 AATCACAACCATCAGCAGATCATTCTAGACAAGGGCATGCTGGGTGGCATCGATGAGCTG 446

Qy        135 LeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeu------Glu 152
              :::|||:::||||||   |||       |||:::   |||   :::||||||       |||
Db        447 ATGCAGTCTCTGAATCATAATGGCGAGACTCTGCGCCAGAA-ACCTCCCTGTGGGGAGAA 505

Qy        153 GluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIle 172
                           :::   |||       :::   |||||||||         |||:::
Db        506 GCAGACCCCTTACAGGAGTGAAAATGAAGCGTCTGAATCCTGCTTTCA------CGCCTT 559

Qy        173 ArgAla---------ValThrIleAsnArg 179
                 |||         ||||||||||||||
Db        560 TCAGCACCCGGCGTCGTGACCATCAACAGG 589


RESULT 10
BI523344/c
LOCUS       BI523344                1099 bp    mRNA    linear   EST 29-AUG-2001
DEFINITION  603175938T1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 3',
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            mRNA sequence.
ACCESSION   BI523344
VERSION     BI523344.1  GI:15348136
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1099)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11605  row: l  column: 09
            High quality sequence start: 40
            High quality sequence stop: 727.
FEATURES             Location/Qualifiers
     source          1. .1099
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240216"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_121"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 017. Note:
                     this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              1.24e-33        Length:         1099
Score:                  374.50          Matches:        90
Percent Similarity:     80.7%           Conservative:   6
Best Local Similarity:  75.6%           Mismatches:     15
Query Match:            39.7%           Indels:         9
DB:                     2               Gaps:           1

US-10-821-670A-102 (1-187) x BI523344 (1-1099)

Qy         72 LeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCys 91
              |||   |||      :::   |||   ||||||:::                  ||||||
Db        776 TTGGATACTTTCCGCAATCTGCTCATGTCACGTCAG--------------GCCCTGTGC 732

Qy         92 LeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAla 111
              ||||||||||||||||||   ||||||||||||||||||||||   |||||||||
Db        731 TTTAGTAGTATTTATGAAGACTG-AAGATGTACCAGGTGGAGTTCAAGACCATGAATGCA 673

Qy        112 LysLeu-LeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIl 131
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||      ||
Db        672 AAGCTTCCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCAGTTAT 613

Qy        131 eAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLe 151
              ||||||||||:::|||||||||||||   ||||||   ||||||||||||   ||||||||
Db        612 TGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCCCT 553

Qy        151 uGluGluProAsp--PheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 170
              |||||||||||||  |||   ||||||:::||||||||||||||||||||||||||||||
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Db        552 TGAAGAACCGGATTGTTTATCAAAACTGAAATCAAGCTCTGCATACTTCTTCATGCTTTC 493

Qy        171 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 187
              ||||||||||||||||||||:::|||:::|||||||||||||||||||||
Db        492 AGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTCC 442

RESULT 11
BG702253
LOCUS       BG702253                812 bp    mRNA    linear   EST 07-MAY-2001
DEFINITION  602683459F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4816118 5',
            mRNA sequence.
ACCESSION   BG702253
VERSION     BG702253.1  GI:13973409
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 812)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10714  row: e  column: 15
            High quality sequence stop: 804.
FEATURES             Location/Qualifiers
     source          1. .812
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4816118"
                     /tissue_type="hippocampus"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_95"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
                     (gtcgag); Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTTTTVN-3', size-selected for  average
                     insert size 2.5 kb and normalized to ROT 5. This is a
                     primary library enriched for  full-length clones and
                     constructed using the Cap-trapper method (Carninci, in
                     preparation).  Library constructed by M. Brownstein
                     (NIMH/NHGRI, National Institutes of Health).  Note: this
                     is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              1.39e-33        Length:         812
Score:                  372.50          Matches:        85
Percent Similarity:     87.0%           Conservative:   2
Best Local Similarity:  85.0%           Mismatches:     13
Query Match:            39.5%           Indels:         3
DB:                     2               Gaps:           0

US-10-821-670A-102 (1-187) x BG702253 (1-812)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              |||||||||   ||||||:::|||||||||   |||||||||||:::||||||   |||
Db        513 GGAATGTTCCCATGCCTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTC 572

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        573 CAGAAGGCCAGACAAACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATCGATCATGAA 632
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Qy          41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         633 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAG 692

Qy          61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
               |||||||||||||      |||||||||   |||   ||||||||||||||||||||||
Db         693 AATGAGAGTTGCT--AAATCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGC- 749

Qy          81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
               ||||||||||||||||||       ||||||||||||||   ||||||||||||||||
Db         750 TCCAGAAAGACCTCTTTTATGATGTGCCTGTGCCTTAGTAGTAT-TATGAAGACTTGAAA 808

RESULT 12
AJ820622/c
LOCUS       AJ820622                778 bp    mRNA    linear   EST 12-MAY-2005
DEFINITION  AJ820622 KN206 Bos sp. cDNA clone C0006020h12, mRNA sequence.
ACCESSION   AJ820622
VERSION     AJ820622.1  GI:51888098
KEYWORDS    EST.
SOURCE      Bos sp.
  ORGANISM  Bos sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 778)
  AUTHORS   McGuire,K. and Glass,E.J.
  TITLE     The expanding role of microarrays in the investigation of
            macrophage responses to pathogens
  JOURNAL   Vet. Immunol. Immunopathol. 105 (3-4), 259-275 (2005)
COMMENT     Contact: McGuire K
            Genomics and Genetics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
            Single pass sequencing. Bases called and trimmed with phred
            v0.020425.c. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options. Vector:pBluescriptII(SK+) R. Site
            1:EcoRV(lost) R. Site 2:NotI Seq Primer: T7 Normalised library
            constructed from pooled monocytes from Bos taurus (Holstein) and
            Bos indicus (Sahiwals) cattle subjected to various stimuli,
            including infection with the protozoan parasite Theileria annulata.
FEATURES             Location/Qualifiers
     source          1. .778
                     /organism="Bos sp."
                     /mol_type="mRNA"
                     /db_xref="taxon:29061"
                     /clone="C0006020h12"
                     /tissue_type="blood"
                     /cell_type="bovine monocyte"
                     /clone_lib="KN206"
                     /note="Vector: pBluescriptII(SK+); Site_1: EcoRV(lost);
                     Site_2: NotI; Normalised library constructed from pooled
                     monocytes from Bos taurus (Holstein) and Bos indicus
                     (Sahiwals) cattle subjected to various stimuli, including
                     infection with the protozoan parasite Theileria annulata"
ORIGIN

Alignment Scores:
Pred. No.:              1.61e-31        Length:         778
Score:                  355.00          Matches:        71
Percent Similarity:     90.8%           Conservative:   8
Best Local Similarity:  81.6%           Mismatches:     8
Query Match:            37.6%           Indels:         0
DB:                     1               Gaps:           0

US-10-821-670A-102 (1-187) x AJ820622 (1-778)

Qy         101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
               ||||||   |||||||||:::||||||||||||||||||||||||||||||||||||||
Db         777 ATGTACCACGTGGAGTTCCAGGCCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAA 718

Qy         121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
               ||||||||||||||||||||||||   ||||||   ||||||:::||||||||||||

Db         717 ATCTTTCTAGACCAGAACATGCTGGCAGCTATTGCTGAGCTGATGCAGGCCCTGAATTTC 658

Qy         141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
               :::|||   ||||||||||||       ||||||:::|||   ||||||||||||||||||
Db         657 GACAGTGAGACTGTGCCACAGAAACCCTCCCTGAAAGAACTGGATTTTTACAAGACAAAA 598

Qy         161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
               :::||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db         597 GTCAAGCTCTGCATCCTTCTTCACGCCTTCAGAATTCGTGCGGTGACCATCGACAGAATG 538

Qy         181 MetSerTyrLeuAsnAlaSer 187
               ||||||||||||::::::|||
Db         537 ATGAGCTATCTGAGTTCTTCC 517

RESULT 13
BU699383
LOCUS       BU699383                561 bp    mRNA    linear   EST 09-OCT-2002
DEFINITION  LL2in11573T7 Hematopoietic Stem Cell Subtracted Library Mus
            musculus cDNA 5' similar to interleukin 12 p35 subunit, mRNA
            sequence.
ACCESSION   BU699383
VERSION     BU699383.1  GI:23615967
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 561)
  AUTHORS   Phillips,R.L., Ernst,R.E., Brunk,B.P., Ivanova,N., Mahan,M.A.,
            Deanehan,J.K., Moore,K.A., Overton,G.C. and Lemischka,I.R.
  TITLE     The genetic program of hematopoietic stem cells
  JOURNAL   Science 288 (5471), 1635-1640 (2000)
   PUBMED   10834841
COMMENT     Contact: Lemischka, Ihor R.
            Department of Molecular Biology
            Princeton University
            Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544, USA
            Tel: 609 258 2838
            Fax: 609 258 2759
            Email: ilemischka@molbio.princeton.edu
            These ESTs are derived from a subtracted cDNA library enriched for
            gene products expressed in day 14-14.5 fetal liver hematopoietic
            stem cells defined as Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E
            (Sca-1)pos
            Seq primer: M13Reverse or T7.
FEATURES             Location/Qualifiers
     source          1. .561
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /tissue_type="Hematopoietic"
                     /cell_type="Stem Cells; Lineageneg/lo, AA4.1pos, cKitpos,
                     Ly6A/E (Sca-1)pos"
                     /dev_stage="Embryonic day 14-14.5"
                     /lab_host="DH10B"
                     /clone_lib="Hematopoietic Stem Cell Subtracted Library"
                     /note="Organ: Fetal Liver; Vector: Sport 1; Site_1: Sal I;
                     Site_2: Not I; Two directionally cloned cDNA libraries
                     were made from fetal liver  hematopoietic stem cells
                     enriched to be Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E
                     (Sca-1)pos called Scapos and from AA4.1neg fetal liver
                     cells. Subtractive hybridization was  performed by
                     hybridization of the target, Scapos, single stranded cDNA
                     library in pSport1 to  biotinylated RNA transcribed from
                     the driver, AA4.1neg cDNA library in pSport2 with  inserts
                     cloned in the complementary orientation. For detailed
                     protocols and additional  information please see our
                     website at http://stemcell.princeton.edu."
ORIGIN

Alignment Scores:
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Pred. No.:              4.56e-31        Length:         561
Score:                  349.50          Matches:        76
Percent Similarity:     68.1%           Conservative:   22
Best Local Similarity:  52.8%           Mismatches:     45
Query Match:            37.0%           Indels:         2
DB:                     3               Gaps:           1

US-10-821-670A-102 (1-187) x BU699383 (1-561)

Qy         37 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 56
              :::|||||||||||||||||||:::|||:::|||||||||:::::::   ||||||||||||
Db        128 CTCGATCATGAAGACATCACACGGGACCAAACCAGCACATTGAAGACCTGTTTACCACTG 187

Qy         57 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 76
              ||||||      ||||||||||||||||||:::|||||||   |||      |||   |||
Db        188 GAACTACACAAGAACGAGAGTTGCCTGGCTACTAGAGAGACTTCTTCCACAACAAGAGGG 247

Qy         77 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 96
              |||||||||       :::|||||||||   |||   ||||||||||||   |||||||||
Db        248 AGCTGCCTGCCCCCACAGAAGACGTCTTTGATGATGACCCTGTGCCTTGGTAGCATCTAT 307

Qy         97 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 116
              ||||||||||||||||||||   ||||||:::|||:::||||||   |||
Db        308 GAGGACTTGAAGATGTACCAGACAGAGTTCCAGGCCATCAACGCAGCACTTCAGAATCAC 367

Qy        117 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 136
                 :::||||||   |||||:::   ||||||      |||||||||||:::|||
Db        368 AACCATCAGCAGATCATTCTAGACAAGGGCATGCTGGTGGGCATCGATGAGCTGATGCAG 427

Qy        137 AlaLeuAsnValAsnSer---ValThrValProGlnAsnSerSerLeuGluGluProAsp 155
              :::|||:::   |||         :::      :::   |||         :::
Db        428 TCTCTGGATCATAATGGGCGAGACTCTGCGGCAAAAANCTCCTGTNGGGNGAAGCAGANC 487

Qy        156 PheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaVal 175
                 |||:::   ::::::||||||      ||||||:::   |||      |||
Db        488 CTTTACAGAGTGGAAATGAAGCTCTG-NATCTGCTTTACGGCTTTAGCANCCGGTTGTGA 546

Qy        176 ThrIleAsnArg 179
                 :::   |||
Db        547 NCATTAAANAGG 558

RESULT 14
BF552757
LOCUS       BF552757                373 bp    mRNA    linear   EST 12-DEC-2000
DEFINITION  UI-R-C0-iz-d-02-0-UI.r1 UI-R-C0 Rattus norvegicus cDNA clone
            UI-R-C0-iz-d-02-0-UI 5', mRNA sequence.
ACCESSION   BF552757
VERSION     BF552757.1  GI:11662487
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 373)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
   PUBMED   8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156  MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            cDNA Library Preparation: M.B. Soares Lab Clone distribution:
            clones will be available through Research Genetics (www.resgen.com)
            This clone is also available through the I.M.A.G.E. Consortium at
            LLNL (info@image.llnl.gov). IMAGE ID= 1782759
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .373
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="UI-R-C0-iz-d-02-0-UI"
                     /dev_stage="adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="UI-R-C0"
                     /note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI;
                     The UI-R-C0 library is a subtracted library derived from
                     the UI-R-A1 and UI-R-E1 libraries. The UI-R-A1 library
                     consisted of a mixture of individually tagged normalized
                     libraries constructed from rat  placenta, adult lung,
                     brain, liver, kidney, heart, spleen, ovary,  and muscle.
                     The UI-R-E1 library  consisted of a mixture of
                     individually tagged normalized libraries constructed from
                     8, 12 and 18-day embryo. The tag is a string of 3-5
                     nucleotides present between the Not I  site and the
                     oligo-dT track which allows identification of the library
                     of origin of a clone within the mixture. The subtracted
                     library (UI-R-C0) was constructed as follows: PCR
                     amplified cDNA inserts from a pool of UI-R-A1 and UI-R-E1
                     clones from which 3' ESTs had been derived was used as a
                     driver in a hybridization with the pooled UI-R-A1 and
                     UI-R-E1 library in the form of single-stranded circles.
                     The remaining single-stranded circles (subtracted library)
                     was purified by hydroxyapatite column chromatography,
                     converted to double-stranded circles and electroporated
                     into DH10B bacteria (Life Technologies) to generate the
                     UI-R-C0 library. This procedure has been previously
                     described (Bonaldo, Lennon and Soares, Genome Research 6:
                     791-806, 1996)"
ORIGIN

Alignment Scores:
Pred. No.:              8.73e-31        Length:         373
Score:                  345.00          Matches:        70
Percent Similarity:     73.8%           Conservative:   20
Best Local Similarity:  57.4%           Mismatches:     32
Query Match:            36.5%           Indels:         0
DB:                     7               Gaps:           0

US-10-821-670A-102 (1-187) x BF552757 (1-373)

Qy         64 CysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLys 83
              |||||||||::::::|||   |||   |||      ||||||||||||      :::|||
Db          8 TGCCTGGCTACTAAAGAGACTTCTTCCATAATAAGAGGGAGCTGCCTGCCTCCACAAAAG 67

Qy         84 ThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGln 103
              ||||||   |||   ||||||||||||   ||||||||||||||||||||||||||||||
Db         68 ACTTCTTTGATGATGACCCTGTGCCTTGGTAGCATCTATGAGGACTTGAAGATGTACCAG 127

Qy        104 ValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeu 123
              ||||||:::|||:::||||||   |||                :::||||||   |||
Db        128 TCAGAGTTCCAGGCCATAAATGCAGCACTTCAGAGCCACAATCATCAGCAGATCACTCTG 187

Qy        124 AspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerVal 143
              |||:::||||||||   ||||||||||||||:::::::::||||||   :::
Db        188 GACAGAAACATGCTGATGGCTATTGATGAGCTAATGCGGTCTCTGAATCACAGCGGCGAG 247

Qy        144 ThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeu 163
                 :::   |||   :::   :::   |||   |||   |||:::   |||:::||||||
Db        248 ATTCTGCACCAGAAAGCTCCCATGGGAGAAGCAGATCCTTACAGAGTGAAGATGAAGCTC 307

Qy        164 CysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyr 183
              ||||||||||||||||||||      |||   :::||||||||||:::|||:::|||
Db        308 TGTATCCTGCTCCATGCCTTCAGCACACGCGTCATGACTATCAACAGGGTGATGAACTAT 367

Qy        184 LeuAsn 185
              |||:::
Db        368 CTGAGC 373
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RESULT 15
CJ137697
LOCUS       CJ137697                692 bp    mRNA    linear   EST 23-SEP-2005
DEFINITION  CJ137697 RIKEN full-length enriched mouse cDNA library, C57BL/6J
            thymus 3 days neonate Mus musculus cDNA clone A630064E02 5', mRNA
            sequence.
ACCESSION   CJ137697
VERSION     CJ137697.1  GI:76238025
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 692)
  AUTHORS   The FANTOM Consortium and RIKEN Genome Exploration Research Group
            and Genome Science Group (Genome Network Project Core Group).
  TITLE     The transcriptional landscape of the mammalian genome
  JOURNAL   Science 309 (5740), 1559-1563 (2005)
   PUBMED   16141072
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. Tissues were provided by Dr. John Todd (
            Dept. of Medical Genetics Wellcome Trust Centre for Molecular
            Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes
            Hospital Cambridge ) whose assistance we gratefully acknowledge.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/.
FEATURES             Location/Qualifiers
     source          1. .692
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="A630064E02"
                     /tissue_type="thymus"
                     /dev_stage="3 days neonate"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library,
                     C57BL/6J thymus 3 days neonate"
ORIGIN

Alignment Scores:
Pred. No.:              2.81e-30        Length:         692
Score:                  344.00          Matches:        80
Percent Similarity:     53.8%           Conservative:   20
Best Local Similarity:  43.0%           Mismatches:     31
Query Match:            36.4%           Indels:         55
DB:                     5               Gaps:           2

US-10-821-670A-102 (1-187) x CJ137697 (1-692)

Qy          15 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 34
               :::   |||           :::||||||:::   |||:::   |||||||||||:::
Db         118 AGCTTCTCCTTATGTTTTTCCCAGGCCAGAGAAAAACTGAAACATTATTCCTGCACTGCT 177

Qy          35 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeu 54
               |||:::||||||||||||||||||||:::|||:::|||||||||:::::   ||||||
Db         178 GAAGACATCGATCATGAAGACATCACACGGGACCAAACCAGCACATTGAAGACCTGTTTA 237

Qy          55 ProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSer--------- 71
               |||||||||||      ||||||||||||||||||:::|||||   |||
Db         238 CCACTGGAACTACACAAGAACGAGAGTTGCCTGGCTACTAGAGAGACTTCTTCCACAACA 297

Qy          71 ------------------------------------------------------------ 71

Db         298 GTAAGTAAGCACTCTAAGGGTTCCTTCCCCATGACGGATTCATAACACTGATGTCTGGTC 357

Qy          72 ---Leu-IleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThr----- 88
                  ||| :::      ||||||||||||      :::|||||||||   |||
Db         358 ATTCTTTCTCTAGAGAGGGAGCTGCCTGCCCCCACAGAAGACGTCTTTGATGATGGTAAG 417

Qy          88 ------------------------------------------------------------ 88

Db         418 CCACATCACTTTTCTGAAATGCAGCAGGGTCCTGTAGTTCCAGCCCATCTCAATGATTCC 477

Qy          89 -------------------------ThrLeuCysLeuSerSerIleTyrGluAspLeuLy 100
                                        ||||||||||||   ||||||||||||||||||||
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Qy         100 sMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGl 120
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Db         538 GATGTACCAGACAGAGTTCCAGGCCATCAACGCAGCACTTCAGAATCACAACCATCAGCA 597

Qy         120 nIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVa 140
               ||||   |||||:::   ||||||   ||||||||||||||||:::|||:::||||||
Db         598 GATCATTCTAGACAAGGGCATGCTGGTGGCCATCGATGAGCTGATGCAGTCTCTGAATCA 657

Qy         140 lAsnSerValThrVal 145
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Db         658 TAATGGCGAGACTCTG 673


Search completed: June 10, 2006, 10:30:49
Job time : 2295 secs
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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 10, 2006, 01:16:39 ; Search time 96.5761 Seconds
(without alignments)
5434.532 Million cell updates/sec

Title: US-10-821-670A-102
Perfect score: 944
Sequence: 1 GMFQCLNHSQTLLRAISNTL.....HAFRIRAVTINRMMSYLNAS 187

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Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	2	944	100.0	561	3	US-09-917-265A-103	Sequence 103, App
	3	944	100.0	591	3	US-09-917-265A-35	Sequence 35, Appl
c	4	944	100.0	591	3	US-09-917-265A-37	Sequence 37, Appl
	5	944	100.0	666	3	US-09-917-265A-32	Sequence 32, Appl
c	6	944	100.0	666	3	US-09-917-265A-34	Sequence 34, Appl
	7	944	100.0	1533	3	US-09-917-265A-43	Sequence 43, Appl
c	8	944	100.0	1533	3	US-09-917-265A-45	Sequence 45, Appl
	9	944	100.0	1599	3	US-09-917-265A-38	Sequence 38, Appl
c	10	944	100.0	1599	3	US-09-917-265A-40	Sequence 40, Appl
	11	941	99.7	591	3	US-09-011-143-9	Sequence 9, Appli
	12	941	99.7	591	3	US-09-302-495-9	Sequence 9, Appli
	13	941	99.7	591	3	US-10-079-616-9	Sequence 9, Appli
	14	941	99.7	689	3	US-09-011-143-26	Sequence 26, Appl
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	16	941	99.7	689	3	US-10-079-616-26	Sequence 26, Appl
	17	941	99.7	1441	3	US-09-011-143-8	Sequence 8, Appli
	18	941	99.7	1441	3	US-09-302-495-8	Sequence 8, Appli
	19	941	99.7	1441	3	US-10-079-616-8	Sequence 8, Appli
	20	903	95.7	1533	3	US-09-917-265A-66	Sequence 66, Appl
c	21	903	95.7	1533	3	US-09-917-265A-68	Sequence 68, Appl
	22	903	95.7	1599	3	US-09-917-265A-61	Sequence 61, Appl
c	23	903	95.7	1599	3	US-09-917-265A-63	Sequence 63, Appl
	24	889	94.2	591	3	US-09-917-265A-49	Sequence 49, Appl
c	25	889	94.2	591	3	US-09-917-265A-51	Sequence 51, Appl
	26	889	94.2	666	3	US-09-917-265A-46	Sequence 46, Appl
c	27	889	94.2	666	3	US-09-917-265A-48	Sequence 48, Appl
	28	889	94.2	669	3	US-09-079-984A-12	Sequence 12, Appl
	29	889	94.2	669	3	US-09-390-729-12	Sequence 12, Appl
	30	889	94.2	1455	3	US-09-917-265A-104	Sequence 104, App
c	31	889	94.2	1455	3	US-09-917-265A-106	Sequence 106, App
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	34	843	89.3	660	2	US-08-186-529-3	Sequence 3, Appli
	35	843	89.3	660	2	US-08-640-386A-3	Sequence 3, Appli
	36	843	89.3	762	3	US-08-848-760B-21	Sequence 21, Appl
	37	843	89.3	762	3	US-09-826-025-21	Sequence 21, Appl
	38	843	89.3	762	5	US-09-543-679A-2890	Sequence 2890, Ap
	39	843	89.3	1019	3	US-09-949-016-2462	Sequence 2462, Ap
	40	843	89.3	1316	2	US-08-684-687-3	Sequence 3, Appli
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	42	843	89.3	1364	2	US-08-265-087-3	Sequence 3, Appli
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	45	843	89.3	1364	3	US-09-260-173-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-917-265A-101
; Sequence 101, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 101
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(561)
US-09-917-265A-101

Alignment Scores:

Pred. No.:	1.14e-116	Length:	561
Score:	944.00	Matches:	187
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-102 (1-187) x US-09-917-265A-101 (1-561)

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Db          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
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Db        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
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Db        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
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Db        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
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Db        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540

Qy        181 MetSerTyrLeuAsnAlaSer 187
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Db        541 ATGAGCTATCTGAATGCTTCC 561
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RESULT 2
US-09-917-265A-103/c
; Sequence 103, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 103
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265A-103

Alignment Scores:

Pred. No.:	1.14e-116	Length:	561
Score:	944.00	Matches:	187
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-102 (1-187) x US-09-917-265A-103 (1-561)

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Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
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Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
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Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
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Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
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Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
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RESULT 3
US-09-917-265A-35
; Sequence 35, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(591)
US-09-917-265A-35

Alignment Scores:

Pred. No.:	1.24e-116	Length:	591
Score:	944.00	Matches:	187
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0

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DB:                    3             Gaps:          0

US-10-821-670A-102 (1-187) x US-09-917-265A-35 (1-591)

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Db         31 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 90

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 210

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
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Db        211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
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Db        271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
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Db        331 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 390

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 450

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 510

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 570

Qy        181 MetSerTyrLeuAsnAlaSer 187
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Db        571 ATGAGCTATCTGAATGCTTCC 591

RESULT 4
US-09-917-265A-37/c
; Sequence 37, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-37

Alignment Scores:
Pred. No.:              1.24e-116      Length:        591
Score:                  944.00         Matches:       187
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            100.0%         Indels:        0
DB:                     3              Gaps:          0

US-10-821-670A-102 (1-187) x US-09-917-265A-37 (1-591)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
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Db       561 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
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Db       381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1

RESULT 5
US-09-917-265A-32
; Sequence 32, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
US-09-917-265A-32

Alignment Scores:
Pred. No.:              1.49e-116      Length:        666
Score:                  944.00         Matches:       187
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
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Query Match:            100.0%      Indels:        0
DB:                     3           Gaps:          0

US-10-821-670A-102 (1-187) x US-09-917-265A-32 (1-666)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 165

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 225

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 285

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 345

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 405

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 465

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 525

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 585

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 645

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db        646 ATGAGCTATCTGAATGCTTCC 666

RESULT 6
US-09-917-265A-34/c
; Sequence 34, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-34

Alignment Scores:
Pred. No.:              1.49e-116   Length:        666
Score:                  944.00      Matches:       187
Percent Similarity:     100.0%      Conservative:  0
Best Local Similarity:  100.0%      Mismatches:    0
Query Match:            100.0%      Indels:        0
DB:                     3           Gaps:          0

US-10-821-670A-102 (1-187) x US-09-917-265A-34 (1-666)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1

RESULT 7
US-09-917-265A-43
; Sequence 43, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-09-917-265A-43

Alignment Scores:
Pred. No.:              5.46e-116   Length:        1533
Score:                  944.00      Matches:       187
Percent Similarity:     100.0%      Conservative:  0
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Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-102 (1-187) x US-09-917-265A-43 (1-1533)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1032

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1092

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1093 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1152

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1153 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1212

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1213 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1272

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1273 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1332

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1333 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1392

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1393 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1452

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1453 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1512

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db       1513 ATGAGCTATCTGAATGCTTCC 1533

RESULT 8
US-09-917-265A-45/c
; Sequence 45, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-45

Alignment Scores:
Pred. No.:              5.46e-116       Length:         1533
Score:                  944.00          Matches:        187
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-102 (1-187) x US-09-917-265A-45 (1-1533)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1

RESULT 9
US-09-917-265A-38
; Sequence 38, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-09-917-265A-38

Alignment Scores:
Pred. No.:              5.83e-116       Length:         1599
Score:                  944.00          Matches:        187
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Percent Similarity:     100.0%          Conservative:  0
Best Local Similarity:  100.0%          Mismatches:    0
Query Match:            100.0%          Indels:        0
DB:                     3               Gaps:          0

US-10-821-670A-102 (1-187) x US-09-917-265A-38 (1-1599)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1098

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1158

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1218

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1219 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1278

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1338

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1398

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1458

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1459 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1518

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1519 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1578

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db       1579 ATGAGCTATCTGAATGCTTCC 1599

RESULT 10
US-09-917-265A-40/c
; Sequence 40, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-40

Alignment Scores:
Pred. No.:              5.83e-116       Length:        1599
Score:                  944.00          Matches:       187
Percent Similarity:     100.0%          Conservative:  0
Best Local Similarity:  100.0%          Mismatches:    0
Query Match:            100.0%          Indels:        0
DB:                     3               Gaps:          0

US-10-821-670A-102 (1-187) x US-09-917-265A-40 (1-1599)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1

RESULT 11
US-09-011-143-9
; Sequence 9, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
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;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  591 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-9

Alignment Scores:
Pred. No.:              3.12e-116      Length:         591
Score:                  941.00         Matches:        186
Percent Similarity:     100.0%         Conservative:   1
Best Local Similarity:  99.5%          Mismatches:     0
Query Match:            99.7%          Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-102 (1-187) x US-09-011-143-9 (1-591)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 90

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 210

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 390

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 450

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 510

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 570

Qy        181 MetSerTyrLeuAsnAlaSer 187
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Db        571 ATGAGCTACCTGAATTCTTCC 591
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```
RESULT 12
US-09-302-495-9
; Sequence 9, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 591 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-302-495-9

Alignment Scores:
Pred. No.:              3.12e-116      Length:         591
Score:                  941.00         Matches:        186
Percent Similarity:     100.0%         Conservative:   1
Best Local Similarity:  99.5%          Mismatches:     0
Query Match:            99.7%          Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-102 (1-187) x US-09-302-495-9 (1-591)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 90

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 210
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Qy          61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

Qy          81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

Qy         101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         331 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 390

Qy         121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         391 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 450

Qy         141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         451 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 510

Qy         161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         511 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 570

Qy         181 MetSerTyrLeuAsnAlaSer 187
               ||||||||||||||:::|||
Db         571 ATGAGCTACCTGAATTCTTCC 591

RESULT 13
US-10-079-616-9
; Sequence 9, Application US/10079616
; Patent No. 6566097
;  GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;  INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 591 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-079-616-9

Alignment Scores:
Pred. No.:              3.12e-116      Length:          591
Score:                  941.00         Matches:         186
Percent Similarity:     100.0%         Conservative:    1
Best Local Similarity:  99.5%          Mismatches:      0
Query Match:            99.7%          Indels:          0
DB:                     3              Gaps:            0

US-10-821-670A-102 (1-187) x US-10-079-616-9 (1-591)

Qy           1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          31 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 90

Qy          21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150

Qy          41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 210

Qy          61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

Qy          81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

Qy         101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         331 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 390

Qy         121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         391 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 450

Qy         141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         451 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 510

Qy         161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         511 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 570

Qy         181 MetSerTyrLeuAsnAlaSer 187
               ||||||||||||||:::|||
Db         571 ATGAGCTACCTGAATTCTTCC 591

RESULT 14
US-09-011-143-26
; Sequence 26, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
```

```
;       CITY:  Washington
;       STATE:  D.C.
;       COUNTRY:  USA
;       ZIP:  20004
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/011,143
;       FILING DATE:  04-FEB-1998
;       CLASSIFICATION:  536
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/JP97/01824
;       FILING DATE:  29-MAY-1997
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 165249/1996
;       FILING DATE:  04-JUN-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  BROWDY, Roger L.
;       REGISTRATION NUMBER:  25,618
;       REFERENCE/DOCKET NUMBER:  IMAMURA=1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-628-5197
;       TELEFAX:  202-737-3528
;   INFORMATION FOR SEQ ID NO:  26:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  689 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-09-011-143-26

Alignment Scores:
Pred. No.:              3.96e-116      Length:         689
Score:                  941.00         Matches:        186
Percent Similarity:     100.0%         Conservative:   1
Best Local Similarity:  99.5%          Mismatches:     0
Query Match:            99.7%          Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-102 (1-187) x US-09-011-143-26 (1-689)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 171

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 231

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATG 291

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 351

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 411

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAG 471

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 531

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 591

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
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Db        592 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 651

Qy        181 MetSerTyrLeuAsnAlaSer 187
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Db        652 ATGAGCTACCTGAATTCTTCC 672

RESULT 15
US-09-302-495-26
; Sequence 26, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/302,495
;            FILING DATE: 30-Apr-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 26:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 689 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-302-495-26

Alignment Scores:
Pred. No.:              3.96e-116      Length:         689
Score:                  941.00         Matches:        186
Percent Similarity:     100.0%         Conservative:   1
Best Local Similarity:  99.5%          Mismatches:     0
Query Match:            99.7%          Indels:         0
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Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
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Db        592 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 651

Qy        181 MetSerTyrLeuAsnAlaSer 187
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Db        652 ATGAGCTACCTGAATTCTTCC 672
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Job time : 100.576 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

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Run on: June 10, 2006, 01:18:38 ; Search time 731.689 Seconds
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Perfect score: 944
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 2	944	100.0	561	3	US-09-917-265-103	Sequence 103, App
3	944	100.0	561	9	US-10-821-670-101	Sequence 101, App
c 4	944	100.0	561	9	US-10-821-670-103	Sequence 103, App
5	944	100.0	591	3	US-09-917-265-35	Sequence 35, Appl
c 6	944	100.0	591	3	US-09-917-265-37	Sequence 37, Appl
7	944	100.0	591	9	US-10-821-670-35	Sequence 35, Appl
c 8	944	100.0	591	9	US-10-821-670-37	Sequence 37, Appl
9	944	100.0	666	3	US-09-917-265-32	Sequence 32, Appl
c 10	944	100.0	666	3	US-09-917-265-34	Sequence 34, Appl
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c 12	944	100.0	666	9	US-10-821-670-34	Sequence 34, Appl
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c 14	944	100.0	1533	3	US-09-917-265-45	Sequence 45, Appl
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c 16	944	100.0	1533	9	US-10-821-670-45	Sequence 45, Appl
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c 18	944	100.0	1599	3	US-09-917-265-40	Sequence 40, Appl
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22	941	99.7	689	6	US-10-079-616-26	Sequence 26, Appl
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24	923	97.8	669	7	US-10-041-672C-2	Sequence 2, Appli
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c 26	903	95.7	1533	3	US-09-917-265-68	Sequence 68, Appl
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c 28	903	95.7	1533	9	US-10-821-670-68	Sequence 68, Appl
29	903	95.7	1599	3	US-09-917-265-61	Sequence 61, Appl
c 30	903	95.7	1599	3	US-09-917-265-63	Sequence 63, Appl
31	903	95.7	1599	9	US-10-821-670-61	Sequence 61, Appl
c 32	903	95.7	1599	9	US-10-821-670-63	Sequence 63, Appl
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c 34	889	94.2	591	3	US-09-917-265-51	Sequence 51, Appl
35	889	94.2	591	9	US-10-821-670-49	Sequence 49, Appl
c 36	889	94.2	591	9	US-10-821-670-51	Sequence 51, Appl
37	889	94.2	666	3	US-09-917-265-46	Sequence 46, Appl
c 38	889	94.2	666	3	US-09-917-265-48	Sequence 48, Appl
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c 40	889	94.2	666	9	US-10-821-670-48	Sequence 48, Appl
41	889	94.2	1455	3	US-09-917-265-104	Sequence 104, App
c 42	889	94.2	1455	3	US-09-917-265-106	Sequence 106, App
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c 44	889	94.2	1455	9	US-10-821-670-106	Sequence 106, App
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ALIGNMENTS

RESULT 1
US-09-917-265-101
; Sequence 101, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(561)
; OTHER INFORMATION:
US-09-917-265-101

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Alignment Scores:
Pred. No.:              1.24e-116       Length:         561
Score:                  944.00          Matches:        187
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
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US-10-821-670A-102 (1-187) x US-09-917-265-101 (1-561)

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Db          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
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Db         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
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Db        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
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Db        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
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Db        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
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Qy        181 MetSerTyrLeuAsnAlaSer 187
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Db        541 ATGAGCTATCTGAATGCTTCC 561

RESULT 2
US-09-917-265-103/c
; Sequence 103, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 103
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-103

Alignment Scores:
Pred. No.:              1.24e-116       Length:         561
Score:                  944.00          Matches:        187
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-102 (1-187) x US-09-917-265-103 (1-561)

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Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
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Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
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RESULT 3
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; Sequence 101, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 101
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(561)
US-10-821-670-101
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Pred. No.:                1.24e-116      Length:          561
Score:                    944.00         Matches:         187
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
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US-10-821-670A-102 (1-187) x US-10-821-670-101 (1-561)

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Db          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db        541 ATGAGCTATCTGAATGCTTCC 561

RESULT 4
US-10-821-670-103/c
; Sequence 103, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 103
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-103

Alignment Scores:
Pred. No.:                1.24e-116      Length:          561
Score:                    944.00         Matches:         187
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       9              Gaps:            0

US-10-821-670A-102 (1-187) x US-10-821-670-103 (1-561)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1

RESULT 5
US-09-917-265-35
; Sequence 35, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(591)
;   OTHER INFORMATION:
US-09-917-265-35
```

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Alignment Scores:
Pred. No.:              1.35e-116       Length:         591
Score:                  944.00          Matches:        187
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-102 (1-187) x US-09-917-265-35 (1-591)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 90

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 210

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 390

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 450

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 510

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 570

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||
Db        571 ATGAGCTATCTGAATGCTTCC 591

RESULT 6
US-09-917-265-37/c
; Sequence 37, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-37

Alignment Scores:
Pred. No.:              1.35e-116       Length:         591
Score:                  944.00          Matches:        187
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-102 (1-187) x US-09-917-265-37 (1-591)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1

RESULT 7
US-10-821-670-35
; Sequence 35, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(591)
US-10-821-670-35
```

```
Alignment Scores:
Pred. No.:                1.35e-116      Length:          591
Score:                    944.00         Matches:         187
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       9              Gaps:            0

US-10-821-670A-102 (1-187) x US-10-821-670-35 (1-591)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 90

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 210

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 390

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 450

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 510

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 570

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db        571 ATGAGCTATCTGAATGCTTCC 591

RESULT 8
US-10-821-670-37/c
; Sequence 37, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-37

Alignment Scores:
Pred. No.:                1.35e-116      Length:          591
Score:                    944.00         Matches:         187
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       9              Gaps:            0

US-10-821-670A-102 (1-187) x US-10-821-670-37 (1-591)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1

RESULT 9
US-09-917-265-32
; Sequence 32, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
;   OTHER INFORMATION:
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US-09-917-265-32

Alignment Scores:

Pred. No.:	1.64e-116	Length:	666
Score:	944.00	Matches:	187
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-102 (1-187) x US-09-917-265-32 (1-666)

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Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
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Db        106 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 165

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 225

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 285

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 345

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 405

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 465

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 525

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 585

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 645

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db        646 ATGAGCTATCTGAATGCTTCC 666
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RESULT 10
US-09-917-265-34/c
; Sequence 34, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265-34

Alignment Scores:

Pred. No.:	1.64e-116	Length:	666
Score:	944.00	Matches:	187
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-102 (1-187) x US-09-917-265-34 (1-666)

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Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
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Db        561 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1
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RESULT 11
US-10-821-670-32
; Sequence 32, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(666)

US-10-821-670-32

Alignment Scores:

Pred. No.:	1.64e-116	Length:	666
Score:	944.00	Matches:	187
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	9	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-821-670-32 (1-666)

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Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 165

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 225

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 285

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 345

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 405

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 465

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 525

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 585

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 645

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||||
Db        646 ATGAGCTATCTGAATGCTTCC 666
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RESULT 12
US-10-821-670-34/c
; Sequence 34, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Felis catus
US-10-821-670-34

Alignment Scores:

Pred. No.:	1.64e-116	Length:	666
Score:	944.00	Matches:	187
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	9	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-821-670-34 (1-666)

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Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
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Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
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Db         21 ATGAGCTATCTGAATGCTTCC 1
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RESULT 13
US-09-917-265-43
; Sequence 43, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)

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;   OTHER INFORMATION:
US-09-917-265-43

Alignment Scores:
Pred. No.:              6.45e-116       Length:         1533
Score:                  944.00          Matches:        187
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-102 (1-187) x US-09-917-265-43 (1-1533)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1032

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1092

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1093 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1152

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1153 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1212

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1213 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1272

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1273 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1332

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1333 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1392

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1393 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1452

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1453 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1512

Qy        181 MetSerTyrLeuAsnAlaSer 187
              |||||||||||||||||||
Db       1513 ATGAGCTATCTGAATGCTTCC 1533

RESULT 14
US-09-917-265-45/c
; Sequence 45, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-45

Alignment Scores:
Pred. No.:              6.45e-116       Length:         1533
Score:                  944.00          Matches:        187
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-102 (1-187) x US-09-917-265-45 (1-1533)

Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        181 MetSerTyrLeuAsnAlaSer 187
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Db         21 ATGAGCTATCTGAATGCTTCC 1

RESULT 15
US-10-821-670-43
; Sequence 43, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
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; LOCATION: (1)..(1533)
US-10-821-670-43

Alignment Scores:

Pred. No.:	6.45e-116	Length:	1533
Score:	944.00	Matches:	187
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	9	Gaps:	0

US-10-821-670A-102 (1-187) x US-10-821-670-43 (1-1533)

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Qy          1 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1032

Qy         21 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1092

Qy         41 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1093 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1152

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1153 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1212

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1213 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1272

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1273 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1332

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1333 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1392

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1393 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1452

Qy        161 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1453 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1512

Qy        181 MetSerTyrLeuAsnAlaSer 187
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Db       1513 ATGAGCTATCTGAATGCTTCC 1533
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Search completed: June 10, 2006, 04:34:07
Job time : 735.689 secs

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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 10, 2006, 01:18:36 ; Search time 9.72915 Seconds
(without alignments)
3659.318 Million cell updates/sec

Title: US-10-821-670A-102
Perfect score: 944
Sequence: 1 GMFQCLNHSQTLLRAISNTL.....HAFRIRAVTINRMMSYLNAS 187

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 253354 seqs, 63461778 residues

Total number of hits satisfying chosen parameters: 506708

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss05h
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-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	90	9.5	2480	6	US-10-953-349-35629	Sequence 35629, A
	2	88.5	9.4	2366	7	US-11-293-697-1960	Sequence 1960, Ap
	3	84	8.9	990	7	US-11-217-529-79916	Sequence 79916, A
c	4	83	8.8	1647	6	US-10-953-349-3750	Sequence 3750, Ap
	5	82	8.7	2406	7	US-11-217-529-76395	Sequence 76395, A
c	6	80	8.5	1798	6	US-10-953-349-5587	Sequence 5587, Ap
	7	80	8.5	1875	7	US-11-217-529-174200	Sequence 174200,
	8	79	8.4	762	7	US-11-217-529-166587	Sequence 166587,
	9	79	8.4	2244	7	US-11-217-529-78602	Sequence 78602, A
	10	79	8.4	3405	7	US-11-217-529-77844	Sequence 77844, A
	11	79	8.4	6429	7	US-11-217-529-4027	Sequence 4027, Ap
	12	77.5	8.2	1374	6	US-10-953-349-13043	Sequence 13043, A
	13	77	8.2	1473	7	US-11-217-529-81075	Sequence 81075, A
c	14	77	8.2	1542	7	US-11-217-529-4965	Sequence 4965, Ap
	15	76.5	8.1	1836	7	US-11-217-529-2301	Sequence 2301, Ap
	16	76.5	8.1	2583	7	US-11-217-529-5733	Sequence 5733, Ap
	17	76	8.1	28605	6	US-10-471-571A-4495	Sequence 4495, Ap
	18	75.5	8.0	1567	6	US-10-953-349-2350	Sequence 2350, Ap
	19	75.5	8.0	1902	7	US-11-217-529-78885	Sequence 78885, A
	20	75.5	8.0	2733	7	US-11-217-529-76578	Sequence 76578, A
	21	75	7.9	2619	7	US-11-217-529-78771	Sequence 78771, A
	22	74.5	7.9	1155	6	US-10-953-349-6668	Sequence 6668, Ap
	23	74.5	7.9	1448	6	US-10-953-349-28874	Sequence 28874, A
	24	74.5	7.9	2463	7	US-11-217-529-79273	Sequence 79273, A
	25	74.5	7.9	2667	7	US-11-217-529-81052	Sequence 81052, A
c	26	74	7.8	1380	7	US-11-302-262-17	Sequence 17, Appl
	27	74	7.8	3093	7	US-11-217-529-1218	Sequence 1218, Ap
	28	73.5	7.8	951	7	US-11-217-529-3315	Sequence 3315, Ap
	29	73.5	7.8	1433	6	US-10-953-349-19986	Sequence 19986, A
	30	73.5	7.8	9588	6	US-10-505-928-101	Sequence 101, App
	31	73	7.7	1905	7	US-11-217-529-81904	Sequence 81904, A
	32	73	7.7	3369	7	US-11-217-529-76775	Sequence 76775, A
	33	72.5	7.7	903	7	US-11-217-529-3808	Sequence 3808, Ap
c	34	72.5	7.7	1315	6	US-10-953-349-20338	Sequence 20338, A
	35	72.5	7.7	3015	7	US-11-217-529-76510	Sequence 76510, A
	36	72.5	7.7	3189	7	US-11-293-697-748	Sequence 748, App
	37	72.5	7.7	4015	7	US-11-293-697-627	Sequence 627, App
	38	72.5	7.7	5787	7	US-11-217-529-76923	Sequence 76923, A
	39	72.5	7.7	10211	6	US-10-505-928-326	Sequence 326, App
	40	72	7.6	2305	6	US-10-953-349-4010	Sequence 4010, Ap
	41	72	7.6	2508	7	US-11-145-307A-5	Sequence 5, Appli
	42	72	7.6	3486	7	US-11-217-529-191019	Sequence 191019,
c	43	72	7.6	8019	7	US-11-217-529-76544	Sequence 76544, A
	44	71.5	7.6	1751	7	US-11-293-697-1794	Sequence 1794, Ap
	45	71.5	7.6	3207	7	US-11-217-529-1062	Sequence 1062, Ap

ALIGNMENTS

RESULT 1
US-10-953-349-35629
; Sequence 35629, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35629
; LENGTH: 2480
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (601)..(601)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (603)..(603)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (621)..(621)
; OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-35629

Alignment Scores:
Pred. No.: 0.132 Length: 2480

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Score:                 90.00          Matches:       38
Percent Similarity:    43.3%          Conservative:  33
Best Local Similarity: 23.2%          Mismatches:    60
Query Match:           9.5%           Indels:        34
DB:                    6              Gaps:          6

US-10-821-670A-102 (1-187) x US-10-953-349-35629 (1-2480)

Qy         30 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 49
Db       1328 TATCTTTGCTTGACCAAGGAAGCAACGCACAACAATCTATTGTTGCACTTGAGCAGGAAA 1387

Qy         50 ValGluAlaCysLeuProLeu----------------------------GluLeuThrMet 60
Db       1388 TTGCACTCCTCAGTCAGTTTGAACATGAAAATATAGTCCAGTATTATGGAACTGACAAG- 1446

Qy         61 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 80
Db       1447 GAAGAATCCAAACTCTATATT---TTTATTGAGCTTGTCACGCAAGGATCT--------- 1494

Qy         81 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 100
Db       1495 ------------------------------CTTTCATCCCTCTACCAAAAGTATAAA 1521

Qy        101 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 120
Db       1522 CTACGAGAATCACAAGTCTCTGCATACACAAGGCAGATTCTT---------AACGGATTG 1572

Qy        121 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 140
Db       1573 GTTTACCTGCATGAGAGAAATGTGGTCCACAGAGAT--------------ATCAAGTGT 1617

Qy        141 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 160
Db       1618 GCCAATATATTGGTGCATGCAAATGGATCTGTAAAGCTTGCAGATTTTGGATTGGCAAAG 1677

Qy        161 ---IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArg 179
Db       1678 GAGGTTACCCTTTGTCTTTCTGTTCATTATTTCCATGTTCGCAGTGTCAAATTGTCTTAT 1737

Qy        180 MetMetSerTyr 183
Db       1738 GGTTGTAGTTTT 1749

RESULT 2
US-11-293-697-1960
; Sequence 1960, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1960
;   LENGTH: 2366
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1960

Alignment Scores:
Pred. No.:             0.189          Length:        2366
Score:                 88.50          Matches:       44
Percent Similarity:    38.5%          Conservative:  25
Best Local Similarity: 24.6%          Mismatches:    75
Query Match:           9.4%           Indels:        35
DB:                    7              Gaps:          8

US-10-821-670A-102 (1-187) x US-11-293-697-1960 (1-2366)

Qy         12 LeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSer 31
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Qy         32 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 51
Db       1003 GCATGT--------------CATAGAGATTTACTAGAAGAT---------GCAAAAGAT 1038

Qy         52 AlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSer 71
Db       1039 GATGCATTGCCAGCTGAGTTATTGGAAGCCCTGAACACATTGTCAGAAGCCAAGGTGGAA 1098

Qy         72 LeuIleThrAsn------------GlySerCysLeuAlaSerArgLysThrSerPheMet 87
Db       1099 ACCATCTGTCACAGAAAAGAGGGAGGTAGCAGTCTCATTGCCAGAAATGAATGTTTAGAA 1158

Qy         88 ThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLys 107
Db       1159 GTGGAGTTCAATACGTCTCAGACCAATGAAGATTGTACACAAATA--------------- 1203

Qy        108 AlaMetAsnAlaLysLeuLeuMetAspProLys---------ArgGlnIlePheLeuAsp 124
Db       1204 ---------GCAGAGACTCTGCAAGACCCAAATCCATCTGGATTGCAAACTTTGGCTCAT 1254

Qy        125 GlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThr 144
Db       1255 CAAAAT---ATCACTTCTTGTGAGCCACTAAGTAATAAGAGAAATTCAAATTCAGTGACA 1311

Qy        145 ValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCys 164
Db       1312 ---------AATAGCTCTGATCAGGAA----------------------ACTGCGTGT 1338

Qy        165 IleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyr 183
Db       1339 GTGTTGAGGAGATCATCCAGACTAGAAAAACTGAAAGTAAGCAGAGATGCAAAGTAC 1395

RESULT 3
US-11-217-529-79916
; Sequence 79916, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79916
;   LENGTH: 990
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-79916

Alignment Scores:
Pred. No.:             0.191          Length:        990
Score:                 84.00          Matches:       46
Percent Similarity:    41.1%          Conservative:  32
Best Local Similarity: 24.2%          Mismatches:    68
Query Match:           8.9%           Indels:        44
DB:                    7              Gaps:          8

US-10-821-670A-102 (1-187) x US-11-217-529-79916 (1-990)

Qy          7 AsnHisSerGlnThrLeuLeuArgAlaIleSer------AsnThrLeuGlnLysAlaArg 24
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Db         40 AATACCTCTGAATCGTTATTAGTTGATATTCAAGAATACAATCAAATTCAAAAACAAATT 99

Qy         25 GlnThrLeuGluPhe---TyrSerCysThrSerGluGluIleAspHisGluAspIleThr 43
Db        100 GAGACCATTCAGGCTGATCTCAACCATGTAACGGAAGAGCTACAGACGCAATATGCTACA 159

Qy         44 LysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu--------------- 58
Db        160 TCGCAAAAAACAAAGACCATTCAAAGTGATTTAAATCTCTCGTTGCATAAATTGGATTTG 219

Qy         59 ---------------------ThrMetAsnGluSerCysLeuAlaSerArgGluIleSer 71
Db        220 GCTAAGCGTAATCTCGACGCGAATCCATCTTCCCAAATAATTGCGAGGAATGAAGAAATT 279

Qy         72 LeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThr---ThrLeu 90
Db        280 TTGAGGGACATTGGAGAATGTGAGAATGAAATCAAAACCAAGCAAATGAGCTTAAAGAAA 339

Qy         91 Cys---------LeuSerSerIleTyrGluAspLeuLysMetTyr--------------- 102
Db        340 TGTCAAGAAGAAGTTTCGACCATTGAAAAAGACATGAAGGAGTACGATAGCGATAAAGGA 399

Qy        103 ------------------GlnValGluPheLysAlaMetAsnAlaLysLeu--------- 113
Db        400 TCCAAGTTAAATGAATTAAAGAAGGAATTGAAACTATTGGCGAAAGAGCTGGAGGAGCAG 459

Qy        114 LeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGlu 133
Db        460 GAATCGGAGTCAGAACGTAAATATGACTTGTTTCAAAACTTGGAATTAGAAACAGAGCAA 519

Qy        134 LeuLeuGlnAlaLeuAsnValAsnSerValThrValPro--------------------- 146
Db        520 TTGAGCTCAGAACTAGATTCTAATAAGACGCTATTGCAAAACCATTTGAAATCTATTGAA 579

Qy        147 ------------GlnAsnSerSerLeuGlu 152
Db        580 AGTTTGAAATTGGAAAATTCTGATTTGGAG 609
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RESULT 4
US-10-953-349-3750/c
; Sequence 3750, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3750
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-3750

Alignment Scores:

Pred. No.:	0.533	Length:	1647
Score:	83.00	Matches:	31
Percent Similarity:	44.8%	Conservative:	12
Best Local Similarity:	32.3%	Mismatches:	31
Query Match:	8.8%	Indels:	22
DB:	6	Gaps:	5

US-10-821-670A-102 (1-187) x US-10-953-349-3750 (1-1647)

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Qy         32 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 51
Db       1098 TGCCTCCTTAGTGAATGTTTTTGGGAAGATATCCTTAAGGAT------------ATTGAG 1051

Qy         52 AlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu------ 69
Db       1050 GCTACTGTCCCATCTTGGCTGAGTCAGATAGATAGTTGTGTCGCTGGCAAATCCAAGCTT 991

Qy         70 ---------------------IleSerLeuIleThrAsnGlySerCysLeuAlaSerArg 82
Db        990 TCTCAAGAATAAAGCAATCTCTTGAGCGTTGTAACA---------TGTCTTGGACCCTAC 940

Qy         83 LysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyr 102
Db        939 TACACCAGTTGTATGGCAATTTTTCTTCTCAAG------TATGTCGATTCTAAGGTCTAC 886

Qy        103 GlnValGlu------------PheLysAlaMetAsnAlaLysLeuLeu 114
Db        885 TGCTATGAAACGGCCACCGGATTTACGGCTATGAGTCCTCAACCGCTC 838
```

RESULT 5
US-11-217-529-76395
; Sequence 76395, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76395
; LENGTH: 2406
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76395

Alignment Scores:

Pred. No.:	1.23	Length:	2406
Score:	82.00	Matches:	36
Percent Similarity:	42.1%	Conservative:	25
Best Local Similarity:	24.8%	Mismatches:	48
Query Match:	8.7%	Indels:	36
DB:	7	Gaps:	6

US-10-821-670A-102 (1-187) x US-11-217-529-76395 (1-2406)

```
Qy         36 GluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuPro 55
Db        277 AAGATAGACGAGTATAAAGTTGTTCTGGATCAAACACGCCAGGTTAATGAT--------- 327

Qy         56 LeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsn 75
Db        328 ---------CAATTGGATAGTTCCATCAAGAAATTTCGGAAAATCTCTCAGGATACT--- 375

Qy         76 GlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIle 95
Db        376 GGAGCTTTCATTGAGGAAACGAAGACGATCTATGAAAAGCAGTCTAAATTAAGCAATCTA 435

Qy         96 TyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMet 115
Db        436 ACTGAGTCAATCCCT-----------------AAAGCTCTCCATTATTTTGAAGTTTTG 477

Qy        116 AspPro----------------------------------------LysArgGlnIle 121
Db        478 GACCCTATAATGCGTCGCTTGAACCATGCCACTTCTCCCGCTATTGTCAAGAAGAGCTCC 537

Qy        122 PheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsn 141
Db        538 TTT------ACGACGATGTTGGCGACTATCGACGAGTCTTTACGTTTTTTGGAT------ 585
```

```
Qy        142 SerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIle 161
                          :::||||||   |||::::::         |||:::   |||
Db        586 --------------GAGAATAGTGACCTCAAGGATGCAGCAGCGTACAGAATCAAGTTC 630

Qy        162 LysLeuCysIleLeu 166
              |||   |||::::::
Db        631 AAGCAATGCTTGATC 645

RESULT 6
US-10-953-349-5587/c
; Sequence 5587, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5587
;   LENGTH: 1798
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-5587

Alignment Scores:
Pred. No.:              1.42          Length:        1798
Score:                  80.00         Matches:       34
Percent Similarity:     42.0%         Conservative:  26
Best Local Similarity:  23.8%         Mismatches:    57
Query Match:            8.5%          Indels:        26
DB:                     6             Gaps:          5

US-10-821-670A-102 (1-187) x US-10-953-349-5587 (1-1798)

Qy         48 SerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAla--- 66
              |||:::         ||||||||||||   :::                   |||:::
Db       1271 TCCTCTGCTGCCTTTTGCCTACCACTCTCAGTTTTGTTCCGCGCCTGCGAGCTGAGTCTG 1212

Qy         67 -----------------------------------------SerArgGluIleSerLeu 72
                                                       :::|||   ||||||
Db       1211 TATCGTCCTACTAAGTCGATGTAATATGGAATTAGCGCCACCAACCGGACAATATCATCC 1152

Qy         73 IleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThr------Leu 90
              |||           ||||||||||||   |||  :::      :::           |||
Db       1151 ATA-----------TGTTTAGCATCAGGTAAAGAAAACTTGAAAAGCATCATCTTCTTG 1104

Qy         91 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 110
              ||||||         :::   |||:::   :::             |||       ::::::
Db       1103 TGCTTGCCAGGGTGTTGGTCAGATATATGCATCGACATGAAATTCTTCCCATACTTATCC 1044

Qy        111 AlaLysLeuLeuMetAspProLys---------ArgGlnIlePheLeuAspGlnAsnMet 127
                 |||         ||||||          |||   :::   :::   ::::::
Db       1043 ACAGCCTTG------TCACCAAAAACCTGATCAAGAACAGTGTCAGTGATCAAATCCGCA 990

Qy        128 LeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGln 147
              |||::::::|||     ::::::|||   :::   ::::::       ::|||
Db        989 GCAACTTCCTTGGATTCAGAGATCAAGGCGAACTCCTCCGACACCCATTTCCTTCCAGCA 930

Qy        148 AsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeu 167
                          :::      |||:::   |||      ||||||:::
Db        929 GGAGGAGACACAATCCCAGCAAATCTTTGCAAATCCCTCATCTCCTTTTGCATAGTTTTT 870

Qy        168 HisAlaPhe 170
              ||||||
Db        869 GCAGCCTTC 861

RESULT 7
US-11-217-529-174200
; Sequence 174200, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174200
;   LENGTH: 1875
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-174200

Alignment Scores:
Pred. No.:              1.51          Length:        1875
Score:                  80.00         Matches:       38
Percent Similarity:     39.9%         Conservative:  31
Best Local Similarity:  22.0%         Mismatches:    57
Query Match:            8.5%          Indels:        47
DB:                     7             Gaps:          8

US-10-821-670A-102 (1-187) x US-11-217-529-174200 (1-1875)

Qy          8 HisSerGlnThrLeuLeuArgAlaIle---------SerAsnThrLeuGlnLysAlaArg 24
              ||||||      |||:::::::::|||         :::|||::::::   :::
Db        223 CACTCAGATTTTTTGGTTAAAAGCATCCAAGATCTTACGAATTCGATGTTACAATTTAGT 282

Qy         25 GlnThrLeuGluPheTyrSerCysThrSerGlu---GluIleAspHisGluAspIleThr 43
                    |||      |||:::         |||   :::|||         |||   :::
Db        283 GATCCATTGACCACATATAATAGGTACAAAGAAGATGACATTAGCTCTTCAGACAGTAGT 342

Qy         44 LysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSer 63
                 |||      |||   :::||||||      |||
Db        343 AGTGATCTCAACTCTAATATAGAAGCTTCAAAACCA---------------------- 378

Qy         64 CysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLys 83
                                              |||||||||
Db        379 --------------------------GCCGCAAATGGTTCTTATACTCTTCAAAATATG 411

Qy         84 ThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGln 103
                 :::            :::   |||:::   :::                    :::
Db        412 CGGAACAAGGCCCTTAATGTAGCCTTAGCGAAATTG--------------------AAA 450

Qy        104 ValGluPheLysAlaMetAsnAlaLysLeuLeuMet---------AspProLysArg--- 119
                 :::      |||   :::      :::|||::::::         ||||||
Db        451 ATAGCATTAAAGGACGTTACCATACGTTTAATAGTAAATGATAGAGATCCTTCCGATAAC 510

Qy        120 ------GlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAla 137
                    ::::::   |||:::         |||       |||      |||:::
Db        511 ATCGTGGAGGTTCATCTAGAAAGCATACAACTTATTACTACAGACGCAAATTTACGACAT 570

Qy        138 LeuAsnValAsnSerValThrVal-ProGlnAsnSerSerLeuGluGluProAspPheTy 157
                 :::|||:::   ::::::|||::: ||||||                       ||
Db        571 ATAAACATTGAAAATATCACCATTTCCTCAA--------------------------TA 603

Qy        157 rLysThrLysIle---------LysLeuCysIleLeu 166
              ||||   |||:::         ||||||||||||
Db        604 CAAAAACAAGCTGTACCCGACTCTCCTGTGCATCCTT 640

RESULT 8
US-11-217-529-166587
; Sequence 166587, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 166587
;   LENGTH: 762
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-166587

Alignment Scores:
Pred. No.:              0.54          Length:          762
Score:                  79.00         Matches:         46
Percent Similarity:     36.6%         Conservative:    18
Best Local Similarity:  26.3%         Mismatches:      66
Query Match:            8.4%          Indels:          45
DB:                     7             Gaps:            7

US-10-821-670A-102 (1-187) x US-11-217-529-166587 (1-762)

Qy         13 LeuArgAla---IleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSer 31
              |||||||||   |||||||||   :::   :::|||:::     |||         |||
Db         48 TTACGTGCTACCATTTCTAATCGGATTAGTGAAGCACAAGGACGTTTGCGC------TCT 101

Qy         32 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 51
              |||   |||                                          :::
Db        102 TGCCGGTCTGGACCCTAT------------------------------CCGATTATA 128

Qy         52 AlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSer 71
                    |||   |||              :::||||||     :::|||   |||
Db        129 CGCTGGCTTGGGCTACATGCCAATCAGAAAAAATCATGTTGCCAGAATCGTCGAATATGT 188

Qy         72 LeuIleThrAsnGlySerCysLeuAla---------SerArgLysThrSerPheMetThr 88
              |||             |||   :::                     |||||||||
Db        189 CTGTTCTTCGGATGTAGTTCTATCGTCGAACCAAACCAAACTGCAACTAGCTTTTATCCA 248

Qy         89 ThrLeu------------------------------------------------------ 90
              ||||||
Db        249 ACACTTCCTGTCAGCAGAATTACTTCAACTAACTGAAGAAGAAAAAAATAAAATCTTGGA 308

Qy         91 ---Cys-LeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMe 109
                 ||| :::|||:::::::|||   :::           ||||||   :::
Db        309 ATTTGTTGTGAGCAACCTGTATAACGAA---------CAATTTGTGGAAGTAAGAGTGCG 359

Qy        109 tAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuTh 129
               |||   :::|||   |||                  ||||||   :::|||
Db        360 TGCTGCAGCCATACTGTCTGATATCGTTCACAACTGGAAGGAAGACCAAGCATTGTTGGA 419

Qy        129 rAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSe 149
               ||||||         :::   |||:::   |||       |||
Db        420 CCTGATCGACAGGTTTGCAAAGGGGCTTGACGCCAACAAATACACT-------------- 465

Qy        149 rSerLeuGluGluProAspPheTyrLysThrLysIleLysLeu 163
               |||   |||:::           ||||||   ||||||:::
Db        466 -TCGAAGGAAAAGCAAAAGTTATCAAAGACAGATATCAAAATC 507

RESULT 9
US-11-217-529-78602
; Sequence 78602, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78602
;   LENGTH: 2244
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-78602

Alignment Scores:
Pred. No.:              2.6           Length:          2244
Score:                  79.00         Matches:         48
Percent Similarity:     40.1%         Conservative:    31
Best Local Similarity:  24.4%         Mismatches:      74
Query Match:            8.4%          Indels:          44
DB:                     7             Gaps:            9

US-10-821-670A-102 (1-187) x US-11-217-529-78602 (1-2244)

Qy          8 HisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeu 27
              ||||||   :::|||         :::|||      |||:::|||:::         |||
Db        220 CATAGTGTTTCATTGAGTTTAAAGTTGTCT---GCCTTGAAGAAGTCAAATAGTGATTTG 276

Qy         28 GluPheTyr------SerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 45
              |||           |||  |||  |||     ::::::|||      ||||||
Db        277 GAGAAACAAGGAAAATCAGTGACATTAGAAAGCAAAGAAAACGAACTCCCTACCAAAAGG 336

Qy         46 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 65
              |||:::                        :::|||   :::   ||||||
Db        337 AAATCGCCTGATGAT-----------------AAACTCAACTTAGAAGAGTCATGGAAG 378

Qy         66 AlaSerArgGluIleSer---------LeuIleThrAsnGlySerCys------------ 78
              |||   :::||||||:::           :::   |||      |||
Db        379 GCTATTAAAGAAATAAACCATTACTGTTTCTTGAAAAACGATCCATGCATAAATCAAACC 438

Qy         79 --------------------------LeuAlaSerArgLysThrSerPheMetThrThr 89
                                        :::   :::|||   |||      |||:::
Db        439 GACGATTTTGCGTTCACAAACTTTATCATAAAAGATAAAAAAAACTCGTTGAGTACATCA 498

Qy         90 LeuCysLeuSer---------SerIleTyrGluAspLeuLysMetTyrGlnValGluPhe 106
              :::   ||||||         |||  :::      ||||||  :::      |||
Db        499 ATACCGCTATCGTCGCAGAATTCATCATTTCCGCCCTTAAAAAAGCATAACAATGAGCTC 558

Qy        107 LysAlaMet--------------------------AsnAlaLysLeuLeuMetAsp--- 116
                 :::                                 |||:::   ::::::
Db        559 CTTGGTATTTTTGTGCCTTGTAACCTGCCGAAAACAACTCGTAAAGTAGCCATTGAGAAT 618

Qy        117 ---------ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGlu 133
                      |||           :::           |||   |||   :::|||
Db        619 TTCAATAGACCAAGTCCTGATGATATAATACAATCGGCCCAACTTAATGCTTTCAATGAA 678

Qy        134 LeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGlu 153
                 |||:::   ||||||:::   ||||||              :::      :::|||
Db        679 AAATTAGAAAACTTAAATATCAAATCTGTG---------CCCAAGGCCGAAAAAAAGGAA 729

Qy        154 ProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 170
              |||         :::|||               |||   :::|||:::|||
Db        730 CCAATTAACCTTCAAACACCACCTACTGAGTCGATTGATATTCATTCATTC 780

RESULT 10
US-11-217-529-77844
; Sequence 77844, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77844
;   LENGTH: 3405
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-77844

Alignment Scores:
Pred. No.:              4.77          Length:        3405
Score:                  79.00         Matches:       41
Percent Similarity:     36.0%         Conservative:  21
Best Local Similarity:  23.8%         Mismatches:    48
Query Match:            8.4%          Indels:        62
DB:                     7             Gaps:          9

US-10-821-670A-102 (1-187) x US-11-217-529-77844 (1-3405)

Qy         35 GluGluIleAspHis----------GluAspIleThrLysAsp------LysThrSer 48
              |||   :::|||||                |||   |||:::      |||::::::
Db        655 GAAAATGTGGATCATTCTATTGATTTACACTCTATAGTCAAAAATTTTGTCAAATCCAAT 714

Qy         49 ThrValGluAlaCysLeuProLeuGlu----------------------------Leu 58
              |||:::|||:::        :::|||
Db        715 ACTCTGGAAAGTGCCTACTTAATTGAAGGAGGGAAGAGCGATGATTCAAAAGATGTAGAG 774

Qy         59 ThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCys 78
              |||   |||   |||   |||            ||||||   :::|||   |||   |||
Db        775 ACTAAAAATCTATCCATTCTA-----------ATAAGCTTTCTAACCAAAGGCGACTGT 822

Qy         79 LeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAsp 98
              |||                                                :::   |||   :::
Db        823 TTG-----------------------------------------AACTTTTACAATAAC 840

Qy         99 LeuLysMetTyrGlnValGluPheLys-----------------AlaMetAsnAlaLys 112
              :::              |||||||||                 |||:::|||   |||
Db        841 ATTTTACAAAGGTTATCTGAATTCAAAACATTTTTGAAATCTGAAGCACTAAATCTGAAA 900

Qy        113 ---------LeuLeuMetAspProLys---ArgGlnIlePheLeuAspGlnAsnMetLeu 128
                     |||      |||||||||           |||::::::         |||
Db        901 TTTGTTTGTCTAAACTATGATCCCAAATGCCTCCCTACCTTTATTGAGAGTGAAGCGTTA 960

Qy        129 ThrAlaIleAspGluLeuLeuGlnAlaLeuAsn-------------------------- 139
              |||          |||               |||
Db        961 ACAGAAAACGCTGAAGAAGCCGACATTACCAATGGTTCAACAATGATCAGTGCTTCGCTG 1020

Qy        140 --------------------------ValAsnSerValThrValProGlnAsnSerSer 150
                                       |||:::   :::         |||
Db       1021 CATCATAATATAGCGAACAAAGATGCTACAAGGTCGATTATAATTGAATTCAAAAGCCCC 1080

Qy        151 LeuGluGluProAspPheTyrLysThrLysIleLys 162
              :::|||:::   |||   :::|||   |||::::::
Db       1081 GTGGAGAAAAGCGATTTATTCAAAAAGAAATTACAA 1116

RESULT 11
US-11-217-529-4027
; Sequence 4027, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4027
;   LENGTH: 6429
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-4027

Alignment Scores:
Pred. No.:              12            Length:        6429
Score:                  79.00         Matches:       46
Percent Similarity:     36.6%         Conservative:  18
Best Local Similarity:  26.3%         Mismatches:    66
Query Match:            8.4%          Indels:        45
DB:                     7             Gaps:          7

US-10-821-670A-102 (1-187) x US-11-217-529-4027 (1-6429)

Qy         13 LeuArgAla---IleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSer 31
              |||||||||   |||||||||   :::   :::|||:::      |||        |||
Db       5712 TTACGTGCTACCATTTCTAATCGGATTAGTGAAGCACAAGGACGTTTGCGC------TCT 5765

Qy         32 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 51
              |||   |||                                                :::
Db       5766 TGCCGGTCTGGACCCTAT--------------------------------CCGATTATA 5792

Qy         52 AlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSer 71
                    |||   |||               :::||||||      :::|||   |||
Db       5793 CGCTGGCTTGGGCTACATGCCAATCAGAAAAAATCATGTTGCCAGAATCGTCGAATATGT 5852

Qy         72 LeuIleThrAsnGlySerCysLeuAla---------SerArgLysThrSerPheMetThr 88
              |||          |||   :::                |||||||||
Db       5853 CTGTTCTTCGGATGTAGTTCTATCGTCGAACCAAACCAAACTGCAACTAGCTTTTATCCA 5912

Qy         89 ThrLeu------------------------------------------------------ 90
              ||||||
Db       5913 ACACTTCCTGTCAGCAGAATTACTTCAACTAACTGAAGAAGAAAAAAATAAAATCTTGGA 5972

Qy         91 ---Cys-LeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMe 109
                  ||| :::|||::::::|||   :::              ||||||   :::
Db       5973 ATTTGTTGTGAGCAACCTGTATAACGAA---------CAATTTGTGGAAGTAAGAGTGCG 6023

Qy        109 tAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuTh 129
              |||   :::|||   |||                          ||||||   :::|||
Db       6024 TGCTGCAGCCATACTGTCTGATATCGTTCACAACTGGAAGGAAGACCAAGCATTGTTGGA 6083

Qy        129 rAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSe 149
              ||||||        :::   |||:::   |||      |||
Db       6084 CCTGATCGACAGGTTTGCAAAGGGGCTTGACGCCAACAAATACACT-------------- 6129

Qy        149 rSerLeuGluGluProAspPheTyrLysThrLysIleLysLeu 163
              |||   |||:::           ||||||   ||||||:::
Db       6130 -TCGAAGGAAAAGCAAAAGTTATCAAAGACAGATATCAAAATC 6171

RESULT 12
US-10-953-349-13043
; Sequence 13043, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
```

```
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13043
;   LENGTH: 1374
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-13043

Alignment Scores:
Pred. No.:              1.95          Length:        1374
Score:                  77.50         Matches:       45
Percent Similarity:     38.3%         Conservative:  35
Best Local Similarity:  21.5%         Mismatches:    66
Query Match:            8.2%          Indels:        63
DB:                     6             Gaps:          8

US-10-821-670A-102 (1-187) x US-10-953-349-13043 (1-1374)

Qy          2 MetPheGlnCysLeuAsnHisSerGln---------ThrLeuLeuArgAlaIleSerAsn 18
              :::   |||   |||:::   |||:::           :::|||      :::|||:::
Db        609 GTGTTGCAGGCTTTAGACAAGTCTAAAAGACGCATTGAAGTGCTCGATGAGCTTTCCTCC 668

Qy         19 ThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAsp 38
                |||   :::|||              |||                :::      :::
Db        669 AAGCTAAGTGAGGCAATATCTTTGAAAGAAAGTCAGCTAATTGGAAATGTTACTGTGAAA 728

Qy         39 HisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGlu--- 57
                ||||||   |||:::|||   :::|||   |||            |||   |||
Db        729 ATTGAAGACACAACAGAAGATGCTTCAAGTCCAGTTCGAATTATTGCTCCAAAGGAGGAA 788

Qy         58 ------------LeuThrMetAsnGluSer-------------------------Cys 64
                         :::|||   :::||||||
Db        789 GTTCAAAATAATGTCACTAAGGATGAGTCAGATCCTGATACGGCGGAATTTGGTGGTGAT 848

Qy         65 LeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThr 84
              :::         ::::::|||:::   :::   ||||||   |||      ::::::|||
Db        849 ATTCAAGATGTGCAACTTTCTATCGAAAGTGAAGGAAGTTCACTGGATGATAAGGAGACT 908

Qy         85 Ser---PheMetThrThrLeuCysLeuSer---------------------------- 93
                    :::   :::|||   :::|||
Db        909 CAGCATCTTCTGGAATCCCTTAGTATCAGCACTCCAAATGAAGACAATATAGCCAGAAAC 968

Qy         94 ------------SerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMet 109
                         |||   |||||||||       |||
Db        969 TCGTCAGAAATATCCTCTTATGAGGACTTCATGGAATAT---------------------- 1007

Qy        110 AsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThr 129
                                                 :::|||      :::
Db       1008 -------------------------------------ATAGATCTAAAACTCAGTGAA 1028

Qy        130 AlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal------------ 145
                     ||||||:::      |||||||||:::::::::   :::
Db       1029 ATTGAAGCTGAACTAGTGACTGTTTTGAATGTCTCAACCTTGGTACTGGATAATGAAGAG 1088

Qy        146 ---ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCys 164
                  :::||||||   |||::::::                       |||:::|||
Db       1089 AGAGCAAAGAATTCTAGGTTGCAACAA-----------------ACAATTGAACTCCTT 1130

Qy        165 IleLeuLeuHisAlaPheArgIleArg 173
                  :::|||      |||   |||
Db       1131 GACAGCATCCATGGCATTAGACAGAGA 1157

RESULT 13
US-11-217-529-81075
; Sequence 81075, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81075
;   LENGTH: 1473
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-81075

Alignment Scores:
Pred. No.:              2.49          Length:        1473
Score:                  77.00         Matches:       28
Percent Similarity:     46.2%         Conservative:  26
Best Local Similarity:  23.9%         Mismatches:    53
Query Match:            8.2%          Indels:        10
DB:                     7             Gaps:          3

US-10-821-670A-102 (1-187) x US-11-217-529-81075 (1-1473)

Qy         36 GluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuPro 55
                ||:::   |||   |||:::      :::        ::::::         :::
Db        565 GAAGTGCCTCATAGAGATATGCCCACTGAAAGTAATAAATCTATAAACGAAACTGTCGGG 624

Qy         56 LeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsn 75
                |||       |||   |||   :::                ::::::   ::::::
Db        625 TTATCATCAACAACAAAT---ACTGTAAAAAAGGTACCCAAAGTTAAAATACTGAAACGA 681

Qy         76 Gly---------SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeu 92
                ||          :::   ||||||:::   |||   :::|||   ::::::      :::
Db        682 GGTGAAACCTTTGCCAGTCTGGCGAATGATAAAAAAGCTTTTGATTCAAGCTCCAATGTG 741

Qy         93 SerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLys 112
                ||||||      :::   |||:::|||   :::          :::      :::
Db        742 TCTTCATCAAAAGATTTATTACAGATGCTAAGAAACCCAATTTCCTCTACTGTATCTTCA 801

Qy        113 LeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAsp 132
                          ||||||   |||                        |||:::
Db        802 AATCAGCAATCACCAAAATCTCAA-----------------CATCTGAGTGGGGATGTA 843

Qy        133 GluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSer 149
                ||::::::      |||      |||||||||:::   ||||||||||||
Db        844 GAAATCATGATGATGTTGAAGAGGAATTCTGTGTCAAAACCTCAAAATAGC 894

RESULT 14
US-11-217-529-4965/c
; Sequence 4965, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4965
;   LENGTH: 1542
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
```

US-11-217-529-4965

Alignment Scores:

Pred. No.:	2.66	Length:	1542
Score:	77.00	Matches:	43
Percent Similarity:	36.2%	Conservative:	28
Best Local Similarity:	21.9%	Mismatches:	78
Query Match:	8.2%	Indels:	47
DB:	7	Gaps:	6

US-10-821-670A-102 (1-187) x US-11-217-529-4965 (1-1542)

```
Qy          3 PheGlnCysLeuAsn-HisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLy 22
              ||||||   :::||| ||||||   :::|||         :::||||||
Db        879 TTCCAACGTATCAATCCATTCAATTAGCCTTTTCATTGGGCTTTCCAATATGTCCTCTAG 820

Qy         22 sAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIl 42
              :::|||   |||  |||       |||:::     :::
Db        819 TTTCAAGCAACCACTTTCCTTTAAACAATGTTCGTACCACATGTTG---------------- 774

Qy         42 eThrLysAspLysThrSerThrValGluAla----------------------------- 52
                      ||||||      :::   |||
Db        773 ----------AAGACATGGCTTTTATTAGCCCTCAATGAAGTAAATAGTTCCATTTGTTT 724

Qy         53 -------------------CysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAl 66
                               :::   ::::::|||   :::|||:::   |||
Db        723 TTGATGGCTAACAAAATAACTCATATAAGTTGACCTGGTCCTTAATAAATGTTGTTCAAA 664

Qy         66 aSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPh 86
              :::   |||||||||             |||       |||
Db        663 CGCCTCTGAAATATCAAAAACTGAATATAACTGCTGTTGGGTCTCAGCATCAGTGGTTAT 604

Qy         86 eMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPh 106
                           |||:::::::::                  :::   ||
Db        603 TTTTCCCCAATCATTTGCGTCTAACGTTTTCCCACGTTGGTTGACCAAAAGCATGTCATT 544

Qy        106 eLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAs 126
              |   |||                                                |||   ||
Db        543 TATTGCT-----------------------------------------------GATACAAA 529

Qy        126 nMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValPr 146
              |:::|||           |||::::::|||:::   |||:::
Db        528 TATCTTG--------------CTAATCGAAGCAATA---GTATCAATATTCCCAAAAAG 487

Qy        146 oGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLe 166
                  ||||||||||||||      ||||||           :::   |||
Db        486 CAACAACTCATCACTTGAGTCA---GACTTTATTAGCTTGTTCTTGAATCTTAGGTCGTC 430

Qy        166 uLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMet 181
                  :::||||||           :::   :::|||:::   :::
Db        429 ATTTAATGCTTTTCTGTATACGTTATTGGCAGTTAATAAAACATTG 384
```

RESULT 15
US-11-217-529-2301
; Sequence 2301, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2301
; LENGTH: 1836
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-2301

Alignment Scores:

Pred. No.:	3.95	Length:	1836
Score:	76.50	Matches:	35
Percent Similarity:	37.4%	Conservative:	29
Best Local Similarity:	20.5%	Mismatches:	85
Query Match:	8.1%	Indels:	22
DB:	7	Gaps:	2

US-10-821-670A-102 (1-187) x US-11-217-529-2301 (1-1836)

```
Qy         14 ArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThr 33
              |||:::   :::|||   |||            ||||||            :::   :::
Db        394 AGATCAAAAAACAATGCCCTTTCCTTACCAACACAGACAACTTCTTCGTCCACCTCCTCT 453

Qy         34 SerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCys 53
              |||                          :::   |||            ||||  :::
Db        454 TCTTCTTCTTCTTCTTCTTCTTCTTCTTATGATTCTGTAAGAAGGACTGATAATAGC 513

Qy         54 LeuProLeuGluLeuThr------------MetAsnGluSerCysLeuAlaSerArgGlu 69
              :::   ::::::                  |||:::            |||||||||
Db        514 GTTAGAATGCAAAAGAATAAACACTCCAGATTCAACAAGGAATTACCCCGCAGCAGGGAA 573

Qy         70 IleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThr 89
                 |||   :::   :::||||||   ::::::                     |||
Db        574 AGCTCAAATATGAATTCTGGATCTATCATCAGTCAATACAATGTCGATACTCAGGCAACC 633

Qy         90 LeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMet 109
                    :::|||   :::   :::       :::       |||:::            :::
Db        634 GCTATAATGAGCGATATGCAAAAACAATATGAGTCGCAGCAACTGCCTTCGTTGTTTATA 693

Qy        110 AsnAlaLysLeuLeuMetAspProLysArgGlnIle---------------------- 121
              |||      ||||||:::||||||      ::::::
Db        694 AACGAGACTTTACTGATTGATCCAAATGGTAAAGTTTCAGAGGTTATAAAGTTGATATTT 753

Qy        122 --------------------------PheLeuAspGlnAsnMetLeuThrAlaIleAsp 132
                                       |||   |||   ::::::      :::
Db        754 GAAGAAGTCGGCTACAAATTTGATGATTTTAGTGATATTTCCGTTTTCCAACTGATGCAA 813

Qy        133 GluLeuLeuGlnAlaLeuAsnValAsnSer-ValThrValProGlnAsnSerSerLeuGl 152
              |||:::   |||   :::       :::||| |||          ||||||      |||
Db        814 GAAATGTATCAATTAATTAAGAAGGATTCTAGTAATAAAAAGTCAAAATTAACTACTTTT 873

Qy        152 uGluProAspPheTyrLysThrLysIleLys 162
                  |||         |||   |||   |||
Db        874 GCCTCCAAAGTAAAAGAAAAAGAAATGCAAG 904
```

Search completed: June 10, 2006, 01:22:41
Job time : 15.7292 secs

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OM nucleic - nucleic search, using sw model

Run on: June 10, 2006, 03:13:25 ; Search time 2310.73 Seconds
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15525.205 Million cell updates/sec

Title: US-10-821-670A-101
Perfect score: 561
Sequence: 1 gggatgttccagtgcctcaa.....tgagctatctgaatgcttcc 561

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	561	100.0	561	2	AR596007	AR596007 Sequence
c	2	561	100.0	561	2	AR596008	AR596008 Sequence
	3	559.4	99.7	666	2	AR595952	AR595952 Sequence
c	4	559.4	99.7	666	2	AR595953	AR595953 Sequence
	5	559.4	99.7	1533	2	AR595959	AR595959 Sequence
c	6	559.4	99.7	1533	2	AR595960	AR595960 Sequence
	7	559.4	99.7	1599	2	AR595956	AR595956 Sequence
c	8	559.4	99.7	1599	2	AR595957	AR595957 Sequence
	9	557.8	99.4	591	2	AR595954	AR595954 Sequence
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	11	557.8	99.4	669	14	FCIL12P35	Y07761 Felis catus
	12	554.6	98.9	591	2	AR242439	AR242439 Sequence
	13	554.6	98.9	591	2	AR280207	AR280207 Sequence
	14	554.6	98.9	591	2	AR322422	AR322422 Sequence
	15	554.6	98.9	669	14	FCU83185	U83185 Felis catus
	16	554.6	98.9	1441	2	AR242438	AR242438 Sequence
	17	554.6	98.9	1441	2	AR280206	AR280206 Sequence
	18	554.6	98.9	1441	2	AR322421	AR322421 Sequence
	19	545	97.1	669	2	AX076201	AX076201 Sequence
	20	545	97.1	669	2	AX076483	AX076483 Sequence
	21	545	97.1	689	2	AR242451	AR242451 Sequence
	22	545	97.1	689	2	AR280219	AR280219 Sequence
	23	545	97.1	689	2	AR322434	AR322434 Sequence
	24	545	97.1	4201	2	AX076477	AX076477 Sequence
	25	513	91.4	657	8	AY191828	AY191828 Synthetic
	26	513	91.4	660	2	AX154617	AX154617 Sequence
	27	511.4	91.2	591	2	BD171284	BD171284 Novel can
	28	511.4	91.2	591	2	AR595963	AR595963 Sequence
c	29	511.4	91.2	591	2	AR595964	AR595964 Sequence
	30	511.4	91.2	660	2	AX154615	AX154615 Sequence
	31	511.4	91.2	660	2	AX154619	AX154619 Sequence
	32	511.4	91.2	666	2	AR595961	AR595961 Sequence
c	33	511.4	91.2	666	2	AR595962	AR595962 Sequence
	34	511.4	91.2	669	2	AR151072	AR151072 Sequence
	35	511.4	91.2	669	2	BD014664	BD014664 Process f
	36	511.4	91.2	669	2	E15018	E15018 Canine mRNA
	37	511.4	91.2	669	2	AR316471	AR316471 Sequence
	38	511.4	91.2	1282	2	BD171283	BD171283 Novel can
	39	511.4	91.2	1455	2	AR596009	AR596009 Sequence
c	40	511.4	91.2	1455	2	AR596010	AR596010 Sequence
	41	508.2	90.6	660	2	AX154616	AX154616 Sequence
	42	508.2	90.6	669	2	AR151062	AR151062 Sequence
	43	508.2	90.6	669	2	BD014654	BD014654 Process f
	44	508.2	90.6	669	2	AR316461	AR316461 Sequence
	45	506.6	90.3	660	2	AX154620	AX154620 Sequence

ALIGNMENTS

RESULT 1
AR596007
LOCUS AR596007 561 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 101 from patent US 6818444.
ACCESSION AR596007
VERSION AR596007.1 GI:56646988
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 561)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 101 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .561
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 100.0%; Score 561; DB 2; Length 561;
Best Local Similarity 100.0%; Pred. No. 5.3e-164;
Matches 561; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
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```
Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db        541 ATGAGCTATCTGAATGCTTCC 561
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RESULT 2
AR596008/c
LOCUS AR596008 561 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 103 from patent US 6818444.
ACCESSION AR596008
VERSION AR596008.1 GI:56646989
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 561)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 103 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .561
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 100.0%; Score 561; DB 2; Length 561;
Best Local Similarity 100.0%; Pred. No. 5.3e-164;
Matches 561; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1
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RESULT 3
AR595952
LOCUS AR595952 666 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 32 from patent US 6818444.
ACCESSION AR595952
VERSION AR595952.1 GI:56646933
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 666)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 32 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .666
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 99.7%; Score 559.4; DB 2; Length 666;
Best Local Similarity 99.8%; Pred. No. 1.7e-163;
Matches 560; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 165

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 225

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 285

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 345

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 405

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 465

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 525

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
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Db        526 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 585

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 645

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db        646 ATGAGCTATCTGAATGCTTCC 666


RESULT 4
AR595953/c
LOCUS       AR595953                 666 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 34 from patent US 6818444.
ACCESSION   AR595953
VERSION     AR595953.1  GI:56646934
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 34 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             99.7%;  Score 559.4;  DB 2;  Length 666;
  Best Local Similarity   99.8%;  Pred. No. 1.7e-163;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              ||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1


RESULT 5
AR595959
LOCUS       AR595959                 1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 43 from patent US 6818444.
ACCESSION   AR595959
VERSION     AR595959.1  GI:56646940
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 43 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             99.7%;  Score 559.4;  DB 2;  Length 1533;
  Best Local Similarity   99.8%;  Pred. No. 1.8e-163;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1032

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1092

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1093 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1152

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1153 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1212

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1213 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1272

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1273 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1332

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1333 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1392

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1393 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1452

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1453 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1512

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              ||||||||||||||||||||
Db       1513 ATGAGCTATCTGAATGCTTCC 1533


RESULT 6
AR595960/c
LOCUS       AR595960                 1533 bp    DNA     linear   PAT 15-DEC-2004
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DEFINITION  Sequence 45 from patent US 6818444.
ACCESSION   AR595960
VERSION     AR595960.1  GI:56646941
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 45 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             99.7%;  Score 559.4;  DB 2;  Length 1533;
  Best Local Similarity   99.8%;  Pred. No. 1.8e-163;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1


RESULT 7
AR595956
LOCUS       AR595956                1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 38 from patent US 6818444.
ACCESSION   AR595956
VERSION     AR595956.1  GI:56646937
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 38 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             99.7%;  Score 559.4;  DB 2;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 1.8e-163;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1098

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1158

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1218

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1219 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1278

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1338

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1398

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1458

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1459 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1518

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1519 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1578

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db       1579 ATGAGCTATCTGAATGCTTCC 1599


RESULT 8
AR595957/c
LOCUS       AR595957                1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 40 from patent US 6818444.
ACCESSION   AR595957
VERSION     AR595957.1  GI:56646938
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 40 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
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                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           99.7%;  Score 559.4;  DB 2;  Length 1599;
  Best Local Similarity  99.8%;  Pred. No. 1.8e-163;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1


RESULT 9
AR595954
LOCUS       AR595954                 591 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 35 from patent US 6818444.
ACCESSION   AR595954
VERSION     AR595954.1  GI:56646935
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 35 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           99.4%;  Score 557.8;  DB 2;  Length 591;
  Best Local Similarity  99.6%;  Pred. No. 5.3e-163;
  Matches  559;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 90

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
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Db        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 210

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
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Db        271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
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Db        331 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 390

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
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Db        391 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 450

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        451 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 510

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 570

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db        571 ATGAGCTATCTGAATGCTTCC 591


RESULT 10
AR595955/c
LOCUS       AR595955                 591 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 37 from patent US 6818444.
ACCESSION   AR595955
VERSION     AR595955.1  GI:56646936
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 37 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           99.4%;  Score 557.8;  DB 2;  Length 591;
  Best Local Similarity  99.6%;  Pred. No. 5.3e-163;
  Matches  559;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
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Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1
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RESULT 11
FCIL12P35
LOCUS       FCIL12P35                669 bp    mRNA    linear   MAM 18-APR-2005
DEFINITION  Felis catus mRNA for interleukin-12 p35 chain.
ACCESSION   Y07761
VERSION     Y07761.1  GI:2102662
KEYWORDS    interleukin-12 subunit p35.
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1
  AUTHORS   Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
  TITLE     Molecular cloning of cat interleukin-12
  JOURNAL   Immunogenetics 45 (6), 462-463 (1997)
   PUBMED   9089110
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Schijns,V.E.C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
            Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
            Utrecht, NETHERLANDS
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Felis catus"
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                     /db_xref="taxon:9685"
                     /cell_type="lymphocyte"
                     /tissue_type="peripheral blood"
     gene            1. .669
                     /gene="IL-12.p35"
     CDS             1. .669
                     /gene="IL-12.p35"
                     /function="heterodimer with IL-12 p40 chain"
                     /codon_start=1
                     /product="interleukin-12 p35 chain"
                     /protein_id="CAA69067.1"
                     /db_xref="GI:2102663"
                     /db_xref="GOA:O02743"
                     /db_xref="InterPro:IPR004281"
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                     LNAS"
ORIGIN

  Query Match           99.4%;  Score 557.8;  DB 14;  Length 669;
  Best Local Similarity   99.6%;  Pred. No. 5.4e-163;
  Matches  559;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 165

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 225

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 285

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
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Db        286 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 345

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 405

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
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Db        406 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 465

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 525

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        526 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 585

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 645

Qy        541 ATGAGCTATCTGAATGCTTCC 561
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Db        646 ATGAGCTATCTGAATGCTTCC 666
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RESULT 12
AR242439
LOCUS       AR242439                 591 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 9 from patent US 6472509.
ACCESSION   AR242439
VERSION     AR242439.1  GI:27288856
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 9 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
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FEATURES             Location/Qualifiers
     source          1. .591
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                     /mol_type="mRNA"
ORIGIN

  Query Match             98.9%;  Score 554.6;  DB 2;  Length 591;
  Best Local Similarity   99.3%;  Pred. No. 5.3e-162;
  Matches  557;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 90

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 210

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
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Db        331 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 390

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 450

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        451 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 510

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 570

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||| |||||| |||||
Db        571 ATGAGCTACCTGAATTCTTCC 591


RESULT 13
AR280207
LOCUS       AR280207                 591 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 9 from patent US 6518045.
ACCESSION   AR280207
VERSION     AR280207.1  GI:29715597
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 9 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
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ORIGIN

  Query Match             98.9%;  Score 554.6;  DB 2;  Length 591;
  Best Local Similarity   99.3%;  Pred. No. 5.3e-162;
  Matches  557;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 90

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
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Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 390

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 450

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
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Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 570

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||| |||||| |||||
Db        571 ATGAGCTACCTGAATTCTTCC 591


RESULT 14
AR322422
LOCUS       AR322422                 591 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 9 from patent US 6566097.
ACCESSION   AR322422
VERSION     AR322422.1  GI:33708175
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 9 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             98.9%;  Score 554.6;  DB 2;  Length 591;
  Best Local Similarity   99.3%;  Pred. No. 5.3e-162;
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Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
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Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
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Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
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Db        331 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 390

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
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Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
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Qy        541 ATGAGCTATCTGAATGCTTCC 561
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Db        571 ATGAGCTACCTGAATTCTTCC 591
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RESULT 15
FCU83185
LOCUS       FCU83185                669 bp    mRNA    linear   MAM 16-JUL-1999
DEFINITION  Felis catus interleukin-12 p35 subunit (IL-12) mRNA, complete cds.
ACCESSION   U83185
VERSION     U83185.1  GI:2735052
KEYWORDS    .
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Nucleotide and predicted peptide sequence of feline interleukin-12
            (IL-12)
  JOURNAL   DNA Seq. 8 (1-2), 77-82 (1997)
   PUBMED   9522125
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal
            Veterinary Medicine, University of Zurich, Winterthurerstrasse 260,
            Zurich, ZH 8057, Switzerland
FEATURES             Location/Qualifiers
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                     LNSS"
ORIGIN
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  Query Match             98.9%;  Score 554.6;  DB 14;  Length 669;
  Best Local Similarity   99.3%;  Pred. No. 5.4e-162;
  Matches  557;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

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              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        166 CAGAAGGCCAGACAAACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAA 225

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 285

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 345

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 405

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
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Db        466 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 525

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        526 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 585

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
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Db        586 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 645

Qy        541 ATGAGCTATCTGAATGCTTCC 561
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Db        646 ATGAGCTATCTGAATTCTTCC 666
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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		561	100.0	561	6	ABK99001	Abk99001 Feline in
2	c	561	100.0	561	6	ABK99002	Abk99002 Feline in
3		561	100.0	561	14	ADV34751	Adv34751 Feline N-
4	c	561	100.0	561	14	ADV34753	Adv34753 Feline N-
5	c	559.4	99.7	666	6	ABK98947	Abk98947 Feline in
6		559.4	99.7	666	6	ABK98946	Abk98946 Feline in
7		559.4	99.7	666	14	ADV34685	Adv34685 Feline si
8	c	559.4	99.7	666	14	ADV34687	Adv34687 Feline si
9	c	559.4	99.7	1533	6	ABK98954	Abk98954 Feline in
10		559.4	99.7	1533	6	ABK98953	Abk98953 Feline in
11	c	559.4	99.7	1533	14	ADV34697	Adv34697 Feline si
12		559.4	99.7	1533	14	ADV34695	Adv34695 Feline si
13		559.4	99.7	1599	6	ABK98950	Abk98950 Feline in
14	c	559.4	99.7	1599	6	ABK98951	Abk98951 Feline in
15		559.4	99.7	1599	14	ADV34691	Adv34691 Feline si
16	c	559.4	99.7	1599	14	ADV34693	Adv34693 Feline si
17		557.8	99.4	591	6	ABK98948	Abk98948 Feline in
18	c	557.8	99.4	591	6	ABK98949	Abk98949 Feline in
19		557.8	99.4	591	14	ADV34688	Adv34688 Feline si
20	c	557.8	99.4	591	14	ADV34690	Adv34690 Feline si
21		554.6	98.9	591	2	AAV56629	Aav56629 Feline FL
22		554.6	98.9	1441	2	AAV56628	Aav56628 Feline FL
23		546.6	97.4	679	4	AAF26097	Aaf26097 Feline fi
24		545	97.1	669	4	AAF26083	Aaf26083 Feline IL
25		545	97.1	669	4	AAF26086	Aaf26086 Feline IL
26		545	97.1	689	2	AAV56641	Aav56641 Feline FL
27		545	97.1	4201	4	AAF26077	Aaf26077 Feline IL
28		543.4	96.9	639	4	AAF26098	Aaf26098 Plasmid p
29		513	91.4	660	5	AAD15216	Aad15216 Modified
30		511.4	91.2	591	2	AAX18179	Aax18179 Canine ma
31	c	511.4	91.2	591	6	ABK98958	Abk98958 Canine in
32		511.4	91.2	591	6	ABK98957	Abk98957 Canine in
33		511.4	91.2	591	14	ADV34701	Adv34701 Canine si
34	c	511.4	91.2	591	14	ADV34703	Adv34703 Canine si
35		511.4	91.2	660	5	AAD15214	Aad15214 Modified
36		511.4	91.2	660	5	AAD15218	Aad15218 Modified
37		511.4	91.2	666	6	ABK98955	Abk98955 Canine in
38	c	511.4	91.2	666	6	ABK98956	Abk98956 Canine in
39	c	511.4	91.2	666	14	ADV34700	Adv34700 Canine si
40		511.4	91.2	666	14	ADV34698	Adv34698 Canine si
41		511.4	91.2	669	2	AAV13819	Aav13819 Canine IL
42		511.4	91.2	669	2	AAX03163	Aax03163 Nucleic a
43		511.4	91.2	669	2	AAX35626	Aax35626 Nucleic a
44		511.4	91.2	669	4	AAI64389	Aai64389 Canine co
45		511.4	91.2	1282	2	AAX18178	Aax18178 Canine fu

ALIGNMENTS

RESULT 1
ABK99001
ID ABK99001 standard; cDNA; 561 BP.
XX
AC ABK99001;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p35-N561 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69315.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Disclosure; Page 92-93; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain

CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 561 BP; 167 A; 134 C; 120 G; 140 T; 0 U; 0 Other;

Query Match 100.0%; Score 561; DB 6; Length 561;
Best Local Similarity 100.0%; Pred. No. 1.2e-164;
Matches 561; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
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Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
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Db         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
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Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
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Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
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Qy        541 ATGAGCTATCTGAATGCTTCC 561
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Db        541 ATGAGCTATCTGAATGCTTCC 561
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RESULT 2
ABK99002/c
ID ABK99002 standard; cDNA; 561 BP.
XX
AC ABK99002;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12nFeIL-12p35-N561 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.

XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Disclosure; Page 94; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 561 BP; 140 A; 120 C; 134 G; 167 T; 0 U; 0 Other;

Query Match 100.0%; Score 561; DB 6; Length 561;
Best Local Similarity 100.0%; Pred. No. 1.2e-164;
Matches 561; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
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Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
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Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1
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RESULT 3
ADV34751
ID ADV34751 standard; cDNA; 561 BP.
XX
AC ADV34751;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline N-terminal single chain IL-12p35 cDNA, nFeIL-12p35-N561.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; gene; ss.
XX
OS Felis catus.
XX
FH Key   Location/Qualifiers
FT CDS   1. .561
FT   /*tag= a
FT   /product= "PFeIL-12p35-N187 protein"
FT   /partial
FT   /note= "No start and stop codon"
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
DR P-PSDB; ADV34752.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Claim 23; SEQ ID NO 101; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline N-terminal single chain IL-12p35 subunit
CC protein encoding cDNA.
XX
SQ Sequence 561 BP; 167 A; 134 C; 120 G; 140 T; 0 U; 0 Other;

  Query Match   100.0%; Score 561; DB 14; Length 561;
  Best Local Similarity 100.0%; Pred. No. 1.2e-164;
  Matches 561; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db        541 ATGAGCTATCTGAATGCTTCC 561
```

RESULT 4
ADV34753/c
ID ADV34753 standard; cDNA; 561 BP.
XX
AC ADV34753;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline N-terminal IL-12p35 complementary DNA, nFeIL-12p35-N561.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; gene; ss.
XX
OS Felis catus.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX

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PS   Disclosure; SEQ ID NO 103; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline N-terminal single chain IL-12p35 subunit
CC   protein complementary DNA.
XX
SQ   Sequence 561 BP; 140 A; 120 C; 134 G; 167 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 561;  DB 14;  Length 561;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-164;
  Matches  561;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1


RESULT 5
ABK98947/c
ID   ABK98947 standard; cDNA; 666 BP.
XX
AC   ABK98947;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p35-666 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 3; Page 56; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 666 BP; 160 A; 138 C; 179 G; 189 T; 0 U; 0 Other;

  Query Match            99.7%;  Score 559.4;  DB 6;  Length 666;
  Best Local Similarity  99.8%;  Pred. No. 4.1e-164;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82
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Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1


RESULT 6
ABK98946
ID   ABK98946 standard; cDNA; 666 BP.
XX
AC   ABK98946;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p35-666 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69304.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 54-55; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 666 BP; 189 A; 179 C; 138 G; 160 T; 0 U; 0 Other;

  Query Match             99.7%;  Score 559.4;  DB 6;  Length 666;
  Best Local Similarity   99.8%;  Pred. No. 4.1e-164;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 165

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 225

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 285

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 345

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 405

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 465

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 525

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 585

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 645

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db        646 ATGAGCTATCTGAATGCTTCC 666


RESULT 7
ADV34685
ID   ADV34685 standard; cDNA; 666 BP.
XX
AC   ADV34685;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12p35 full-length cDNA, nFeIL-12p35 666.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .666
FT                   /*tag=  a
FT                   /product= "PFeIL-12p35 222 protein "
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
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DR   P-PSDB; ADV34686.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 23; SEQ ID NO 32; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12p35 subunit protein
CC   encoding full-length cDNA.
XX
SQ   Sequence 666 BP; 189 A; 179 C; 138 G; 160 T; 0 U; 0 Other;

  Query Match            99.7%;  Score 559.4;  DB 14;  Length 666;
  Best Local Similarity  99.8%;  Pred. No. 4.1e-164;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 165

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 225

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 285

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 345

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 405

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 465

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 525

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 585

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 645

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db        646 ATGAGCTATCTGAATGCTTCC 666


RESULT 8
ADV34687/c
ID   ADV34687 standard; DNA; 666 BP.
XX
AC   ADV34687;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12p35 complementary DNA, nFeIL-12p35 666.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 34; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12p35 subunit full-length
CC   complementary DNA.
XX
SQ   Sequence 666 BP; 160 A; 138 C; 179 G; 189 T; 0 U; 0 Other;

  Query Match            99.7%;  Score 559.4;  DB 14;  Length 666;
  Best Local Similarity  99.8%;  Pred. No. 4.1e-164;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1


RESULT 9
ABK98954/c
ID   ABK98954 standard; cDNA; 1533 BP.
XX
AC   ABK98954;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1533 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 66-67; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

  Query Match             99.7%;  Score 559.4;  DB 6;  Length 1533;
  Best Local Similarity   99.8%;  Pred. No. 6.2e-164;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1


RESULT 10
ABK98953
ID   ABK98953 standard; cDNA; 1533 BP.
XX
AC   ABK98953;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1533 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69307.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
```

PS Claim 6; Page 63-64; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

Query Match 99.7%; Score 559.4; DB 6; Length 1533;
Best Local Similarity 99.8%; Pred. No. 6.2e-164;
Matches 560; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1032

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1092

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1093 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1152

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1153 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1212

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1213 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1272

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1273 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1332

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1333 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1392

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1393 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1452

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1453 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1512

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db       1513 ATGAGCTATCTGAATGCTTCC 1533
```

RESULT 11
ADV34697/c
ID ADV34697 standard; DNA; 1533 BP.
XX
AC ADV34697;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain IL-12 complementary DNA, nFeIL-12 1533.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Felis catus.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 3; SEQ ID NO 45; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain IL-12 complementary DNA.
XX
SQ Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

Query Match 99.7%; Score 559.4; DB 14; Length 1533;
Best Local Similarity 99.8%; Pred. No. 6.2e-164;
Matches 560; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy         541 ATGAGCTATCTGAATGCTTCC 561
               |||||||||||||||||||||
Db          21 ATGAGCTATCTGAATGCTTCC 1


RESULT 12
ADV34695
ID   ADV34695 standard; cDNA; 1533 BP.
XX
AC   ADV34695;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1533
FT                   /*tag=  a
FT                   /product= "PFeIL-12 511 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34696.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 43; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

  Query Match            99.7%;  Score 559.4;  DB 14;  Length 1533;
  Best Local Similarity  99.8%;  Pred. No. 6.2e-164;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1032

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       1033 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1092

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1093 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1152

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1153 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1212

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1213 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1272

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1273 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1332

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1333 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1392

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1393 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1452

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1453 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1512

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db       1513 ATGAGCTATCTGAATGCTTCC 1533


RESULT 13
ABK98950
ID   ABK98950 standard; cDNA; 1599 BP.
XX
AC   ABK98950;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1599 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69306.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 58-60; 106pp; English.
```

```
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

  Query Match             99.7%;  Score 559.4;  DB 6;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 6.4e-164;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
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Db       1039 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1098

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1158

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
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Db       1159 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1218

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1219 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1278

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1338

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1398

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1458

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1459 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1518

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1519 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1578

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db       1579 ATGAGCTATCTGAATGCTTCC 1599


RESULT 14
ABK98951/c
ID   ABK98951 standard; cDNA; 1599 BP.
XX
AC   ABK98951;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1599 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 61-62; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

  Query Match             99.7%;  Score 559.4;  DB 6;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 6.4e-164;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
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Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142
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Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
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Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1


RESULT 15
ADV34691
ID   ADV34691 standard; cDNA; 1599 BP.
XX
AC   ADV34691;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1599
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FT                   /product= "PFeIL-12p533 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34692.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 38; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

  Query Match             99.7%;  Score 559.4;  DB 14;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 6.4e-164;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1098

Qy         61 CAGAAGGCCAGACAAACTCTAGAAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 CAGAAGGCCAGACAAACTCTAGAAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1158

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1218

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1219 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1278

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1338

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1398

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1458

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1459 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1518

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1519 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1578

Qy        541 ATGAGCTATCTGAATGCTTCC 561
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Gapop 10.0 , Gapext 1.0

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	28	86.2	15.4	592	12	CE159257	CE159257 tigr-gss-
	29	81	14.4	342	2	BM257856	BM257856 521721 MA
	30	77.6	13.8	840	11	BZ261813	BZ261813 CH230-420
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c	32	74.6	13.3	940	14	BX963061	BX963061 Forward s
	33	69	12.3	558	9	CX570753	CX570753 RVL1941 W
	34	64	11.4	382	4	CB809298	CB809298 AMGNNUC:T
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c	37	59.4	10.6	528	1	AI332701	AI332701 qq19a07.x
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ALIGNMENTS

RESULT 1
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LOCUS DQ033872 762 bp DNA linear GSS 02-JUN-2005
DEFINITION Homo sapiens IL12A gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION DQ033872
VERSION DQ033872.1 GI:66885081
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 762)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 762)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.
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ORIGIN

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  Matches  513;  Conservative    0;  Mismatches   48;  Indels    0;  Gaps    0;

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Db        199 GGAATGTTCCCATGCCTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTC 258

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              |||||||||||||||||||||||||||||| | ||||||||  ||||||||||||||||||
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Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              |||||||||||||||||||||||||||||||||||||||| ||||||  |||||||||||| |
Db        319 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAG 378

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              |||||||||||||   ||||||||||| |||| | ||||||||||||||||||||||||
Db        379 AATGAGAGTTGCCTAAATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCC 438

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              |||||||||||||||||||| | |||||||||||||| ||||| ||||| |||||||||
Db        439 TCCAGAAAGACCTCTTTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAG 498

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              |||||||||||||||||||| ||||||||||||||   | ||||||||||| ||||||
Db        499 ATGTACCAGGTGGAGTTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAG 558

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||| |||||||||||||||| ||| |||||||||||| | ||||||||||| ||
Db        559 ATCTTTCTAGATCAAAACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTC 618

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||| |||||||||||| || |||||||| |||||||||||||||||||||||||||
Db        619 AACAGTGAGACTGTGCCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAA 678

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              |||||||||||||||||||||||||||||||||||||| |||||||| ||  ||||| ||
Db        679 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTG 738

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              ||||||||||||||||||||
Db        739 ATGAGCTATCTGAATGCTTCC 759
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```
RESULT 2
DQ033873
LOCUS       DQ033873                762 bp    DNA     linear   GSS 02-JUN-2005
DEFINITION  Pan troglodytes IL12A gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   DQ033873
VERSION     DQ033873.1  GI:66885082
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     A Scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
  JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
   PUBMED   15869325
REFERENCE   2  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.  Translation starts at the beginning of
            alignment.
FEATURES             Location/Qualifiers
     source          1. .762
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     gene            <1. .>762
                     /gene="IL12A"
                     /locus_tag="HC3464"
ORIGIN
```

```
  Query Match             85.7%;  Score 481;  DB 14;  Length 762;
  Best Local Similarity   91.1%;  Pred. No. 6.1e-131;
  Matches  511;  Conservative    0;  Mismatches   50;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              || |||||||  |||||  |||||||||||| |||||||  | |||  |||||||||  |||
Db        199 GGAATGTTCCCATGCCTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTC 258

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              |||||||||||||||||||||||||||||| | ||||||||  ||||||||||||||||||
Db        259 CAGAAGGCCAGACAAACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAA 318

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              |||||||||||||||||||||||||||||||||||||||| ||||||  |||||||||||| |
Db        319 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAG 378

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              |||||||||||||   ||||||||||| |||| | ||||||||||||||||||||||||
Db        379 AATGAGAGTTGCCTAAATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCC 438

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              |||||||||||||||||||| | |||||||||||||| ||||| ||||| |||||||||
Db        439 TCCAGAAAGACCTCTTTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAG 498

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              |||||||||||||||||||| ||||||||||||||   | ||||||||||| ||||||
Db        499 ATGTACCAGGTGGAGTTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAG 558

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||| |||||||||||||||| ||| |||||| |||||| | |||||||||||| ||
Db        559 ATCTTTCTAGATCAAAACATGCTGGCAGTTATTGACGAGCTGATGCAGGCCCTGAATTTC 618

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||| |||||||||||| || |||||||| |||||||||||||||||||||||||||
Db        619 AACAGTGAGACTGTGCCACAAAAATCCTCCCTTGAAGAACTGGATTTTTATAAAACTAAA 678

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              |||||||||||||||||||||||||||||||||||||| |||||||| ||  ||||| ||
Db        679 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTG 738

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              ||||||||||||||||||||
Db        739 ATGAGCTATCTGAATGCTTCC 759
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RESULT 3
CD013914
LOCUS       CD013914                935 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION  90138124 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD013914
VERSION     CD013914.1  GI:37777444
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 935)
  AUTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
            Au-Young,J. and Stuve,L.L.
```

```
  TITLE     PCR isolation and cloning of novel splice variant mRNAs from known
            drug target genes
  JOURNAL   Genomics 83 (4), 566-571 (2004)
   PUBMED   15028279
COMMENT     Contact: Jin, P.
            Incyte Corporation
            3160 Porter Drive, Palo Alto, CA 94304, USA
            Tel: 650 621 8639
            Fax: 650 621 8965
            Email: pjin@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .935
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Single gene library"
                     /note="Vector: pDrive Cloning Vector; RT-PCR was performed
                     using gene-specific primers flanking the open-reading
                     frame. PCR products were subcloned into pDrive Cloning
                     Vector and sequenced completely using M13 forward and
                     reverse primers. Sequencing gaps were closed by
                     re-sequencig using primers flanking the gapped areas."
ORIGIN

  Query Match            71.3%;  Score 399.8;  DB 4;  Length 935;
  Best Local Similarity  85.0%;  Pred. No. 7.8e-107;
  Matches  477;  Conservative    0;  Mismatches   42;  Indels   42;  Gaps    1;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              || |||||||  |||||  |||||||||||| ||||||| | ||| |||||||||| |||
Db        302 GGAATGTTCCCATGCCTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTC 361

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              |||||||||||||||||||||||||||||| | |||||||| ||||||||||||||||||
Db        362 CAGAAGGCCAGACAAACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAA 421

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              |||||||||||||||||||||||||||||||||||||||||| |||||| |||||||||||| |
Db        422 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAG 481

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
                                                    ||||||||||||||||||||
Db        482 ----------------------------------------AATGGGAGTTGCCTGGCC 499

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              |||||||||||||||||||| | |||||||||||| ||||| ||||| |||||||||
Db        500 TCCAGAAAGACCTCTTTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAG 559

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              |||||||||||||||||||| |||||||||||||| | |||||||||| ||||||
Db        560 ATGTACCAGGTGGAGTTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAG 619

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              |||||||| |||||||||||||| ||| |||||||||||| | |||||||||||| ||
Db        620 ATCTTTCTAGATCAAAACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTC 679

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||| |||||||||||| || |||||||| |||||||||||||||||||||||||||
Db        680 AACAGTGAGACTGTGCCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAA 739

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              |||||||||||||||||||||||||||||||||||| |||||||| ||  ||||| ||
Db        740 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTG 799

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db        800 ATGAGCTATCTGAATGCTTCC 820


RESULT 4
CD013915
LOCUS       CD013915               1136 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION  90138132 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD013915
VERSION     CD013915.1  GI:37777445
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1136)
  AUTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
            Au-Young,J. and Stuve,L.L.
  TITLE     PCR isolation and cloning of novel splice variant mRNAs from known
            drug target genes
  JOURNAL   Genomics 83 (4), 566-571 (2004)
   PUBMED   15028279
COMMENT     Contact: Jin, P.
            Incyte Corporation
            3160 Porter Drive, Palo Alto, CA 94304, USA
            Tel: 650 621 8639
            Fax: 650 621 8965
            Email: pjin@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .1136
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Single gene library"
                     /note="Vector: pDrive Cloning Vector; RT-PCR was performed
                     using gene-specific primers flanking the open-reading
                     frame. PCR products were subcloned into pDrive Cloning
                     Vector and sequenced completely using M13 forward and
                     reverse primers. Sequencing gaps were closed by
                     re-sequencig using primers flanking the gapped areas."
ORIGIN

  Query Match            71.2%;  Score 399.2;  DB 4;  Length 1136;
  Best Local Similarity  80.7%;  Pred. No. 1.3e-106;
  Matches  513;  Conservative    0;  Mismatches   48;  Indels   75;  Gaps    1;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              || |||||||  |||||  |||||||||||| ||||||| | ||| |||||||||| |||
Db        386 GGAATGTTCCCATGCCTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTC 445

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              |||||||||||||||||||||||||||||| | |||||||| ||||||||||||||||||
Db        446 CAGAAGGCCAGACAAACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAA 505

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              |||||||||||||||||||||||||||||||||||||||||| |||||| |||||||||||| |
Db        506 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAG 565

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT------------------ 222
              |||||||||||||||   |||||||||| |||| | ||||||
Db        566 AATGAGAGTTGCCTAAATTCCAGAGAGACCTCTTTCATAACTGTAAGTCAAAAAATGAAA 625

Qy        223 ----------------------------------------------------------AAT 225
                                                                        |||
Db        626 AGTTTCAGCCTGTATGATGAATTCATATCACTGATGTCTGATTATTTTTTCCTCTAGAAT 685

Qy        226 GGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATC 285
              |||||||||||||||||||||||||||||||||||| | |||||||||||| |||||
Db        686 GGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATGGCCCTGTGCCTTAGTAGTATT 745

Qy        286 TATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATG 345
              ||||| |||||||||||||||||||||||||||||| |||||||||||||||   | |||
Db        746 TATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAATGCAAAGCTTCTGATG 805

Qy        346 GATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTA 405
              |||||||| |||||||||||||| |||||||||||||||| ||| |||||||||||||| |
Db        806 GATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCAGTTATTGATGAGCTGATG 865

Qy        406 CAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGAT 465
              |||||||||||| ||||||||| |||||||||||| || |||||||| ||||||||||||
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Db        866 CAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCCCTTGAAGAACCGGAT 925

Qy        466 TTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTG 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        926 TTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGGGCAGTG 985

Qy        526 ACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 561
              || ||  ||||| |||||||||||||||||||||||
Db        986 ACTATTGATAGAGTGATGAGCTATCTGAATGCTTCC 1021


RESULT 5
CD013916
LOCUS       CD013916                 863 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION  90138296 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD013916
VERSION     CD013916.1  GI:37777446
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 863)
  AUTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
            Au-Young,J. and Stuve,L.L.
  TITLE     PCR isolation and cloning of novel splice variant mRNAs from known
            drug target genes
  JOURNAL   Genomics 83 (4), 566-571 (2004)
   PUBMED   15028279
COMMENT     Contact: Jin, P.
            Incyte Corporation
            3160 Porter Drive, Palo Alto, CA 94304, USA
            Tel: 650 621 8639
            Fax: 650 621 8965
            Email: pjin@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .863
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Single gene library"
                     /note="Vector: pDrive Cloning Vector; RT-PCR was performed
                     using gene-specific primers flanking the open-reading
                     frame. PCR products were subcloned into pDrive Cloning
                     Vector and sequenced completely using M13 forward and
                     reverse primers. Sequencing gaps were closed by
                     re-sequencig using primers flanking the gapped areas."
ORIGIN

  Query Match           59.3%;  Score 332.8;  DB 4;  Length 863;
  Best Local Similarity   91.7%;  Pred. No. 5.6e-87;
  Matches  352;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy        178 ATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTG 237
              | |||||||||||||||   |||||||||||| |||| | ||||||||||||||||||||
Db        365 AAGAATGAGAGTTGCCTAAATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTG 424

Qy        238 GCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTG 297
              |||||||||||||||||||||||| | |||||||||||| ||||| ||||| ||||||
Db        425 GCCTCCAGAAAGACCTCTTTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTG 484

Qy        298 AAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGG 357
              |||||||||||||||||||||||| ||||||||||||||  | |||||||||| |||
Db        485 AAGATGTACCAGGTGGAGTTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGG 544

Qy        358 CAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAAT 417
              |||||||||| |||||||||||||||| ||| |||||||||||| | ||||||||||||
Db        545 CAGATCTTTCTAGATCAAAACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAAT 604

Qy        418 GTCAACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACT 477
              |||||||| |||||||||||| || |||||||| |||||||||||||||||||||||||
Db        605 TTCAACAGTGAGACTGTGCCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACT 664

Qy        478 AAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGA 537
              |||||||||||||||||||||||||||||||||||||||||||| |||||||| ||   |||||
Db        665 AAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGA 724

Qy        538 ATGATGAGCTATCTGAATGCTTCC 561
              ||||||||||||||||||||||||
Db        725 GTGATGAGCTATCTGAATGCTTCC 748


RESULT 6
BC035571
LOCUS       BC035571                 1938 bp    mRNA    linear   HTC 04-MAR-2003
DEFINITION  Homo sapiens, clone IMAGE:5240216, mRNA.
ACCESSION   BC035571
VERSION     BC035571.1  GI:23958681
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1938)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 69 Row: b Column: 15
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 4504638
            This clone has the following problem: retained intron.
FEATURES             Location/Qualifiers
     source          1. .1938
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240216"
                     /tissue_type="Brain, fetal, whole pooled"
                     /clone_lib="NIH_MGC_121"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
ORIGIN

  Query Match           46.3%;  Score 259.6;  DB 6;  Length 1938;
  Best Local Similarity   91.9%;  Pred. No. 3.7e-65;
  Matches  274;  Conservative    0;  Mismatches   24;  Indels    0;  Gaps    0;

Qy        264 GACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGC 323
              | |||||||||||||| ||||| ||||| |||||||||||||||||||||||||||||| |
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Db       1145 GGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGAC 1204

Qy        324 CATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCT 383
              |||||||||||||||  | ||||||||||| |||||||||||||| ||||||||||||||
Db       1205 CATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCT 1264

Qy        384 GACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAA 443
              | ||| |||||||||||||| | |||||||||||| ||||||||| |||||||||||| ||
Db       1265 GGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAA 1324

Qy        444 CTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCA 503
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1325 ATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCA 1384

Qy        504 TGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||| |||||||| ||  ||||| ||||||||||||||||||||||
Db       1385 TGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTCC 1442


RESULT 7
BI523344/c
LOCUS       BI523344               1099 bp    mRNA    linear   EST 29-AUG-2001
DEFINITION  603175938T1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 3',
            mRNA sequence.
ACCESSION   BI523344
VERSION     BI523344.1  GI:15348136
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1099)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11605  row: 1  column: 09
            High quality sequence start: 40
            High quality sequence stop: 727.
FEATURES             Location/Qualifiers
     source          1. .1099
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240216"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_121"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 017. Note:
                     this is a NIH_MGC Library."
ORIGIN

  Query Match             38.6%;  Score 216.6;  DB 2;  Length 1099;
  Best Local Similarity   89.0%;  Pred. No. 1.7e-52;
  Matches  268;  Conservative    0;  Mismatches   29;  Indels    4;  Gaps    3;

Qy        264 GACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGC 323
              | |||||||| |||| ||||| ||||| ||| |||||||||||||||||||||||||| |
Db        741 GGCCCTGTGCTTTAGTAGTATTTATGAAGAC-TGAAGATGTACCAGGTGGAGTTCAAGAC 683

Qy        324 CATGAATGCAAAGC-TGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGC 382
              |||||||||||||| |  | |||||||||| |||||||||||||| ||||||||||||
Db        682 CATGAATGCAAAGCTTCCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGC 623

Qy        383 TGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGA 442
              || ||| |||||||||||||| | |||||||||||| ||||||||| |||||||||||| |
Db        622 TGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAA 563

Qy        443 ACTCCTCCCTGGAAGAACCGGAT--TTTTATAAAACTAAAATCAAGCTCTGCATACTTCT 500
              | |||||||| ||||||||||||  |||   |||||| ||||||||||||||||||||||
Db        562 AATCCTCCCTTGAAGAACCGGATTGTTTATCAAAACTGAAATCAAGCTCTGCATACTTCT 503

Qy        501 TCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTC 560
              |||||||||||||||||| |||||||| ||  ||||| ||||||||||||||||||||||
Db        502 TCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTC 443

Qy        561 C 561
              |
Db        442 C 442


RESULT 8
AI050362
LOCUS       AI050362               589 bp    mRNA    linear   EST 09-JUL-1998
DEFINITION  ub30a07.r1 Soares_thymus_2NbMT Mus musculus cDNA clone
            IMAGE:1379220 5' similar to gb:M65291 INTERLEUKIN-12 ALPHA CHAIN
            PRECURSOR (HUMAN); gb:M86672 Mus musculus interleukin 12 p35
            subunit, complete cds (MOUSE);, mRNA sequence.
ACCESSION   AI050362
VERSION     AI050362.1  GI:3299479
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 589)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:901688
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 60.
FEATURES             Location/Qualifiers
     source          1. .589
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1379220"
                     /sex="male"
                     /tissue_type="Thymus"
                     /dev_stage="4 weeks"
                     /lab_host="DH10B"
                     /clone_lib="Soares_thymus_2NbMT"
                     /note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI;
                     1st strand cDNA was primed with a Not I - oligo(dT) primer
```

[5'
TGTTACCAATCTGAAGTGGGAGCGGCCGCGTTTTTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 38.6%; Score 216.4; DB 1; Length 589;
Best Local Similarity 72.5%; Pred. No. 1.6e-52;
Matches 280; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

```
Qy         65 AGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATA 124
              |||||||| |||  ||  ||  ||| ||||||||| | ||||| || ||||||||||| |
Db        109 AGGCCAGAGAAAAACTGAAACATTATTCCTGCACTGCTGAAGACATCGATCATGAAGACA 168

Qy        125 TCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATG 184
              |||||   ||  |||||||||||| || || |||| |||||||||||| ||  || ||| |
Db        169 TCACACGGGACCAAACCAGCACATTGAAGACCTGTTTACCACTGGAACTACACAAGAACG 228

Qy        185 AGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCA 244
              ||||||||||||| | |||||||  |||   | ||| |  ||||| |||||| || |
Db        229 AGAGTTGCCTGGCTACTAGAGAGACTTCTTCCACAACAAGAGGGAGCTGCCTGCCCCCAC 288

Qy        245 GAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGT 304
                |||||  ||||| |||| |||||||||||||| | || ||||||||||||||||||||
Db        289 AGAAGACGTCTTTGATGATGACCCTGTGCCTTGGTAGCATCTATGAGGACTTGAAGATGT 348

Qy        305 ACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCT 364
              |||||   |||||| ||||||| || |||   ||    |   |     |   |||||||
Db        349 ACCAGACAGAGTTCCAGGCCATCAACGCAGCACTTCAGAATCACAACCATCAGCAGATCA 408

Qy        365 TTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACA 424
              |||| ||  |   |||||||   |  || ||||||||| | ||| | ||||||   ||
Db        409 TTCTAGACAAGGGCATGCTGGGTGGCATCGATGAGCTGATGCAGTCTCTGAATCATAATG 468

Qy        425 GTGTGACTGTGCCACAGAACTCCTCC 450
              | | |||| |||  |||||  |  ||
Db        469 GCGAGACTCTGCGCCAGAAACCTCCC 494
```

RESULT 9
BG702253
LOCUS BG702253 812 bp mRNA linear EST 07-MAY-2001
DEFINITION 602683459F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4816118 5', mRNA sequence.
ACCESSION BG702253
VERSION BG702253.1 GI:13973409
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 812)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10714 row: e column: 15
High quality sequence stop: 804.
FEATURES Location/Qualifiers
source 1. .812
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4816118"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_95"
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 38.3%; Score 214.6; DB 2; Length 812;
Best Local Similarity 86.1%; Pred. No. 6.1e-52;
Matches 261; Conservative 0; Mismatches 39; Indels 3; Gaps 2;

```
Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              || |||||||  |||||  |||||||||||| ||||||| | ||| |||||||||  |||
Db        513 GGAATGTTCCCATGCCTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTC 572

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              |||||||||||||||||||||||||||||| | |||||||| |||||||| |||||||||
Db        573 CAGAAGGCCAGACAAACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATCGATCATGAA 632

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              |||||||||||||||||||||||||||||||||||||||| |||||| |||||||||||| |
Db        633 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAG 692

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||      |||||||||| |||| | |||||||||||||||||||||| |
Db        693 AATGAGAGTTGC--TAAATCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGG-C 749

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              |||||||||||||||||||| |  |||||||||||| |||||     ||   |  |||
Db        750 TCCAGAAAGACCTCTTTTATGATGTGCCTGTGCCTTAGTAGTATTATGAAGACTTGAAAG 809

Qy        301 ATG 303
              |||
Db        810 ATG 812
```

RESULT 10
BU698113
LOCUS BU698113 563 bp mRNA linear EST 09-OCT-2002
DEFINITION LL2in12067T7 Hematopoietic Stem Cell Subtracted Library Mus musculus cDNA 5' similar to interleukin 12 p35 subunit, mRNA sequence.
ACCESSION BU698113
VERSION BU698113.1 GI:23610620
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 563)
AUTHORS Phillips,R.L., Ernst,R.E., Brunk,B.P., Ivanova,N., Mahan,M.A., Deanehan,J.K., Moore,K.A., Overton,G.C. and Lemischka,I.R.
TITLE The genetic program of hematopoietic stem cells
JOURNAL Science 288 (5471), 1635-1640 (2000)
PUBMED 10834841
COMMENT Contact: Lemischka, Ihor R.
Department of Molecular Biology
Princeton University
Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544, USA

```
            Tel: 609 258 2838
            Fax: 609 258 2759
            Email: ilemischka@molbio.princeton.edu
            These ESTs are derived from a subtracted cDNA library enriched for
            gene products expressed in day 14-14.5 fetal liver hematopoietic
            stem cells defined as Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E
            (Sca-1)pos
            Seq primer: M13Reverse or T7.
FEATURES              Location/Qualifiers
     source           1. .563
                      /organism="Mus musculus"
                      /mol_type="mRNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /tissue_type="Hematopoietic"
                      /cell_type="Stem Cells; Lineageneg/lo, AA4.1pos, cKitpos,
                      Ly6A/E (Sca-1)pos"
                      /dev_stage="Embryonic day 14-14.5"
                      /lab_host="DH10B"
                      /clone_lib="Hematopoietic Stem Cell Subtracted Library"
                      /note="Organ: Fetal Liver; Vector: Sport 1; Site_1: Sal I;
                      Site_2: Not I; Two directionally cloned cDNA libraries
                      were made from fetal liver  hematopoietic stem cells
                      enriched to be Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E
                      (Sca-1)pos called Scapos and from AA4.1neg fetal liver
                      cells. Subtractive hybridization was  performed by
                      hybridization of the target, Scapos, single stranded cDNA
                      library in pSport1 to  biotinylated RNA transcribed from
                      the driver, AA4.1neg cDNA library in pSport2 with  inserts
                      cloned in the complementary orientation. For detailed
                      protocols and additional  information please see our
                      website at http://stemcell.princeton.edu."
ORIGIN

  Query Match           38.2%;  Score 214.2;  DB 3;  Length 563;
  Best Local Similarity  69.6%;  Pred. No. 7.2e-52;
  Matches  305;  Conservative    0;  Mismatches  129;  Indels    4;  Gaps    1;

Qy         65 AGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATA 124
              |||||||| |||  ||  ||  ||| |||||||| | ||||| || ||||||||||| |
Db        100 AGGCCAGAGAAAAACTGAAACATTATTCCTGCACTGCTGAAGACATCGATCATGAAGACA 159

Qy        125 TCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATG 184
              |||||   ||  |||||||||||| || || |||| |||||||||||| ||  || ||| |
Db        160 TCACACGGGACCAAACCAGCACATTGAAGACCTGTTTACCACTGGAACTACACAAGAACG 219

Qy        185 AGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCA 244
              |||||||||||||| | |||||||  |||   | ||| |  ||||| |||||| || |
Db        220 AGAGTTGCCTGGCTACTAGAGAGACTTCTTCCACAACAAGAGGGAGCTGCCTGCCCCCAC 279

Qy        245 GAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGT 304
                |||||  ||||| |||| |||||||||||| | || ||||||||||||||||||||||
Db        280 AGAAGACGTCTTTGATGATGACCCTGTGCCTTGGTAGCATCTATGAGGACTTGAAGATGT 339

Qy        305 ACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCT 364
              |||||   |||||| |||||||| || |||   ||     |   |      |   |||||||
Db        340 ACCAGACAGAGTTCCAGGCCATCAACGCAGCACTTCAGAATCACAACCATCAGCAGATCA 399

Qy        365 TTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACA 424
              ||||  ||  |   |||||||   || || |||||||||  | |||  | ||||||   ||
Db        400 TTCTAGACAAGGGCATGCTGGTGGCCATCGATGAGCTGATGCAGTCTCTGAATCATAATG 459

Qy        425 GTG----TGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |          || |||| | | || |     |||  | | |||   ||| | |   |||
Db        460 GGNGAGACTCTTGCGCCAGAAACCTTCCTGTGGGAGAAGCAGGACCCTTACAGAGTGAAA 519

Qy        481 ATCAAGCTCTGCATACTT 498
              || |||||||  || | |
Db        520 ATGAAGCTCTTGATTCCT 537


RESULT 11
AJ820622/c
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LOCUS       AJ820622                778 bp    mRNA    linear   EST 12-MAY-2005
DEFINITION  AJ820622 KN206 Bos sp. cDNA clone C0006020h12, mRNA sequence.
ACCESSION   AJ820622
VERSION     AJ820622.1  GI:51888098
KEYWORDS    EST.
SOURCE      Bos sp.
  ORGANISM  Bos sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 778)
  AUTHORS   McGuire,K. and Glass,E.J.
  TITLE     The expanding role of microarrays in the investigation of
            macrophage responses to pathogens
  JOURNAL   Vet. Immunol. Immunopathol. 105 (3-4), 259-275 (2005)
COMMENT     Contact: McGuire K
            Genomics and Genetics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
            Single pass sequencing. Bases called and trimmed with phred
            v0.020425.c. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options. Vector:pBluescriptII(SK+) R. Site
            1:EcoRV(lost) R. Site 2:NotI Seq Primer: T7 Normalised library
            constructed from pooled monocytes from Bos taurus (Holstein) and
            Bos indicus (Sahiwals) cattle subjected to various stimuli,
            including infection with the protozoan parasite Theileria annulata.
FEATURES              Location/Qualifiers
     source           1. .778
                      /organism="Bos sp."
                      /mol_type="mRNA"
                      /db_xref="taxon:29061"
                      /clone="C0006020h12"
                      /tissue_type="blood"
                      /cell_type="bovine monocyte"
                      /clone_lib="KN206"
                      /note="Vector: pBluescriptII(SK+); Site_1: EcoRV(lost);
                      Site_2: NotI; Normalised library constructed from pooled
                      monocytes from Bos taurus (Holstein) and Bos indicus
                      (Sahiwals) cattle subjected to various stimuli, including
                      infection with the protozoan parasite Theileria annulata"
ORIGIN

  Query Match           37.3%;  Score 209.2;  DB 1;  Length 778;
  Best Local Similarity  87.4%;  Pred. No. 2.4e-50;
  Matches  229;  Conservative    0;  Mismatches   33;  Indels    0;  Gaps    0;

Qy        300 GATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCA 359
              |||||||| |||||||| |||||||||||||||||||  | |||||||||| |||||
Db        778 GATGTACCACGTGGAGTTCCAGGCCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCA 719

Qy        360 GATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGT 419
              ||||||||  || || ||||||||| |||||||| ||||||| | |||||||||||| |
Db        718 AATCTTTCTAGACCAGAACATGCTGGCAGCTATTGCTGAGCTGATGCAGGCCCTGAATTT 659

Qy        420 CAACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAA 479
              | |||||| ||||||||||||||||  |||||||| |||||| |||||||| || || ||
Db        658 CGACAGTGAGACTGTGCCACAGAAACCCTCCCTGAAAGAACTGGATTTTTACAAGACAAA 599

Qy        480 AATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAAT 539
              | |||||||||||||| |||||||| || |||||||||||||| ||||||||| | |||||
Db        598 AGTCAAGCTCTGCATCCTTCTTCACGCCTTCAGAATTCGTGCGGTGACCATCGACAGAAT 539

Qy        540 GATGAGCTATCTGAATGCTTCC 561
              |||||||||||||| | |||||
Db        538 GATGAGCTATCTGAGTTCTTCC 517


RESULT 12
BF552757
LOCUS       BF552757                373 bp    mRNA    linear   EST 12-DEC-2000
DEFINITION  UI-R-C0-iz-d-02-0-UI.r1 UI-R-C0 Rattus norvegicus cDNA clone
            UI-R-C0-iz-d-02-0-UI 5', mRNA sequence.
ACCESSION   BF552757
```

```
VERSION     BF552757.1  GI:11662487
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 373)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  PUBMED    8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156  MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            cDNA Library Preparation: M.B. Soares Lab Clone distribution:
            clones will be available through Research Genetics (www.resgen.com)
            This clone is also available through the I.M.A.G.E. Consortium at
            LLNL (info@image.llnl.gov). IMAGE ID= 1782759
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .373
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="UI-R-C0-iz-d-02-0-UI"
                     /dev_stage="adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="UI-R-C0"
                     /note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI;
                     The UI-R-C0 library is a subtracted library derived from
                     the UI-R-A1 and UI-R-E1 libraries. The UI-R-A1 library
                     consisted of a mixture of individually tagged normalized
                     libraries constructed from rat  placenta, adult lung,
                     brain, liver, kidney, heart, spleen, ovary,  and muscle.
                     The UI-R-E1 library  consisted of a mixture of
                     individually tagged normalized libraries constructed from
                     8, 12 and 18-day embryo. The tag is a string of 3-5
                     nucleotides present between the Not I  site and the
                     oligo-dT track which allows identification of the library
                     of origin of a clone within the mixture. The subtracted
                     library (UI-R-C0) was constructed as follows: PCR
                     amplified cDNA inserts from a pool of UI-R-A1 and UI-R-E1
                     clones from which 3' ESTs had been derived was used as a
                     driver in a hybridization with the pooled UI-R-A1 and
                     UI-R-E1 library in the form of single-stranded circles.
                     The remaining single-stranded circles (subtracted library)
                     was purified by hydroxyapatite column chromatography,
                     converted to double-stranded circles and electroporated
                     into DH10B bacteria (Life Technologies) to generate the
                     UI-R-C0 library. This procedure has been previously
                     described (Bonaldo, Lennon and Soares, Genome Research 6:
                     791-806, 1996)"
ORIGIN

  Query Match             35.7%;  Score 200;  DB 7;  Length 373;
  Best Local Similarity   71.5%;  Pred. No. 1e-47;
  Matches  263;  Conservative    0;  Mismatches  105;  Indels    0;  Gaps    0;

Qy        186 GAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAG 245
              ||| |||||||| | | |||||  |||   ||||  |  ||||| |||||| |  |
Db          4 GAGGTGCCTGGCTACTAAAGAGACTTCTTCCATAATAAGAGGGAGCTGCCTGCCTCCACA 63

Qy        246 AAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTA 305
              |||||| ||||| |||| |||||||||||| | || ||||||||||||||||||||||
Db         64 AAAGACTTCTTTGATGATGACCCTGTGCCTTGGTAGCATCTATGAGGACTTGAAGATGTA 123

Qy        306 CCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTT 365
              ||||  |||||| ||||||| ||||||   ||     |   |   | |   |||||||
Db        124 CCAGTCAGAGTTCCAGGCCATAAATGCAGCACTTCAGAGCCACAATCATCAGCAGATCAC 183

Qy        366 TCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAG 425
              ||||||   |||||||||||  ||||||||||||||  | | | | ||||||  || | |
Db        184 TCTGGACAGAAACATGCTGATGGCTATTGATGAGCTAATGCGGTCTCTGAATCACAGCGG 243

Qy        426 TGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAA 485
              | || | |||  |||||  |  || ||| |||| | |||  ||| | |   || || ||
Db        244 CGAGATTCTGCACCAGAAAGCTCCCATGGGAGAAGCAGATCCTTACAGAGTGAAGATGAA 303

Qy        486 GCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAG 545
              |||||| || || || ||||| ||||| |  || |   |||| ||||| ||  ||||||
Db        304 GCTCTGTATCCTGCTCCATGCCTTCAGCACACGCGTCATGACTATCAACAGGGTGATGAA 363

Qy        546 CTATCTGA 553
              ||||||||
Db        364 CTATCTGA 371


RESULT 13
BU699383
LOCUS       BU699383                561 bp    mRNA    linear   EST 09-OCT-2002
DEFINITION  LL2in11573T7 Hematopoietic Stem Cell Subtracted Library Mus
            musculus cDNA 5' similar to interleukin 12 p35 subunit, mRNA
            sequence.
ACCESSION   BU699383
VERSION     BU699383.1  GI:23615967
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 561)
  AUTHORS   Phillips,R.L., Ernst,R.E., Brunk,B.P., Ivanova,N., Mahan,M.A.,
            Deanehan,J.K., Moore,K.A., Overton,G.C. and Lemischka,I.R.
  TITLE     The genetic program of hematopoietic stem cells
  JOURNAL   Science 288 (5471), 1635-1640 (2000)
  PUBMED    10834841
COMMENT     Contact: Lemischka, Ihor R.
            Department of Molecular Biology
            Princeton University
            Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544, USA
            Tel: 609 258 2838
            Fax: 609 258 2759
            Email: ilemischka@molbio.princeton.edu
            These ESTs are derived from a subtracted cDNA library enriched for
            gene products expressed in day 14-14.5 fetal liver hematopoietic
            stem cells defined as Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E
            (Sca-1)pos
            Seq primer: M13Reverse or T7.
FEATURES             Location/Qualifiers
     source          1. .561
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /tissue_type="Hematopoietic"
                     /cell_type="Stem Cells; Lineageneg/lo, AA4.1pos, cKitpos,
                     Ly6A/E (Sca-1)pos"
                     /dev_stage="Embryonic day 14-14.5"
                     /lab_host="DH10B"
                     /clone_lib="Hematopoietic Stem Cell Subtracted Library"
                     /note="Organ: Fetal Liver; Vector: Sport 1; Site_1: Sal I;
                     Site_2: Not I; Two directionally cloned cDNA libraries
                     were made from fetal liver  hematopoietic stem cells
                     enriched to be Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E
                     (Sca-1)pos called Scapos and from AA4.1neg fetal liver
                     cells. Subtractive hybridization was  performed by
                     hybridization of the target, Scapos, single stranded cDNA
                     library in pSport1 to  biotinylated RNA transcribed from
```

the driver, AA4.1neg cDNA library in pSport2 with inserts cloned in the complementary orientation. For detailed protocols and additional information please see our website at http://stemcell.princeton.edu."

ORIGIN

Query Match 33.9%; Score 190; DB 3; Length 561;
Best Local Similarity 68.2%; Pred. No. 1.1e-44;
Matches 275; Conservative 0; Mismatches 125; Indels 3; Gaps 1;

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Qy        110 TTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGG 169
              | |||||||||||| ||||||   ||  |||||||||||| || || |||| ||||||||||
Db        129 TCGATCATGAAGACATCACACGGGACCAAACCAGCACATTGAAGACCTGTTTACCACTGG 188

Qy        170 AATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGA 229
              || ||  || ||| |||||||||||||| | |||||||  |||   | ||| |  ||||
Db        189 AACTACACAAGAACGAGAGTTGCCTGGCTACTAGAGAGACTTCTTCCACAACAAGAGGGA 248

Qy        230 GTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATG 289
              | ||||| || |    ||||| ||||| |||| |||||||||||| | || |||||||
Db        249 GCTGCCTGCCCCCACAGAAGACGTCTTTGATGATGACCCTGTGCCTTGGTAGCATCTATG 308

Qy        290 AGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATC 349
              ||||||||||||||||||||   |||||| ||||||| || |||   ||    |   |
Db        309 AGGACTTGAAGATGTACCAGACAGAGTTCCAGGCCATCAACGCAGCACTTCAGAATCACA 368

Qy        350 CTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGG 409
                |   ||||||| |||| ||  |   |||||||   |  || ||||||||| | |||
Db        369 ACCATCAGCAGATCATTCTAGACAAGGGCATGCTGGTGGGCATCGATGAGCTGATGCAGT 428

Qy        410 CCCTGAATGTCAA---CAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATT 466
              | ||| ||   ||      | |   ||| | || | | |||||    ||   | | |
Db        429 CTCTGGATCATAATGGGCGAGACTCTGCGGCAAAAANCTCCTGTNGGGNGAAGCAGANCC 488

Qy        467 TTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTT 509
              |||| | |    |||| |||||||| ||      ||   |||||
Db        489 TTTACAGAGTGGAAATGAAGCTCTGNATCTGCTTTACGGCTTT 531
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RESULT 14
CB168830/c
LOCUS CB168830 777 bp mRNA linear EST 30-JAN-2003
DEFINITION CWI602769160.R1 CSEQFXL41 testes Bos taurus cDNA, mRNA sequence.
ACCESSION CB168830
VERSION CB168830.1 GI:28154956
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 777)
AUTHORS Adelson,D.L. and Gill,C.A.
TITLE Bovine ESTs (Adelson and Gill)
JOURNAL Unpublished (2003)
COMMENT Contact: David L. Adelson
Animal Breeding and Genetics
Texas A&M University
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471, USA
Tel: 9798452616
Fax: 9798456970
Email: david.adelson@tamu.edu.
FEATURES Location/Qualifiers
source 1. .777
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="testes"
/clone_lib="CSEQFXL41 testes"
/note="Organ: testes; Vector: pBluescript SK+; Site_1: NotI; Site_2: EcoRI; sequence 5' of the insert (5'-NNN. . .NNNinsert)
GCGAATTGGAGCTCCACCGCGGTGGCGGCCGCGGCTCGAG. Sequence 3' of the inserts (AAGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG. non-normalized library, sequenced 3' with M13R primer."

ORIGIN

Query Match 31.3%; Score 175.4; DB 4; Length 777;
Best Local Similarity 86.5%; Pred. No. 2.5e-40;
Matches 205; Conservative 0; Mismatches 31; Indels 1; Gaps 1;

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Qy        325 ATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 384
              ||||||||||||||  | |||||||||||| | ||| |||||||| || || |||||||||
Db        777 ATGAATGCAAAGCTTCTGATGGATCCTAAGA-GCAAATCTTTCTAGACCAGAACATGCTG 719

Qy        385 ACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAAC 444
              ||||||||| ||||||| | |||||||||||| || |||||| ||||||||||||||||
Db        718 GCAGCTATTGCTGAGCTGATGCAGGCCCTGAATTTCGACAGTGAGACTGTGCCACAGAAA 659

Qy        445 TCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 504
              |||||||| |||||| ||||||||| || || ||| |||||||||||| ||||||||
Db        658 CCCTCCCTGAAAGAACTGGATTTTTACAAGACAAAAGTCAAGCTCTGCATCCTTCTTCAC 599

Qy        505 GCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 561
              || |||||||||||||| ||||||||| | |||||||||||||||||||| | |||||
Db        598 GCCTTCAGAATTCGTGCGGTGACCATCGACAGAATGATGAGCTATCTGAGTTCTTCC 542
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RESULT 15
CB801533
LOCUS CB801533 412 bp mRNA linear EST 16-MAY-2003
DEFINITION AMGNNUC:SRPB2-00244-H1-A srpb2 (10220) Rattus norvegicus cDNA clone srpb2-00244-h1 5', mRNA sequence.
ACCESSION CB801533
VERSION CB801533.1 GI:29914888
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 412)
AUTHORS Amgen EST Program.
TITLE Amgen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00244 row: h column: 1.
FEATURES Location/Qualifiers
source 1. .412
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="srpb2-00244-h1"
/tissue_type="prostate tissue"
/clone_lib="srpb2 (10220)"
/note="Vector: pSPORT1; Site_1: Sal1; Site_2: NotI; rat prostate normalized double selected poly(A+) mRNA size fraction > 1 kb"

ORIGIN

Query Match 31.2%; Score 175.2; DB 4; Length 412;
Best Local Similarity 69.5%; Pred. No. 2.4e-40;
Matches 248; Conservative 0; Mismatches 108; Indels 1; Gaps 1;

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Qy        205 GAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACG 264
              | |  |  | |  ||   |  ||||| ||||||  |  |   |||||| ||||| |||| |
Db          5 GCGTCCGNTNTCCTATANAGAGGGAGCTGCCTGCCTCCACAAAAGACTTCTTTGATGATG 64

Qy        265 ACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCC 324
              |||||||||||| | || |||||||||||||| |||||||| ||||   |||||| |||||
Db         65 ACCCTGTGCCTTGGTAGCATCTATGAGGACTNGAAGATGTNCCAGTCAGAGTTCCAGGCC 124
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Qy        325 ATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 384
              || ||||||   ||    |   |   | |   |||||||  ||||||   ||||||||||
Db        125 ATAAATGCAGCACTTCAGAGCCACAATCATCAGCAGATCACTCTGGACAGAAACATGCTG 184

Qy        385 ACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAAC 444
              |  ||||||||||||||  | | ||| ||||||  || | | | |||| |||  |||||
Db        185 ATGGCTATTGATGAGCTAATGC-GGCTCTGAATCACAGCGGCGAGACTCTGCACCAGAAA 243

Qy        445 TCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 504
              |  || ||| |||| | |||  ||| | |   || || |||||||| || || || |||
Db        244 GCTCCCATGGGAGAAGCAGATCCTTACAGAGTGAAGATGAAGCTCTGTATCCTGCTCCAT 303

Qy        505 GCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 561
              || ||||| |  || |   |||| ||||| ||  |||||| ||||||||   | |||
Db        304 GCCTTCAGCACCCGCGTCATGACTATCAACAGGGTGATGAACTATCTGAGCTCCTCC 360
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Search completed: June 10, 2006, 17:40:16
Job time : 3276.2 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 10, 2006, 04:51:14 ; Search time 121.102 Seconds
(without alignments)
8667.862 Million cell updates/sec

Title: US-10-821-670A-101
Perfect score: 561
Sequence: 1 gggatgttccagtgcctcaa.....tgagctatctgaatgcttcc 561

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
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9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	561	100.0	561	3	US-09-917-265A-101	Sequence 101, App
c	2	561	100.0	561	3	US-09-917-265A-103	Sequence 103, App
	3	559.4	99.7	666	3	US-09-917-265A-32	Sequence 32, Appl
c	4	559.4	99.7	666	3	US-09-917-265A-34	Sequence 34, Appl
	5	559.4	99.7	1533	3	US-09-917-265A-43	Sequence 43, Appl
c	6	559.4	99.7	1533	3	US-09-917-265A-45	Sequence 45, Appl
	7	559.4	99.7	1599	3	US-09-917-265A-38	Sequence 38, Appl
c	8	559.4	99.7	1599	3	US-09-917-265A-40	Sequence 40, Appl
	9	557.8	99.4	591	3	US-09-917-265A-35	Sequence 35, Appl
c	10	557.8	99.4	591	3	US-09-917-265A-37	Sequence 37, Appl
	11	554.6	98.9	591	3	US-09-011-143-9	Sequence 9, Appli
	12	554.6	98.9	591	3	US-09-302-495-9	Sequence 9, Appli
	13	554.6	98.9	591	3	US-10-079-616-9	Sequence 9, Appli
	14	554.6	98.9	1441	3	US-09-011-143-8	Sequence 8, Appli
	15	554.6	98.9	1441	3	US-09-302-495-8	Sequence 8, Appli
	16	554.6	98.9	1441	3	US-10-079-616-8	Sequence 8, Appli
	17	545	97.1	689	3	US-09-011-143-26	Sequence 26, Appl
	18	545	97.1	689	3	US-09-302-495-26	Sequence 26, Appl
	19	545	97.1	689	3	US-10-079-616-26	Sequence 26, Appl
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	22	511.4	91.2	666	3	US-09-917-265A-46	Sequence 46, Appl
c	23	511.4	91.2	666	3	US-09-917-265A-48	Sequence 48, Appl
	24	511.4	91.2	669	3	US-09-079-984A-12	Sequence 12, Appl
	25	511.4	91.2	669	3	US-09-390-729-12	Sequence 12, Appl
	26	511.4	91.2	1455	3	US-09-917-265A-104	Sequence 104, App
c	27	511.4	91.2	1455	3	US-09-917-265A-106	Sequence 106, App
	28	508.2	90.6	669	3	US-09-079-984A-2	Sequence 2, Appli
	29	508.2	90.6	669	3	US-09-390-729-2	Sequence 2, Appli
	30	500.2	89.2	1533	3	US-09-917-265A-66	Sequence 66, Appl
c	31	500.2	89.2	1533	3	US-09-917-265A-68	Sequence 68, Appl
	32	500.2	89.2	1599	3	US-09-917-265A-61	Sequence 61, Appl
c	33	500.2	89.2	1599	3	US-09-917-265A-63	Sequence 63, Appl
	34	484.2	86.3	660	2	US-08-186-529-3	Sequence 3, Appli
	35	484.2	86.3	660	2	US-08-640-386A-3	Sequence 3, Appli
	36	484.2	86.3	762	3	US-08-848-760B-21	Sequence 21, Appl
	37	484.2	86.3	762	3	US-09-826-025-21	Sequence 21, Appl
	38	484.2	86.3	762	5	US-09-543-679A-2890	Sequence 2890, Ap
	39	484.2	86.3	1019	3	US-09-949-016-2462	Sequence 2462, Ap
	40	484.2	86.3	1316	2	US-08-684-687-3	Sequence 3, Appli
	41	484.2	86.3	1316	3	US-09-851-520-3	Sequence 3, Appli
	42	484.2	86.3	1364	2	US-08-265-087-3	Sequence 3, Appli
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	44	484.2	86.3	1364	2	US-08-965-688-3	Sequence 3, Appli
	45	484.2	86.3	1364	3	US-09-260-173-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-917-265A-101
; Sequence 101, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 101
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(561)
US-09-917-265A-101

Query Match 100.0%; Score 561; DB 3; Length 561;
Best Local Similarity 100.0%; Pred. No. 4.1e-178;
Matches 561; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
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Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
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Db        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300

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Db        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
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Db        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540

Qy        541 ATGAGCTATCTGAATGCTTCC 561
                |||||||||||||||||||||
Db        541 ATGAGCTATCTGAATGCTTCC 561


RESULT 2
US-09-917-265A-103/c
; Sequence 103, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 103
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-103

  Query Match            100.0%;  Score 561;  DB 3;  Length 561;
  Best Local Similarity  100.0%;  Pred. No. 4.1e-178;
  Matches  561;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
                |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1


RESULT 3
US-09-917-265A-32
; Sequence 32, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
US-09-917-265A-32

  Query Match            99.7%;  Score 559.4;  DB 3;  Length 666;
  Best Local Similarity  99.8%;  Pred. No. 1.6e-177;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
                || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 165

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 225

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 285

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 345

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 405

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 465

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        466 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 525

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 585

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 645

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db        646 ATGAGCTATCTGAATGCTTCC 666


RESULT 4
US-09-917-265A-34/c
; Sequence 34, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-34

  Query Match             99.7%;  Score 559.4;  DB 3;  Length 666;
  Best Local Similarity   99.8%;  Pred. No. 1.6e-177;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1


RESULT 5
US-09-917-265A-43
; Sequence 43, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-09-917-265A-43

  Query Match             99.7%;  Score 559.4;  DB 3;  Length 1533;
  Best Local Similarity   99.8%;  Pred. No. 2.6e-177;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1032

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1092

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1093 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1152

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1153 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1212

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1213 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1272

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1273 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1332

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1333 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1392

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1393 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1452

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1453 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1512
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Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db       1513 ATGAGCTATCTGAATGCTTCC 1533
```

RESULT 6
US-09-917-265A-45/c
; Sequence 45, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265A-45

Query Match 99.7%; Score 559.4; DB 3; Length 1533;
Best Local Similarity 99.8%; Pred. No. 2.6e-177;
Matches 560; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1
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RESULT 7
US-09-917-265A-38
; Sequence 38, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1599)
US-09-917-265A-38

Query Match 99.7%; Score 559.4; DB 3; Length 1599;
Best Local Similarity 99.8%; Pred. No. 2.7e-177;
Matches 560; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1098

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1158

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1218

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1219 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1278

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1338

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1398

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1458

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1459 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1518

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1519 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1578

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db       1579 ATGAGCTATCTGAATGCTTCC 1599
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RESULT 8
US-09-917-265A-40/c
; Sequence 40, Application US/09917265A

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; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-40

  Query Match             99.7%;  Score 559.4;  DB 3;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 2.7e-177;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1


RESULT 9
US-09-917-265A-35
; Sequence 35, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(591)
US-09-917-265A-35

  Query Match             99.4%;  Score 557.8;  DB 3;  Length 591;
  Best Local Similarity   99.6%;  Pred. No. 5.1e-177;
  Matches  559;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 90

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 210

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 390

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 450

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        451 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 510

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 570

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db        571 ATGAGCTATCTGAATGCTTCC 591


RESULT 10
US-09-917-265A-37/c
; Sequence 37, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
```

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;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-37

  Query Match             99.4%;  Score 557.8;  DB 3;  Length 591;
  Best Local Similarity   99.6%;  Pred. No. 5.1e-177;
  Matches  559;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1


RESULT 11
US-09-011-143-9
; Sequence 9, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  591 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-9

  Query Match             98.9%;  Score 554.6;  DB 3;  Length 591;
  Best Local Similarity   99.3%;  Pred. No. 6.1e-176;
  Matches  557;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 90

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 210

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 390

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 450

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        451 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 510

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 570

Qy        541 ATGAGCTATCTGAATGCTTCC 561
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Db        571 ATGAGCTACCTGAATTCTTCC 591


RESULT 12
US-09-302-495-9
; Sequence 9, Application US/09302495
; Patent No. 6518045
;  GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/302,495
;            FILING DATE: 30-Apr-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;  INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 591 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-302-495-9

  Query Match             98.9%;  Score 554.6;  DB 3;  Length 591;
  Best Local Similarity   99.3%;  Pred. No. 6.1e-176;
  Matches  557;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 90

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 210

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 390

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 450

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        451 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAA 510

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 570

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||| |||||| |||||
Db        571 ATGAGCTACCTGAATTCTTCC 591


RESULT 13
US-10-079-616-9
; Sequence 9, Application US/10079616
; Patent No. 6566097
;  GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;  INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 591 base pairs
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;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-079-616-9

  Query Match            98.9%;  Score 554.6;  DB 3;  Length 591;
  Best Local Similarity  99.3%;  Pred. No. 6.1e-176;
  Matches  557;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
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Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
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Db         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
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Db        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 210

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
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Db        211 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 270

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
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Db        271 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 330

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
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Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
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Qy        541 ATGAGCTATCTGAATGCTTCC 561
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RESULT 14
US-09-011-143-8
; Sequence 8, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1441 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-8

  Query Match            98.9%;  Score 554.6;  DB 3;  Length 1441;
  Best Local Similarity  99.3%;  Pred. No. 1e-175;
  Matches  557;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

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Db        248 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 307

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
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Db        308 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 367

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
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Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
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Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
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Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
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Qy        541 ATGAGCTATCTGAATGCTTCC 561
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Db        788 ATGAGCTACCTGAATTCTTCC 808
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; Sequence 8, Application US/09302495
; Patent No. 6518045
;  GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/302,495
;            FILING DATE: 30-Apr-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;  INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1441 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-302-495-8

  Query Match             98.9%;  Score 554.6;  DB 3;  Length 1441;
  Best Local Similarity   99.3%;  Pred. No. 1e-175;
  Matches  557;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
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Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
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Qy        541 ATGAGCTATCTGAATGCTTCC 561
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	2	561	100.0	561	3	US-09-917-265-103	Sequence 103, App
	3	561	100.0	561	9	US-10-821-670-101	Sequence 101, App
c	4	561	100.0	561	9	US-10-821-670-103	Sequence 103, App
	5	559.4	99.7	666	3	US-09-917-265-32	Sequence 32, Appl
c	6	559.4	99.7	666	3	US-09-917-265-34	Sequence 34, Appl
	7	559.4	99.7	666	9	US-10-821-670-32	Sequence 32, Appl
c	8	559.4	99.7	666	9	US-10-821-670-34	Sequence 34, Appl
	9	559.4	99.7	1533	3	US-09-917-265-43	Sequence 43, Appl
c	10	559.4	99.7	1533	3	US-09-917-265-45	Sequence 45, Appl
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c	12	559.4	99.7	1533	9	US-10-821-670-45	Sequence 45, Appl
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c	14	559.4	99.7	1599	3	US-09-917-265-40	Sequence 40, Appl
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	21	554.6	98.9	591	6	US-10-079-616-9	Sequence 9, Appli
	22	554.6	98.9	1441	6	US-10-079-616-8	Sequence 8, Appli
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c	42	500.2	89.2	1599	3	US-09-917-265-63	Sequence 63, Appl
	43	500.2	89.2	1599	9	US-10-821-670-61	Sequence 61, Appl
c	44	500.2	89.2	1599	9	US-10-821-670-63	Sequence 63, Appl
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ALIGNMENTS

RESULT 1
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; Sequence 101, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(561)
; OTHER INFORMATION:
US-09-917-265-101

Query Match 100.0%; Score 561; DB 3; Length 561;
Best Local Similarity 100.0%; Pred. No. 7.9e-169;
Matches 561; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
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Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540

Qy        541 ATGAGCTATCTGAATGCTTCC 561
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Db        541 ATGAGCTATCTGAATGCTTCC 561
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RESULT 2
US-09-917-265-103/c
; Sequence 103, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 103
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265-103

Query Match 100.0%; Score 561; DB 3; Length 561;
Best Local Similarity 100.0%; Pred. No. 7.9e-169;
Matches 561; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1
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RESULT 3
US-10-821-670-101
; Sequence 101, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 101
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(561)
US-10-821-670-101

Query Match 100.0%; Score 561; DB 9; Length 561;
Best Local Similarity 100.0%; Pred. No. 7.9e-169;
Matches 561; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
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Db        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540

Qy        541 ATGAGCTATCTGAATGCTTCC 561
                 |||||||||||||||||||||
Db        541 ATGAGCTATCTGAATGCTTCC 561


RESULT 4
US-10-821-670-103/c
; Sequence 103, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 103
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-103

  Query Match            100.0%;  Score 561;  DB 9;  Length 561;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-169;
  Matches  561;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
                 |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1


RESULT 5
US-09-917-265-32
; Sequence 32, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
;   OTHER INFORMATION:
US-09-917-265-32

  Query Match            99.7%;  Score 559.4;  DB 3;  Length 666;
  Best Local Similarity   99.8%;  Pred. No. 2.8e-168;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
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Db        106 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 165

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 225

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 285

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 345

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 405

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 465

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 525

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        526 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 585

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 645

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db        646 ATGAGCTATCTGAATGCTTCC 666


RESULT 6
US-09-917-265-34/c
; Sequence 34, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-34

  Query Match             99.7%;  Score 559.4;  DB 3;  Length 666;
  Best Local Similarity   99.8%;  Pred. No. 2.8e-168;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1


RESULT 7
US-10-821-670-32
; Sequence 32, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
US-10-821-670-32

  Query Match             99.7%;  Score 559.4;  DB 9;  Length 666;
  Best Local Similarity   99.8%;  Pred. No. 2.8e-168;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 165

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 225

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 285

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 345

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 405

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 465

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 525

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 585

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 645

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db        646 ATGAGCTATCTGAATGCTTCC 666
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RESULT 8
US-10-821-670-34/c
; Sequence 34, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-34

  Query Match             99.7%;  Score 559.4;  DB 9;  Length 666;
  Best Local Similarity   99.8%;  Pred. No. 2.8e-168;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1


RESULT 9
US-09-917-265-43
; Sequence 43, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
;   OTHER INFORMATION:
US-09-917-265-43

  Query Match             99.7%;  Score 559.4;  DB 3;  Length 1533;
  Best Local Similarity   99.8%;  Pred. No. 4.4e-168;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1032

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1092

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1093 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1152

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1153 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1212

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1213 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1272

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1273 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1332

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1333 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1392

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1393 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1452

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1453 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1512

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db       1513 ATGAGCTATCTGAATGCTTCC 1533


RESULT 10
US-09-917-265-45/c
; Sequence 45, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
```

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;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-45

  Query Match             99.7%;  Score 559.4;  DB 3;  Length 1533;
  Best Local Similarity   99.8%;  Pred. No. 4.4e-168;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1


RESULT 11
US-10-821-670-43
; Sequence 43, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-10-821-670-43

  Query Match             99.7%;  Score 559.4;  DB 9;  Length 1533;
  Best Local Similarity   99.8%;  Pred. No. 4.4e-168;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1032

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1092

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1093 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1152

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1153 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1212

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1213 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1272

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1273 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1332

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1333 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1392

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1393 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1452

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1453 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1512

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db       1513 ATGAGCTATCTGAATGCTTCC 1533


RESULT 12
US-10-821-670-45/c
; Sequence 45, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 1533
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;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-45

  Query Match             99.7%;  Score 559.4;  DB 9;  Length 1533;
  Best Local Similarity   99.8%;  Pred. No. 4.4e-168;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 262

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        141 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 82

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 22

Qy        541 ATGAGCTATCTGAATGCTTCC 561
              |||||||||||||||||||||
Db         21 ATGAGCTATCTGAATGCTTCC 1


RESULT 13
US-09-917-265-38
; Sequence 38, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
US-09-917-265-38

  Query Match             99.7%;  Score 559.4;  DB 3;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 4.5e-168;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1098

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 1158

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 1218

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1219 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 1278

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 1338

Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1398

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1458

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1459 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1518

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
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Db       1519 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1578

Qy        541 ATGAGCTATCTGAATGCTTCC 561
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Db       1579 ATGAGCTATCTGAATGCTTCC 1599


RESULT 14
US-09-917-265-40/c
; Sequence 40, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-40

  Query Match             99.7%;  Score 559.4;  DB 3;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 4.5e-168;
  Matches  560;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
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Db        561 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 502

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
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Db        501 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 442

Qy        121 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 180
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Db        441 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 382

Qy        181 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 240
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Db        381 AATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCC 322

Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
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Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
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Db        261 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 202

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
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Db        201 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 142

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
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Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
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Qy        541 ATGAGCTATCTGAATGCTTCC 561
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RESULT 15
US-10-821-670-38
; Sequence 38, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1599)
US-10-821-670-38

Query Match 99.7%; Score 559.4; DB 9; Length 1599;
Best Local Similarity 99.8%; Pred. No. 4.5e-168;
Matches 560; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 60
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Db       1039 GGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTT 1098

Qy         61 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 120
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Qy        241 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 300
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Qy        301 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 360
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Db       1339 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 1398

Qy        361 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 420
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Db       1399 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 1458

Qy        421 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 480
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Db       1459 AACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 1518

Qy        481 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 540
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Db       1519 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 1578

Qy        541 ATGAGCTATCTGAATGCTTCC 561
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Search completed: June 10, 2006, 18:16:34
Job time : 640.581 secs

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 10, 2006, 01:16:39 ; Search time 169.396 Seconds
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Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	2	1757	100.0	985	3	US-09-917-265A-57	Sequence 57, Appl
	3	1757	100.0	987	3	US-09-917-265A-29	Sequence 29, Appl
c	4	1757	100.0	987	3	US-09-917-265A-31	Sequence 31, Appl
	5	1751	99.7	2193	3	US-09-011-143-5	Sequence 5, Appli
	6	1751	99.7	2193	3	US-09-302-495-5	Sequence 5, Appli
	7	1751	99.7	2193	3	US-10-079-616-5	Sequence 5, Appli
	8	1743	99.2	1599	3	US-09-917-265A-38	Sequence 38, Appl
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	13	1653	94.1	990	3	US-09-390-729-11	Sequence 11, Appl
	14	1653	94.1	1599	3	US-09-917-265A-61	Sequence 61, Appl
c	15	1653	94.1	1599	3	US-09-917-265A-63	Sequence 63, Appl
	16	1653	94.1	2267	3	US-09-917-265A-107	Sequence 107, App
c	17	1653	94.1	2267	3	US-09-917-265A-109	Sequence 109, App
	18	1643	93.5	921	3	US-09-011-143-6	Sequence 6, Appli
	19	1643	93.5	921	3	US-09-011-143-7	Sequence 7, Appli
	20	1643	93.5	921	3	US-09-302-495-6	Sequence 6, Appli
	21	1643	93.5	921	3	US-09-302-495-7	Sequence 7, Appli
	22	1643	93.5	921	3	US-10-079-616-6	Sequence 6, Appli
	23	1643	93.5	921	3	US-10-079-616-7	Sequence 7, Appli
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c	25	1635	93.1	921	3	US-09-917-265A-28	Sequence 28, Appl
	26	1635	93.1	1533	3	US-09-917-265A-43	Sequence 43, Appl
c	27	1635	93.1	1533	3	US-09-917-265A-45	Sequence 45, Appl
	28	1620	92.2	990	3	US-09-079-984A-1	Sequence 1, Appli
	29	1620	92.2	990	3	US-09-390-729-1	Sequence 1, Appli
	30	1550	88.2	921	3	US-09-917-265A-52	Sequence 52, Appl
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	32	1550	88.2	1533	3	US-09-917-265A-66	Sequence 66, Appl
c	33	1550	88.2	1533	3	US-09-917-265A-68	Sequence 68, Appl
	34	1498.5	85.3	1623	2	US-08-751-767A-9	Sequence 9, Appli
	35	1498.5	85.3	6139	2	US-08-751-767A-7	Sequence 7, Appli
	36	1497.5	85.2	987	2	US-08-186-529-1	Sequence 1, Appli
	37	1497.5	85.2	987	2	US-08-640-386A-1	Sequence 1, Appli
	38	1497.5	85.2	1018	2	US-08-184-009-194	Sequence 194, App
	39	1497.5	85.2	1018	2	US-08-458-356-194	Sequence 194, App
	40	1497.5	85.2	1018	3	US-08-460-736-194	Sequence 194, App
	41	1497.5	85.2	1018	3	US-09-535-370-194	Sequence 194, App
	42	1497.5	85.2	1018	3	US-09-663-667-194	Sequence 194, App
	43	1497.5	85.2	1389	3	US-09-634-368-4	Sequence 4, Appli
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	45	1497.5	85.2	2362	2	US-08-265-087-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-917-265A-55
; Sequence 55, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
; LENGTH: 985
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(984)
US-09-917-265A-55

Alignment Scores:

Pred. No.:	6.13e-201	Length:	985
Score:	1757.00	Matches:	328
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
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US-10-821-670A-56 (1-328) x US-09-917-265A-55 (1-985)

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Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
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Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
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Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
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Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
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Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
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RESULT 2
US-09-917-265A-57/c

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; Sequence 57, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-57
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Alignment Scores:

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Best Local Similarity:	100.0%	Mismatches:	0
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Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326
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Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGC 2
```

RESULT 3
US-09-917-265A-29
; Sequence 29, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(987)
US-09-917-265A-29

Alignment Scores:

Pred. No.:	6.15e-201	Length:	987
Score:	1757.00	Matches:	328
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-56 (1-328) x US-09-917-265A-29 (1-987)

```
Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984
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RESULT 4
US-09-917-265A-31/c
; Sequence 31, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 987

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;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-31

Alignment Scores:
Pred. No.:              6.15e-201       Length:         987
Score:                  1757.00         Matches:        328
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-56 (1-328) x US-09-917-265A-31 (1-987)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGC 4

RESULT 5
US-09-011-143-5
; Sequence 5, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2193 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-5

Alignment Scores:
Pred. No.:              1.14e-199       Length:         2193
Score:                  1751.00         Matches:        327
Percent Similarity:     99.7%           Conservative:   0
Best Local Similarity:  99.7%           Mismatches:     1
Query Match:            99.7%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-56 (1-328) x US-09-011-143-5 (1-2193)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db         64 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTACCTGGTTTTGCTGGCACCTCCTCTC 123
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Qy          21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         124 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 183

Qy          41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         184 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 243

Qy          61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         244 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 303

Qy          81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         304 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 363

Qy         101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         364 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 423

Qy         121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         424 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 483

Qy         141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         484 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 543

Qy         161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         544 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 603

Qy         181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         604 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 663

Qy         201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         664 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 723

Qy         221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         724 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 783

Qy         241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         784 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 843

Qy         261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         844 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 903

Qy         281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         904 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 963

Qy         301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         964 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 1023

Qy         321 SerAsnTrpAlaSerValSerCys 328
               |||||||||||||||||||||||
Db        1024 AGCAACTGGGCATCCGTGTCCTGC 1047

RESULT 6
US-09-302-495-5
; Sequence 5, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2193 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-302-495-5

Alignment Scores:
Pred. No.:                1.14e-199      Length:          2193
Score:                    1751.00        Matches:         327
Percent Similarity:       99.7%          Conservative:    0
Best Local Similarity:    99.7%          Mismatches:      1
Query Match:              99.7%          Indels:          0
DB:                       3              Gaps:            0

US-10-821-670A-56 (1-328) x US-09-302-495-5 (1-2193)

Qy           1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
               ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db          64 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTACCTGGTTTTGCTGGCACCTCCTCTC 123

Qy          21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         124 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 183

Qy          41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         184 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 243

Qy          61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         244 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 303

Qy          81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         304 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 363
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Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
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Db        364 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 423

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 483

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
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Db        484 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 543

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
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Db        544 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 603

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
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Db        604 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 663

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
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Db        664 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 723

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 783

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 843

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 903

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 963

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 1023

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db       1024 AGCAACTGGGCATCCGTGTCCTGC 1047

RESULT 7
US-10-079-616-5
; Sequence 5, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2193 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-079-616-5

Alignment Scores:
Pred. No.:                1.14e-199      Length:          2193
Score:                    1751.00        Matches:         327
Percent Similarity:       99.7%          Conservative:    0
Best Local Similarity:    99.7%          Mismatches:      1
Query Match:              99.7%          Indels:          0
DB:                       3              Gaps:            0

US-10-821-670A-56 (1-328) x US-10-079-616-5 (1-2193)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db         64 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTACCTGGTTTTGCTGGCACCTCCTCTC 123

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
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Db        124 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 183

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 243

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 303

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 363

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
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Db        364 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 423

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
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Db        424 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 483

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 543

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 603
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Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 663

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 723

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 783

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
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Db        784 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 843

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 903

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
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Db        904 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 963

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 1023

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||||
Db       1024 AGCAACTGGGCATCCGTGTCCTGC 1047
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RESULT 8
US-09-917-265A-38
; Sequence 38, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1599)
US-09-917-265A-38

Alignment Scores:

Pred. No.:	6.33e-199	Length:	1599
Score:	1743.00	Matches:	326
Percent Similarity:	99.4%	Conservative:	0
Best Local Similarity:	99.4%	Mismatches:	2
Query Match:	99.2%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-56 (1-328) x US-09-917-265A-38 (1-1599)

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Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
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Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
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Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              |||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
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Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
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Db        961 AGCAACTGGGCATCCGTGTCCTGC 984
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RESULT 9
US-09-917-265A-40/c
; Sequence 40, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A

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;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-40

Alignment Scores:
Pred. No.:              6.33e-199       Length:         1599
Score:                  1743.00         Matches:        326
Percent Similarity:     99.4%           Conservative:   0
Best Local Similarity:  99.4%           Mismatches:     2
Query Match:            99.2%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-56 (1-328) x US-09-917-265A-40 (1-1599)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||    ||||||||||||||||||||||||||||
Db       1599 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 1540

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
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Db       1539 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 1420

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1359 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 1300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1299 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 1240

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1179 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 1120

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db       1119 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 1060

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        999 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 940

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        939 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 880

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        879 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 820

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 760

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        759 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 640

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db        639 AGCAACTGGGCATCCGTGTCCTGC 616

RESULT 10
US-09-917-265A-58
; Sequence 58, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
US-09-917-265A-58

Alignment Scores:
Pred. No.:              1.9e-188        Length:         987
Score:                  1653.00         Matches:        307
Percent Similarity:     96.6%           Conservative:   10
Best Local Similarity:  93.6%           Mismatches:     11
Query Match:            94.1%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-56 (1-328) x US-09-917-265A-58 (1-987)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||:::||||||||||||||||||||||||||||||
Db          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||:::||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||   ||||||||||||||||||||||||||||||||:::|||||||||   |||
Db        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
                  ||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
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Db        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              |||   ||||||||||||||||||||||||||||||   ||||||||||||||:::|||
Db        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||   :::|||   ||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              |||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||:::||||||||||||||||||
Db        961 AGCGACTGGGCATCTGTGTCATGC 984

RESULT 11
US-09-917-265A-60/c
; Sequence 60, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-60

Alignment Scores:
Pred. No.:              1.9e-188        Length:         987
Score:                  1653.00         Matches:        307
Percent Similarity:     96.6%           Conservative:   10
Best Local Similarity:  93.6%           Mismatches:     11

Query Match:            94.1%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-56 (1-328) x US-09-917-265A-60 (1-987)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||:::||||||||||||||||||||||||   ||||||
Db        987 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 928

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 808

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||   ||||||||||||||||||||||||||||||||||:::|||||||||   |||
Db        747 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 688

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
                  ||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        687 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 628

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db        567 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 508

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              |||   ||||||||||||||||||||||||||||||   ||||||||||||||:::|||
Db        507 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 448

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 328

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 268

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 208

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||   :::|||   ||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 148

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              |||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        147 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 28

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||:::||||||||||||||||||
Db         27 AGCGACTGGGCATCTGTGTCATGC 4
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```
RESULT 12
US-09-079-984A-11
; Sequence 11, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,984A
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  990 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 987
;      IDENTIFICATION METHOD:  Similarity
US-09-079-984A-11

Alignment Scores:
Pred. No.:              1.91e-188      Length:          990
Score:                  1653.00        Matches:         307
Percent Similarity:     96.6%          Conservative:    10
Best Local Similarity:  93.6%          Mismatches:      11
Query Match:            94.1%          Indels:          0
DB:                     3              Gaps:            0

US-10-821-670A-56 (1-328) x US-09-079-984A-11 (1-990)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              |||||||||||||||||||||||||:::|||||||||||||||||||||||||   ||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              |||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              |||||||||||||||||||||||||||:::|||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||   ||||||||||||||||||||||||||||||||:::|||||||||   |||
Db        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              |||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||:::||||||||||||||||
Db        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              |||   ||||||||||||||||||||||||||||   ||||||||||||||:::|||
Db        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              |||||||||||||||||||||||||||||||||||||||||   :::|||   ||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              |||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
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Db        961 AGCGACTGGGCATCTGTGTCCTGC 984

RESULT 13
US-09-390-729-11
; Sequence 11, Application US/09390729
; Patent No. 6562334
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
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;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/390,729
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/079,984
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  990 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 987
;      IDENTIFICATION METHOD:  Similarity
US-09-390-729-11

Alignment Scores:
Pred. No.:              1.91e-188      Length:         990
Score:                  1653.00        Matches:        307
Percent Similarity:     96.6%          Conservative:   10
Best Local Similarity:  93.6%          Mismatches:     11
Query Match:            94.1%          Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-56 (1-328) x US-09-390-729-11 (1-990)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||:::|||||||||||||||||||||||||||||    ||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||:::|||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||   ||||||||||||||||||||||||||||||||:::|||||||||   |||
Db        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
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Db        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
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Db        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
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Db        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              |||   ||||||||||||||||||||||||||||||   |||||||||||||||:::|||
Db        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
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Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
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Db        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||   :::|||   ||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||:::|||||||||||||||||||
Db        961 AGCGACTGGGCATCTGTGTCCTGC 984

RESULT 14
US-09-917-265A-61
; Sequence 61, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-09-917-265A-61

Alignment Scores:
Pred. No.:              4.07e-188      Length:         1599
Score:                  1653.00        Matches:        307
Percent Similarity:     96.6%          Conservative:   10
Best Local Similarity:  93.6%          Mismatches:     11
Query Match:            94.1%          Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-56 (1-328) x US-09-917-265A-61 (1-1599)
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Db          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
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Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||:::|||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
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Db        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||  ||||||||||||||||||||||||||||||||||:::|||||||||   |||
Db        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              |||   ||||||||||||||||||||||||||||||   ||||||||||||||:::|||
Db        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||  :::|||   ||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
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Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
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Db        961 AGCGACTGGGCATCTGTGTCATGC 984

RESULT 15
US-09-917-265A-63/c
; Sequence 63, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-63

Alignment Scores:
Pred. No.:              4.07e-188       Length:         1599
Score:                  1653.00         Matches:        307
Percent Similarity:     96.6%           Conservative:   10
Best Local Similarity:  93.6%           Mismatches:     11
Query Match:            94.1%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-56 (1-328) x US-09-917-265A-63 (1-1599)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
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Db       1599 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 1540

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
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Db       1539 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
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Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 1420

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
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Db       1419 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
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Db       1359 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 1300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
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Db       1299 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 1240

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db       1179 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 1120

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
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Db       1119 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 1060

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
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Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
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Db        999 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 940

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
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Db        939 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 880

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
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Db        879 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 820

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              |||||||||||||||||||||||||||||||||||||||   :::|||   ||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 760

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
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Db        759 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
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Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 640

Qy        321 SerAsnTrpAlaSerValSerCys 328
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GenCore version 5.1.9
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Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1757	100.0	985	3	US-09-917-265-55	Sequence 55, Appl
c	2	1757	100.0	985	3	US-09-917-265-57	Sequence 57, Appl
	3	1757	100.0	985	9	US-10-821-670-55	Sequence 55, Appl
c	4	1757	100.0	985	9	US-10-821-670-57	Sequence 57, Appl
	5	1757	100.0	987	3	US-09-917-265-29	Sequence 29, Appl
c	6	1757	100.0	987	3	US-09-917-265-31	Sequence 31, Appl
	7	1757	100.0	987	9	US-10-821-670-29	Sequence 29, Appl
c	8	1757	100.0	987	9	US-10-821-670-31	Sequence 31, Appl
	9	1757	100.0	990	7	US-10-041-672C-1	Sequence 1, Appli
	10	1757	100.0	4522	7	US-10-041-672C-10	Sequence 10, Appl
	11	1751	99.7	2193	6	US-10-079-616-5	Sequence 5, Appli
	12	1743	99.2	1599	3	US-09-917-265-38	Sequence 38, Appl
c	13	1743	99.2	1599	3	US-09-917-265-40	Sequence 40, Appl
	14	1743	99.2	1599	9	US-10-821-670-38	Sequence 38, Appl
c	15	1743	99.2	1599	9	US-10-821-670-40	Sequence 40, Appl
	16	1653	94.1	987	3	US-09-917-265-58	Sequence 58, Appl
c	17	1653	94.1	987	3	US-09-917-265-60	Sequence 60, Appl
	18	1653	94.1	987	9	US-10-821-670-58	Sequence 58, Appl
c	19	1653	94.1	987	9	US-10-821-670-60	Sequence 60, Appl
	20	1653	94.1	1599	3	US-09-917-265-61	Sequence 61, Appl
c	21	1653	94.1	1599	3	US-09-917-265-63	Sequence 63, Appl
	22	1653	94.1	1599	9	US-10-821-670-61	Sequence 61, Appl
c	23	1653	94.1	1599	9	US-10-821-670-63	Sequence 63, Appl
	24	1653	94.1	2267	3	US-09-917-265-107	Sequence 107, App
c	25	1653	94.1	2267	3	US-09-917-265-109	Sequence 109, App
	26	1653	94.1	2267	9	US-10-821-670-107	Sequence 107, App
c	27	1653	94.1	2267	9	US-10-821-670-109	Sequence 109, App
	28	1643	93.5	921	6	US-10-079-616-6	Sequence 6, Appli
	29	1643	93.5	921	6	US-10-079-616-7	Sequence 7, Appli
	30	1635	93.1	921	3	US-09-917-265-26	Sequence 26, Appl
c	31	1635	93.1	921	3	US-09-917-265-28	Sequence 28, Appl
	32	1635	93.1	921	9	US-10-821-670-26	Sequence 26, Appl
c	33	1635	93.1	921	9	US-10-821-670-28	Sequence 28, Appl
	34	1635	93.1	1533	3	US-09-917-265-43	Sequence 43, Appl
c	35	1635	93.1	1533	3	US-09-917-265-45	Sequence 45, Appl
	36	1635	93.1	1533	9	US-10-821-670-43	Sequence 43, Appl
c	37	1635	93.1	1533	9	US-10-821-670-45	Sequence 45, Appl
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c	39	1550	88.2	921	3	US-09-917-265-54	Sequence 54, Appl
	40	1550	88.2	921	9	US-10-821-670-52	Sequence 52, Appl
c	41	1550	88.2	921	9	US-10-821-670-54	Sequence 54, Appl
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c	43	1550	88.2	1533	3	US-09-917-265-68	Sequence 68, Appl
	44	1550	88.2	1533	9	US-10-821-670-66	Sequence 66, Appl
c	45	1550	88.2	1533	9	US-10-821-670-68	Sequence 68, Appl

ALIGNMENTS

RESULT 1
US-09-917-265-55
; Sequence 55, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 985
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(984)
; OTHER INFORMATION:
US-09-917-265-55

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Alignment Scores:
Pred. No.:              4.39e-206       Length:         985
Score:                  1757.00         Matches:        328
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-56 (1-328) x US-09-917-265-55 (1-985)

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Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
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Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
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Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
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Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
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Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
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Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
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Qy        321 SerAsnTrpAlaSerValSerCys 328
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RESULT 2
US-09-917-265-57/c
; Sequence 57, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-57

Alignment Scores:
Pred. No.:              4.39e-206       Length:         985
Score:                  1757.00         Matches:        328
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

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Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
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Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
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Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
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Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
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Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

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Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

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Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
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Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
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Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        321 SerAsnTrpAlaSerValSerCys 328
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Db         25 AGCAACTGGGCATCCGTGTCCTGC 2

RESULT 3
US-10-821-670-55
; Sequence 55, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(984)
US-10-821-670-55

Alignment Scores:
Pred. No.:              4.39e-206       Length:         985
Score:                  1757.00         Matches:        328
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-56 (1-328) x US-10-821-670-55 (1-985)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
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Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
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Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
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Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
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Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
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Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
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Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
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Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
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Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
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Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
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Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
                 ||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984

RESULT 4
US-10-821-670-57/c
; Sequence 57, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
```

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;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-57

Alignment Scores:
Pred. No.:              4.39e-206      Length:         985
Score:                  1757.00        Matches:        328
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     9              Gaps:           0

US-10-821-670A-56 (1-328) x US-10-821-670-57 (1-985)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGC 2

RESULT 5
US-09-917-265-29
; Sequence 29, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
;   OTHER INFORMATION:
US-09-917-265-29

Alignment Scores:
Pred. No.:              4.41e-206      Length:         987
Score:                  1757.00        Matches:        328
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-56 (1-328) x US-09-917-265-29 (1-987)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
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Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984

RESULT 6
US-09-917-265-31/c
; Sequence 31, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-31

Alignment Scores:
Pred. No.:              4.41e-206       Length:         987
Score:                  1757.00         Matches:        328
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0
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US-10-821-670A-56 (1-328) x US-09-917-265-31 (1-987)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGC 4

RESULT 7
US-10-821-670-29
```

```
; Sequence 29, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
US-10-821-670-29

Alignment Scores:
Pred. No.:              4.41e-206      Length:         987
Score:                  1757.00        Matches:        328
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     9              Gaps:           0

US-10-821-670A-56 (1-328) x US-10-821-670-29 (1-987)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984

RESULT 8
US-10-821-670-31/c
; Sequence 31, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-31

Alignment Scores:
Pred. No.:              4.41e-206      Length:         987
Score:                  1757.00        Matches:        328
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     9              Gaps:           0

US-10-821-670A-56 (1-328) x US-10-821-670-31 (1-987)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
```

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        321 SerAsnTrpAlaSerValSerCys 328
                ||||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGC 4

RESULT 9
US-10-041-672C-1
; Sequence 1, Application US/10041672C
; Publication No. US20030157059A1
; GENERAL INFORMATION:
;  APPLICANT: Mologen Forschungs-, Entwicklungs- und Vetriebs GmbH
;  APPLICANT:  Universitat Zurich
;  TITLE OF INVENTION: FELINE INTERLEUKIN-12 AS IMMUNOSTIMULANT
;  FILE REFERENCE: NHL-NP-36
;  CURRENT APPLICATION NUMBER: US/10/041,672C
;  CURRENT FILING DATE:  2002-01-08
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 990
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: feline IL-12 p40
US-10-041-672C-1

Alignment Scores:
Pred. No.:              4.43e-206       Length:         990
Score:                  1757.00         Matches:        328
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     7               Gaps:           0

US-10-821-670A-56 (1-328) x US-10-041-672C-1 (1-990)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Qy       301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy       321 SerAsnTrpAlaSerValSerCys 328
            |||||||||||||||||||||||||
Db       961 AGCAACTGGGCATCCGTGTCCTGC 984

RESULT 10
US-10-041-672C-10
; Sequence 10, Application US/10041672C
; Publication No. US20030157059A1
; GENERAL INFORMATION:
;  APPLICANT: Mologen Forschungs-, Entwicklungs- und Vetriebs GmbH
;  APPLICANT:  Universitat Zurich
;  TITLE OF INVENTION: FELINE INTERLEUKIN-12 AS IMMUNOSTIMULANT
;  FILE REFERENCE: NHL-NP-36
;  CURRENT APPLICATION NUMBER: US/10/041,672C
;  CURRENT FILING DATE:  2002-01-08
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 4522
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pMol-fil12p40
US-10-041-672C-10

Alignment Scores:
Pred. No.:              4.33e-205      Length:         4522
Score:                  1757.00        Matches:        328
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     7              Gaps:           0

US-10-821-670A-56 (1-328) x US-10-041-672C-10 (1-4522)

Qy         1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy        21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

Qy        41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy        61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy        81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy       101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy       121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy       141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy       161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db      3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

Qy       181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy       201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy       221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy       241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy       261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy       281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy       301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

Qy       321 SerAsnTrpAlaSerValSerCys 328
             |||||||||||||||||||||||||
Db      4007 AGCAACTGGGCATCCGTGTCCTGC 4030

RESULT 11
US-10-079-616-5
; Sequence 5, Application US/10079616
; Publication No. US20020107366A1
;  GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
```

```
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2193 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-079-616-5

Alignment Scores:
Pred. No.:              8.06e-205      Length:         2193
Score:                  1751.00        Matches:        327
Percent Similarity:     99.7%          Conservative:   0
Best Local Similarity:  99.7%          Mismatches:     1
Query Match:            99.7%          Indels:         0
DB:                     6              Gaps:           0

US-10-821-670A-56 (1-328) x US-10-079-616-5 (1-2193)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db         64 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTACCTGGTTTTGCTGGCACCTCCTCTC 123

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 183

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 243

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 303

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 363

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 423

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 483

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 543

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 603

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 663

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 723

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 783

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 843

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 903

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 963

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 1023

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db       1024 AGCAACTGGGCATCCGTGTCCTGC 1047

RESULT 12
US-09-917-265-38
; Sequence 38, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
US-09-917-265-38

Alignment Scores:
Pred. No.:              4.89e-204      Length:         1599
Score:                  1743.00        Matches:        326
Percent Similarity:     99.4%          Conservative:   0
Best Local Similarity:  99.4%          Mismatches:     2
Query Match:            99.2%          Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-56 (1-328) x US-09-917-265-38 (1-1599)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
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Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984

RESULT 13
US-09-917-265-40/c
; Sequence 40, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-40

Alignment Scores:
Pred. No.:              4.89e-204       Length:         1599
Score:                  1743.00         Matches:        326
Percent Similarity:     99.4%           Conservative:   0

Best Local Similarity:  99.4%           Mismatches:     2
Query Match:            99.2%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-56 (1-328) x US-09-917-265-40 (1-1599)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db       1599 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 1540

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 1420

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1359 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 1300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1299 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 1240

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1179 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 1120

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db       1119 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 1060

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        999 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 940

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        939 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 880

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        879 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 820

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 760

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        759 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 640

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db        639 AGCAACTGGGCATCCGTGTCCTGC 616
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RESULT 14
US-10-821-670-38
; Sequence 38, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-10-821-670-38

Alignment Scores:
Pred. No.:              4.89e-204      Length:         1599
Score:                  1743.00        Matches:        326
Percent Similarity:     99.4%          Conservative:   0
Best Local Similarity:  99.4%          Mismatches:     2
Query Match:            99.2%          Indels:         0
DB:                     9              Gaps:           0

US-10-821-670A-56 (1-328) x US-10-821-670-38 (1-1599)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984

RESULT 15
US-10-821-670-40/c
; Sequence 40, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-40

Alignment Scores:
Pred. No.:              4.89e-204      Length:         1599
Score:                  1743.00        Matches:        326
Percent Similarity:     99.4%          Conservative:   0
Best Local Similarity:  99.4%          Mismatches:     2
Query Match:            99.2%          Indels:         0
DB:                     9              Gaps:           0

US-10-821-670A-56 (1-328) x US-10-821-670-40 (1-1599)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db       1599 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 1540

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
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Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 1420

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1359 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 1300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1299 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 1240

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1179 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 1120

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              |||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db       1119 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 1060

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
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Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        999 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 940

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        939 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 880

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        879 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 820

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 760

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        759 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 640

Qy        321 SerAsnTrpAlaSerValSerCys 328
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Db        639 AGCAACTGGGCATCCGTGTCCTGC 616


Search completed: June 10, 2006, 04:34:15
Job time : 1291.39 secs
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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 10, 2006, 01:18:36 ; Search time 17.065 Seconds
(without alignments)
3659.318 Million cell updates/sec

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Perfect score: 1757
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 253354 seqs, 63461778 residues

Total number of hits satisfying chosen parameters: 506708

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_New:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	177	10.1	1363	6	US-10-827-684B-6	Sequence 6, Appli
2	177	10.1	1369	6	US-10-827-684B-5	Sequence 5, Appli
3	176	10.0	1923	7	US-11-145-307A-52	Sequence 52, Appl
4	130.5	7.4	1161	7	US-11-297-134-9	Sequence 9, Appli
5	108	6.1	2341	6	US-10-511-937-349	Sequence 349, App
6	106	6.0	2582	7	US-11-293-697-2331	Sequence 2331, Ap
7	104.5	5.9	2534	7	US-11-293-697-1946	Sequence 1946, Ap
8	99.5	5.7	3597	6	US-10-505-928-651	Sequence 651, App
9	99.5	5.7	3597	6	US-10-511-937-2802	Sequence 2802, Ap
10	99	5.6	5997	7	US-11-313-450-1	Sequence 1, Appli
11	99	5.6	8370	7	US-11-263-326-90	Sequence 90, Appl
12	99	5.6	8377	7	US-11-263-326-95	Sequence 95, Appl
13	99	5.6	8380	7	US-11-263-326-89	Sequence 89, Appl
14	99	5.6	8381	7	US-11-263-326-1	Sequence 1, Appli
15	99	5.6	8381	7	US-11-263-326-3	Sequence 3, Appli
16	99	5.6	8381	7	US-11-263-326-5	Sequence 5, Appli
17	99	5.6	8381	7	US-11-263-326-7	Sequence 7, Appli
18	99	5.6	8381	7	US-11-263-326-8	Sequence 8, Appli
19	99	5.6	8381	7	US-11-263-326-11	Sequence 11, Appl
20	99	5.6	8381	7	US-11-263-326-91	Sequence 91, Appl
21	99	5.6	8381	7	US-11-263-326-92	Sequence 92, Appl
22	99	5.6	8381	7	US-11-263-326-93	Sequence 93, Appl
23	99	5.6	8381	7	US-11-263-326-96	Sequence 96, Appl
24	99	5.6	8381	7	US-11-263-326-97	Sequence 97, Appl
25	99	5.6	8381	7	US-11-263-326-108	Sequence 108, App
26	99	5.6	8381	7	US-11-263-326-136	Sequence 136, App
27	99	5.6	8381	7	US-11-263-326-137	Sequence 137, App
28	99	5.6	8381	7	US-11-263-326-138	Sequence 138, App
29	99	5.6	8381	7	US-11-263-326-139	Sequence 139, App
30	99	5.6	8381	7	US-11-263-326-140	Sequence 140, App
31	99	5.6	8381	7	US-11-263-326-141	Sequence 141, App
32	99	5.6	8381	7	US-11-263-326-142	Sequence 142, App
33	99	5.6	8381	7	US-11-263-326-143	Sequence 143, App
34	99	5.6	8381	7	US-11-263-326-144	Sequence 144, App
35	99	5.6	8388	7	US-11-263-326-94	Sequence 94, Appl
36	97.5	5.5	3646	6	US-10-511-937-358	Sequence 358, App
37	95	5.4	887	6	US-10-511-937-350	Sequence 350, App
38	94	5.4	5193	7	US-11-270-040-5	Sequence 5, Appli
39	94	5.4	8381	7	US-11-263-326-9	Sequence 9, Appli
c 40	93.5	5.3	2208	6	US-10-953-349-3367	Sequence 3367, Ap
41	90.5	5.2	2062	6	US-10-953-349-4146	Sequence 4146, Ap
42	90.5	5.2	3084	6	US-10-511-937-448	Sequence 448, App
43	87.5	5.0	1219	6	US-10-953-349-15072	Sequence 15072, A
44	87.5	5.0	1560	7	US-11-217-529-1952	Sequence 1952, Ap
45	87.5	5.0	2100	7	US-11-217-529-126	Sequence 126, App

ALIGNMENTS

RESULT 1
US-10-827-684B-6
; Sequence 6, Application US/10827684B
; Publication No. US20060115807A1
; GENERAL INFORMATION:
; APPLICANT: Chambers, Ian P
; TITLE OF INVENTION: Improved episomal expression system
; FILE REFERENCE: 78870/00003
; CURRENT APPLICATION NUMBER: US/10/827,684B
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 09/359,672
; PRIOR FILING DATE: 1999-07-23
; PRIOR APPLICATION NUMBER: GB 9701492.2
; PRIOR FILING DATE: 1997-01-24
; PRIOR APPLICATION NUMBER: PCT/GB98/00216
; PRIOR FILING DATE: 1998-01-26
; PRIOR APPLICATION NUMBER: GB 0407043.9
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1363
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-827-684B-6

Alignment Scores:

Pred. No.:	4.57e-10	Length:	1363
Score:	177.00	Matches:	76
Percent Similarity:	40.5%	Conservative:	50
Best Local Similarity:	24.4%	Mismatches:	125

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Query Match:           10.1%          Indels:        61
DB:                    6              Gaps:          13

US-10-821-670A-56 (1-328) x US-10-827-684B-6 (1-1363)

Qy         37 TrpHisProAsp-Ala---ProGlyGluMetValValLeuThrCysAsnThrProGlu-- 54
Db         76 TGGCACAGTGACAAGCCTGCCAGGGGCCACCGTTACCCTGATTTGCCCCGGGAAGGAAGC 135

Qy         55 -GluAspAspIleThr------------TrpThrSerAspGlnSerSerGluValLeuGl 70
Db        136 AGCAGGCAATGTTACCATTCACTGGGTGTACTCTGGCTCACAAAACAGAGAATGGACTAC 195

Qy         70 ySerGlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCy 90
Db        196 CACAGGAAACACACTGGTTCTGAGGGACGTGCAGCTCAGCGACACTGGGGACTATTTATG 255

Qy         90 sHisLysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGl 110
Db        256 CTCCCTGAATGATCACCTGGTGGGGACTGTGCCCTTGCTGGTG---------------- 298

Qy        110 yIleTrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLy 130
Db        299 ------------GATGTTCCCCCAGAGGAGCCCAAG-----------------CTCTC 327

Qy        130 sCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerTh 150
Db        328 CTGCTTCCGGAAGAACCCCCTTGTCAACGCCATCTGTGAGTGG---------------- 370

Qy        150 rAspLeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCy 170
Db        371 ----------------------------CGTCCGAGCAGCACCCCCTCTCCAACCACG-- 400

Qy        170 sGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTy 190
Db        401 ----AAGGCTGTGCTGTTTGCAAAGAAAATCAACACCACCAAC---GGGAAGAGTGACTT 453

Qy        190 rThrValGluCysGlnGluGlySerAlaCys----------------------------Pr 201
Db        454 CCAGGTGCCCTGCCAGTATTC-TCAGCAGCTGAAAAGCTTCTCCTGCCAGGTGGAGATCC 512

Qy        201 oAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTy 221
Db        513 TGGAGGGTGACAAAGTATACCACATAGTGTCACTGTGCGTTGCAAACAGTGTGGGAAGCA 572

Qy        221 r-GluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysA 241
Db        573 AGTCCAGCCACAACGAAGCGTTTCACAGCTTAAAAATGGTGCAGCCGGATCCACCTGCCA 632

Qy        241 snLeuGlnLeuLysProLeuLys---AsnSerArgHisValGluValSerTrpGluTyrP 260
Db        633 ACCTTGTGGTATCAGCCATACCTGGAAGGCCGCGCTGGCTCAAAGTCAGCTGGCAGCACC 692

Qy        260 roAspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnG 280
Db        693 CTGAGACCTGGGACCCG------AGTTACTACTTGCTGCAGTTCCAGCTTCGATACCGAC 746

Qy        280 lyLysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValV 300
Db        747 CTGTATGGTCAAAGGAG---TTCACGGTGTTGCTGCTCCCGGTGGCCCAGTACCAATGCG 803

Qy        300 alCysHisLysAspAlaLys--------------IleArgValGlnAlaArgAspArgT 315
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Qy        315 yrTyrSerSerSerTrpSerAsnTrpAla 324
Db        864 TTGACCTTGGCCAGTGGAGTGAATGGTCC 892

RESULT 2
US-10-827-684B-5
; Sequence 5, Application US/10827684B
; Publication No. US20060115807A1
; GENERAL INFORMATION:
;  APPLICANT: Chambers, Ian P
;  TITLE OF INVENTION: Improved episomal expression system
;  FILE REFERENCE: 78870/00003
;  CURRENT APPLICATION NUMBER: US/10/827,684B
;  CURRENT FILING DATE:  2004-04-19
;  PRIOR APPLICATION NUMBER: US 09/359,672
;  PRIOR FILING DATE: 1999-07-23
;  PRIOR APPLICATION NUMBER: GB 9701492.2
;  PRIOR FILING DATE: 1997-01-24
;  PRIOR APPLICATION NUMBER: PCT/GB98/00216
;  PRIOR FILING DATE: 1998-01-26
;  PRIOR APPLICATION NUMBER: GB 0407043.9
;  PRIOR FILING DATE: 2004-03-29
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 1369
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-827-684B-5

Alignment Scores:
Pred. No.:             4.6e-10        Length:        1369
Score:                 177.00         Matches:       76
Percent Similarity:    40.5%          Conservative:  50
Best Local Similarity: 24.4%          Mismatches:    125
Query Match:           10.1%          Indels:        61
DB:                    6              Gaps:          13

US-10-821-670A-56 (1-328) x US-10-827-684B-5 (1-1369)

Qy         37 TrpHisProAsp-Ala---ProGlyGluMetValValLeuThrCysAsnThrProGlu-- 54
Db         82 TGGCACAGTGACAAGCCTGCCAGGGGCCACCGTTACCCTGATTTGCCCCGGGAAGGAAGC 141

Qy         55 -GluAspAspIleThr------------TrpThrSerAspGlnSerSerGluValLeuGl 70
Db        142 AGCAGGCAATGTTACCATTCACTGGGTGTACTCTGGCTCACAAAACAGAGAATGGACTAC 201

Qy         70 ySerGlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCy 90
Db        202 CACAGGAAACACACTGGTTCTGAGGGACGTGCAGCTCAGCGACACTGGGGACTATTTATG 261

Qy         90 sHisLysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGl 110
Db        262 CTCCCTGAATGATCACCTGGTGGGGACTGTGCCCTTGCTGGTG---------------- 304

Qy        110 yIleTrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLy 130
Db        305 ------------GATGTTCCCCCAGAGGAGCCCAAG-----------------CTCTC 333

Qy        130 sCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerTh 150
Db        334 CTGCTTCCGGAAGAACCCCCTTGTCAACGCCATCTGTGAGTGG---------------- 376

Qy        150 rAspLeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCy 170
Db        377 ----------------------------CGTCCGAGCAGCACCCCCTCTCCAACCACG-- 406

Qy        170 sGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTy 190
Db        407 ----AAGGCTGTGCTGTTTGCAAAGAAAATCAACACCACCAAC---GGGAAGAGTGACTT 459

Qy        190 rThrValGluCysGlnGluGlySerAlaCys----------------------------Pr 201
Db        460 CCAGGTGCCCTGCCAGTATTC-TCAGCAGCTGAAAAGCTTCTCCTGCCAGGTGGAGATCC 518

Qy        201 oAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTy 221
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Qy        221 r-GluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysA 241
Db        579 AGTCCAGCCACAACGAAGCGTTTCACAGCTTAAAAATGGTGCAGCCGGATCCACCTGCCA 638

Qy        241 snLeuGlnLeuLysProLeuLys---AsnSerArgHisValGluValSerTrpGluTyrP 260
Db        639 ACCTTGTGGTATCAGCCATACCTGGAAGGCCGCGCTGGCTCAAAGTCAGCTGGCAGCACC 698

Qy        260 roAspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnG 280
Db        699 CTGAGACCTGGGACCCG------AGTTACTACTTGCTGCAGTTCCAGCTTCGATACCGAC 752

Qy        280 lyLysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValV 300
Db        753 CTGTATGGTCAAAGGAG---TTCACGGTGTTGCTGCTCCCGGTGGCCCAGTACCAATGCG 809

Qy        300 alCysHisLysAspAlaLys--------------IleArgValGlnAlaArgAspArgT 315
Db        810 TCATCCATGATGCCTTGCGAGGAGTGAAGCACGTGGTCCAGGTCCGTGGGAAGGAGGAGC 869

Qy        315 yrTyrSerSerSerTrpSerAsnTrpAla 324
Db        870 TTGACCTTGGCCAGTGGAGTGAATGGTCC 898
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RESULT 3
US-11-145-307A-52
; Sequence 52, Application US/11145307A
; Publication No. US20060094035A1
; GENERAL INFORMATION:
; APPLICANT: Arcturus Bioscience, Inc.
; APPLICANT: Erlander, Mark G.
; APPLICANT: Ma, Xiao-Jun
; TITLE OF INVENTION: Identification of Tumors
; FILE REFERENCE: 022041-002020US
; CURRENT APPLICATION NUMBER: US/11/145,307A
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 60/577,084
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 1923
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-145-307A-52

Alignment Scores:

Pred. No.:	9.67e-10	Length:	1923
Score:	176.00	Matches:	79
Percent Similarity:	37.8%	Conservative:	40
Best Local Similarity:	25.1%	Mismatches:	105
Query Match:	10.0%	Indels:	93
DB:	7	Gaps:	17

US-10-821-670A-56 (1-328) x US-11-145-307A-52 (1-1923)

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Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAsp---AspIleThrTrpThr 61
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Qy         62 ---------SerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGln 78
Db        324 GTAAATGGGACAGACCTGGCCCCTGACCTGCTC---AACGGCTCTCAGCTGGTGCTCCAT 380

Qy         79 ValLysGluPheAlaAspAlaGlyGlnTyrThrCys---HisLysGlyGlyGluValLeu 97
Db        381 GGCCTGGAACTGGGCCACAGTGGCCTCTACGCCTGCTTCCACCGTGACTCCTGGCACCTG 440

Qy         98 SerHisSerPheLeuLeu---------IleHisLysLysGluAspGlyIleTrpSerThr 114
Db        441 CGCCACCAAGTCCTGCTGCATGTGGGCTTGCCGCCGCGGGAGCCT-------------- 485
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Qy        115 AspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLys 134
Db        486 ------------------------------------GTGCTCAGCTGCCGCTCCAAC 506

Qy        135 AsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPhe 154
Db        507 ACTTACCCCAAGGGCTTCTACTGCAGCTGGCATCTGCCCACCCCCACCTACATT------ 560

Qy        155 ThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThr 174
Db        561 ----------------------------CCCAAC------ACCTTCAATGTGACTGTG 584

Qy        175 LeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrValGluCys 194
Db        585 CTGCATGGCTCCAAAATTATGGTC--------------------------------TGT 611

Qy        195 GlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValValValAsp 214
Db        612 GA-GAAGGA---------CCCAGCCCTCAAGAACCGCTGCCACATTCGCTACATGCACCT 661

Qy        215 AlaIleHisLysLeuLysTyrGlu--------------------------------Asn 223
Db        662 GTTCTCCACC--ATCAAGTACAAGGTCTCCATAAGTGTCAGCAATGCCCTGGGCCACAAT 719

Qy        224 TyrThrSerSerPhePheIleArg---AspIleIleLysProAspProProLysAsnLeu 242
Db        720 GCCACAGCTATCACCTTTGACGAGTTCACCATTGTGAAGCCTGATCCTCCAGAAAATGTG 779

Qy        243 GlnLeuLysProLeu---LysAsnSerArgHisValGluValSerTrpGluTyrProAsp 261
Db        780 GTAGCCCGGCCAGTGCCCAGCAACCCTCGCCGGCTGGAGGTGACGTGGCAGACCCCCTCG 839

Qy        262 ThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLys 281
Db        840 ACCTGGCCTGACCCTGAGTCT---TTTCCTCTCAAGTTCTTTCTGCGCTACCGA------ 890

Qy        282 AsnAsnArgGluLysLysAspArgLeuSerValAspLys---------------------- 294
Db        891 ----------------------CCCCTCATCCTGGACCAGTGGCAGCATGTGGAGCTGTCC 929

Qy        295 ---------------ThrSerAlaLysValValCysHisLysAspAlaLysIleArgVal 309
Db        930 GACGGCACAGCACACACCATCACAGATGCCTACGCCGGGAAGGAGTACATTATCCAGGTG 989

Qy        310 GlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAla 324
Db        990 GCAGCCAAGGACAATGAGATT---GGGACATGGAGTGACTGGAGC 1031
```

RESULT 4
US-11-297-134-9
; Sequence 9, Application US/11297134
; Publication No. US20060111297A1
; GENERAL INFORMATION:
; APPLICANT: Genzyme Corporation
; APPLICANT: Roberts, Bruce
; TITLE OF INVENTION: BLOOD FACTOR DOMAINS
; FILE REFERENCE: 5270C
; CURRENT APPLICATION NUMBER: US/11/297,134
; CURRENT FILING DATE: 2005-12-08
; PRIOR APPLICATION NUMBER: PCT/US2005/018461
; PRIOR FILING DATE: 2004-06-09
; PRIOR APPLICATION NUMBER: US 60/477,291
; PRIOR FILING DATE: 2003-06-09
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 1161
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-297-134-9

Alignment Scores:

Pred. No.:	3.97e-05	Length:	1161

```
Score:                 130.50        Matches:       47
Percent Similarity:    40.8%         Conservative:  39
Best Local Similarity: 22.3%         Mismatches:    82
Query Match:           7.4%          Indels:        43
DB:                    7             Gaps:          9

US-10-821-670A-56 (1-328) x US-11-297-134-9 (1-1161)

Qy       129 LeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIle 148
Db       110 GTGCAATGCCGAGCCTCTCGGTAC----------------------------CCGATC 139

Qy       149 SerThrAspLeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyVal 168
Db       140 GCCGTGGATTGCTCCTGGACCCTGCCGCCTGCTCCAAACTCCACCAGCCCC--------- 190

Qy       169 ThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLys 188
Db       191 ---------GTGTCCTTCATTGCCACGTACAGGCTCGGCATGGCTGCCCGGGGCCACAGC 241

Qy       189 ---LysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeu 207
Db       242 TGGCCCTGCCTGCAGCAGACGCCAACGTCCACCAGCTGCACCATCACGGATGTCCAGCTG 301

Qy       208 ------------ProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsn 223
Db       302 TTCTCCATGGCTCCCTACGTGCTCAATGTCACCGCCGTCCACCCCTGGGGCTCCAGCAGC 361

Qy       224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
Db       362 AGCTTCGTGCCTTTCATAACAGAGCACATCATCAAGCCCGACCCTCCAGAAGGCGTGCGC 421

Qy       244 LeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThrTrp 263
Db       422 CTAAGCCCCCTCGCT---GAGCGCCACGTACAGGTGCAGTGGGAGCCTCCCGGGTCCTGG 478

Qy       264 SerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsnAsn 283
Db       479 CCCTTCCCA---GAGATCTTCTCACTGAAGTACTGGATCCGTTACAAG---CGTCAGGGA 532

Qy       284 ArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHisLys 303
Db       533 GCTGCGCGCTTCCACCGGGTGGGGCCCATTGAAGCCACGTCCTTCATCCTC--------- 583

Qy       304 AspAlaLysIleArgValGlnAlaArgAspArgTyrTyr---------------------- 316
Db       584 ---------AGGGCTGTGCGGCCCCGAGCCAGGTACTACGTCCAAGTGGCGGCTCAGGAC 634

Qy       317 ------------------SerSerSerTrpSer 321
Db       635 CTCACAGACTACGGGGAACTGAGTGACTGGAGT 667

RESULT 5
US-10-511-937-349
; Sequence 349, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
;  APPLICANT: EXPRESSION DIAGNOSTICS, INC.
;  APPLICANT:  Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  APPLICANT:  Prentice, James
;  APPLICANT:  Morris, MacDonald
;  APPLICANT:  Rosenberg, Steven
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
;  TITLE OF INVENTION:  AND MONITORING TRANSPLANT REJECTION
;  FILE REFERENCE: 506612000104
;  CURRENT APPLICATION NUMBER: US/10/511,937
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: PCT/US2003/012946
;  PRIOR FILING DATE: 2003-04-24
;  PRIOR APPLICATION NUMBER: US 10/131,831
;  PRIOR FILING DATE: 2002-04-24
;  PRIOR APPLICATION NUMBER: US 10/325,899
;  PRIOR FILING DATE: 2002-12-20
;  NUMBER OF SEQ ID NOS: 3117
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 349
;   LENGTH: 2341
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-511-937-349

Alignment Scores:
Pred. No.:             0.0302        Length:        2341
Score:                 108.00        Matches:       76
Percent Similarity:    31.9%         Conservative:  39
Best Local Similarity: 21.1%         Mismatches:    102
Query Match:           6.1%          Indels:        144
DB:                    6             Gaps:          15

US-10-821-670A-56 (1-328) x US-10-511-937-349 (1-2341)

Qy         3 ProGlnGlnLeuValIleAlaTrp--------------PheSerLeuValLeuLeuAla 17
Db       275 CCTCTCCAGTGTGGCATCATGTGGCAGCTGCTCCTCCCAACTGCTCTGCTACTTCTAGTT 334

Qy        18 ProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrp 37
Db       335 TCAGCTGGCATGCGGACTGAAGATCTCCCAAAGGCTGTGGTGTTCCTGGAGCCTCAATGG 394

Qy        38 HisProAspAlaProGlyGluMetValValLeuThrCysAsn---------ThrProGlu 54
Db       395 TACAGGGTGCTCGAGAAGGACAGTGTGACTCTGAAGTGCCAGGGAGCCTACTCCCCTGAG 454

Qy        55 GluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGlyLysThr 74
Db       455 GACAATTCCACACAGTGGTTTCACAATGAGAGCCTC---ATCTCAAGCCAGGCCTCGAGC 511

Qy        75 LeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGly 94
Db       512 TACTTCATTGACGCTGCCACAGTCGACGACAGTGGAGAGTACAGGTGCCAGACAAACCTC 571

Qy        95 GluValLeuSerHisSerPheLeuLeu---------------------------------- 103
Db       572 TCCACCCTCAGTGACCCGGTGCAGCTAGAAGTCCATATCGGCTGGCTGTTGCTCCAGGCC 631

Qy       104 ---------IleHisLysLysGluAspGlyIle------------------TrpSerThr 114
Db       632 CCTCGGTGGGTGTTCAAGGAGGAAGACCCTATTCACCTGAGGTGTCACAGCTGGAAGAAC 691

Qy       115 AspIleLeu------------------------------------------------------ 117
Db       692 ACTGCTCTGCATAAGGTCACATATTTACAGAATGGCAAAGGCAGGAAGTATTTTCATCAT 751

Qy       118 ----------------------------------------------------------Arg 118
Db       752 AATTCTGACTTCTACATTCCAAAAGCCACACTCAAAGACAGCGGCTCCTACTTCTGCAGG 811

Qy       119 GluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGly 138
Db       812 GGGCTTGTTGGGAGTAAAAATGT-GTCTTCAGAGACTGTGAACATCACCATCACTCA--- 867

Qy       139 ArgPhe-------------------------ThrCysTrp-Trp-------------- 144
Db       868 AGGTTTGGCAGTGTCAACCATCTCATCATTCTTTCCACCTGGGTACCAAGTCTCTTTCTG 927

Qy       145 ----------------LeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSe 159
Db       928 CTTGGTGATGGTACTCCTTTTTGCAGTGGACACAGGACTATATTTCTCTGTGAAGACAAA 987

Qy       159 rArgGlySerSer-------------------------------------AspProGl 166
Db       988 CATTCGAAGCTCAACAAGAGACTGGAAGGACCATAAATTTAAATGGAGAAAGGACCCTCA 1047
```

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Qy        166 nGlyVal---------------------------------------------------- 168
              |
Db       1048 AGACAAATGACCCCCATCCCATGGGGGTAATAAGAGCAGTAGCAGCAGCATCTCTGAACA 1107

Qy        169 -ThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLy 188
               |||   |||||||||||:::     :::         :::|||  :::::
Db       1108 TTTCTCTGGATTTGCAACCCTATCATCCTCAGGCCTCTCTACAAGCAGCAGGAAACATAG 1167

Qy        188 sLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeu-- 207
              :          |||          |||     :::   ||||||
Db       1168 A---------------ACTCAGAGCCAGATCCCTTATCCAACTCTCGACTTTTCCTTGGT 1212

Qy        208 ----------------------------------------ProIleGluValValVa 213
                                                       |||   |||
Db       1213 CTCCAGTGGAAGGGAAAAGCCCATGATCTTCAAGCAGGGAAGCCCCAGTGAG-------- 1264

Qy        213 lAspAlaIleHis------LysLeuLysTyrGluAsnTyrThrSerSerPhePheIle 230
                  :::|||      |||||||||:::::::::|||||:::::|||   :::
Db       1265 ----TAGCTGCATTCCTAGAAATTGAAGTTTCAGAGCTACACAAACACTTTTTCTGTC 1318

RESULT 6
US-11-293-697-2331
; Sequence 2331, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2331
;   LENGTH: 2582
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-2331

Alignment Scores:
Pred. No.:              0.0575          Length:         2582
Score:                  106.00          Matches:        68
Percent Similarity:     35.3%           Conservative:   44
Best Local Similarity:  21.5%           Mismatches:     136
Query Match:            6.0%            Indels:         69
DB:                     7               Gaps:           14

US-10-821-670A-56 (1-328) x US-11-293-697-2331 (1-2582)

Qy          7 ValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeu 26
              ::::::   |||      |||::::::|||   |||
Db        223 ATGCTTCTGTGGCTGCTGCTGCTGATCCTGACTCCTGGAAGAGAACAATCAGGGGTGGCC 282

Qy         27 GluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaProGlyGluMetVal 46
               |||   |||   ::::::         |||                |||||   |||
Db        283 CCAAAAGCTGTACTTCTCCTCAATCCTCCATGGTCCACAGCCTTCAAAGGAGAAAAAGTG 342

Qy         47 ValLeuThrCysAsnThrProGlu-----------GluAspAspIleThrTrpThrSer 62
              |||   |||::::::                  :::  |||      |||
Db        343 GCTCTCATATGCAGCAGCATATCACATTCCCTAGCCCAGGGAGACACATATTGGTATCAC 402

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              |||:::          :::        |||         ||||||:::   |||
Db        403 GATGAGAAGTTGTTGAAAATAAAACATGACAAG---------ATCCAAATTACAGAG--- 450

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              |||   |||   |||         |||      ||||||   :::
Db        451 ------CCTGGAAATTACCAATGTAAGACCCGAGGATCCTCCCTCAGTGATGCC------ 498

Qy        103 LeuIleHisLysLysGluAspGlyIleTrp---SerThrAspIleLeuArgGluGlnLys 121
              :::|||   :::         |||             |||
Db        499 ---GTGCATGTGGAATTTTCACCTGACTGGCTGATCCTGCAGGCTTTACATCCTGTCTTT 555

Qy        122 GluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThr 141
              |||      |||   :::   |||:::|||:::   |||:::
Db        556 GAAGGAGACAAT---GTCATTCTGAGATGTCAGGGGAAAGACAACAAA------------ 600

Qy        142 CysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGly 161
                                  :::|||      |||        |||        |||
Db        601 --------------------AACACTCATCAAAAGGTTTACTACAAGGAT------GGA 633

Qy        162 SerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArg 181
                    |||                          :::   :::   ||||||:::
Db        634 AAACAGCTTCCTAAT--------------------AGTTATAATTTAGAGAAGATCACA 672

Qy        182 ValAsp------AsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAla 199
              |||:::      :::||||||     ||||||
Db        673 GTGAATTCAGTCTCCAGGGATAATAGCAAATAT----------------------CAT 708

Qy        200 CysProAlaAlaGluGlu------SerLeuProIleGluValValValAspAlaIleHis 217
              |||   |||      :::        |||   |||||||||                ::::::
Db        709 TGTACTGCTTATAGGAAGTTTTACATACTTGACATTGAAGTAACTTCAAAACCCCTAAAT 768

Qy        218 LysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAsp 237
                    |||                  |||:::      :::::::::
Db        769 ATCCAAGTTCAAGAG--------------CTGTTTCTACATCCTGTGCTGAGAGCCAGC 813

Qy        238 ProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrp 257
                    ::::::      |||:::      :::        ::::::|||
Db        814 TCTTCCACGCCCATAGAGGGGAGTCCCATGACCCTGACCTGTGAGACCCAGCTCTCTCCA 873

Qy        258 GluTyrProAspThr---------------------------------------------- 262
              :::   ||||||
Db        874 CAGAGGCCAGATGTCCAGCTGCAATTCTCCCTCTTCAGAGATAGCCAGACCCTCGGATTG 933

Qy        263 ---TrpSerThr-ProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLy 281
                 ||||||    |||   :::      ||||||      |||::::::   ||||||
Db        934 GGCTGGAGCAGGTCCCCCAAACTCCAGATCCCTGCCATGTGGACTGAAGACTCAGGGTCT 993

Qy        281 sAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAla 297
                          :::      |||:::      |||      |||
Db        994 TACTGGTGTGAGGTGGAGACAGTGACTCACAGCATCAAAAAAAGGAGCC 1042

RESULT 7
US-11-293-697-1946
; Sequence 1946, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1946
;   LENGTH: 2534
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1946

Alignment Scores:
Pred. No.:              0.0813          Length:         2534
Score:                  104.50          Matches:        62
Percent Similarity:     35.6%           Conservative:   33
Best Local Similarity:  23.2%           Mismatches:     107
Query Match:            5.9%            Indels:         65
DB:                     7               Gaps:           13

US-10-821-670A-56 (1-328) x US-11-293-697-1946 (1-2534)

Qy         46 ValValLeuThrCysAsnThrProGlu---GluAspAspIleThrTrpThrSerAsp--- 63
              :::   |||   |||         :::   |||      :::   |||      |||
```

```
Db        298 CTGGCCCTGCAGTGTGAAGTCTCTGACCCCGAGGCCCATGTGGTGTGGCGCAAAGATGGC 357

Qy         64 -----------------GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIle 77

Db        358 GTGCAGCTGGGCCCCAGTGACAAGTATGACTTCCTGCACACGGCGGGCACGCGGGGGCTC 417

Qy         78 GlnValLysGluPheAla------AspAlaGlyGlnTyrThrCysHisLysGlyGlyGlu 95

Db        418 GTGGTGCATGACGTGAGCCCTGAAGACGCCGGCCTGTACACCTGCCACGTGGGCTCCGAG 477

Qy         96 ValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAsp 115

Db        478 GAG---ACCCGGGCCCGGGTCCGCGTGCACGATCTGCACGTGGGCATC------------ 522

Qy        116 IleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsn 135

Db        523 ------------ACCAAGAGGCTGAAGACAATGGAGGTGCTGGAAGGGGAA--------- 561

Qy        136 TyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThr 155

Db        562 ---AGCTGCAGCTTTGAGTGC------------------------------------- 579

Qy        156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175

Db        580 GTCCTGTCCCACGAGAGTGCCAGCGACCCGGCCATGTGGACAGTCGGTGGGAAGACAGTG 639

Qy        176 SerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGln 195

Db        640 GGCAGCTCCAGCCGCTTCCAGGCCACACGTCAGGGCCGAAAATACATCCTGGTGGTCCGG 699

Qy        196 GluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValValValAspAla 215

Db        700 GAGGCTGCACCAAGTGATGCCGGGGAG--------------------GTGGTCTTCTCT 738

Qy        216 IleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLys 235

Db        739 GTGCGGGGCCTCACCTCCAAG---------GCCTCACTCATTGTCAGA------------ 777

Qy        236 ProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluVal 255

Db        778 ---GAGAGGCCGGCCACCATC---ATCAAGCCCCTGGAA--------------------- 810

Qy        256 SerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGly 275

Db        811 --------------GACCAGTGGGTGGCGCCAGGGGAGGACGTGGAGCTGCGCTGTGAG 855

Qy        276 ValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThr 295

Db        856 CTGTCACGGGCGGGAACGCCCGTGCACTGGCTGAAGGACAGGAAGGCCATCCGCAAGAGC 915

Qy        296 SerAla---LysValValCys 301

Db        916 CAGAAGTATGATGTGGTCTGC 936

RESULT 8
US-10-505-928-651
; Sequence 651, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
;  APPLICANT: Ludwig Institute for Cancer Research et al.
;  TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
;  FILE REFERENCE: 28967/39178
;  CURRENT APPLICATION NUMBER: US/10/505,928
;  CURRENT FILING DATE:  2004-08-27
;  PRIOR APPLICATION NUMBER: US 60/363,019
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: PatentIn 3.2
; SEQ ID NO 651
;   LENGTH: 3597
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-505-928-651

Alignment Scores:
Pred. No.:                0.471          Length:          3597
Score:                    99.50          Matches:         56
Percent Similarity:       34.4%          Conservative:    28
Best Local Similarity:    23.0%          Mismatches:      72
Query Match:              5.7%           Indels:          89
DB:                       6              Gaps:            11

US-10-821-670A-56 (1-328) x US-10-505-928-651 (1-3597)

Qy        135 AsnTyrSerGlyArgPheThrCysTrpTrpLeu-----------ThrAlaIleSerThr 150

Db        284 GACTACATGAGCATCTCTACTTGCGAGTGGAAGATGAATGGTCCCACCAATTGCAGCACC 343

Qy        151 AspLeuLysPheThrValLys--------------SerSerArgGlySerSerAspPro 165

Db        344 GAGCTCCGCCTGTTGTACCAGCTGGTTTTTCTGCTCTCCGAAGCCCACACGTGTATCCCT 403

Qy        166 Gln---------GlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182

Db        404 GAGAACAACGGAGGCGCGGGGTGCGTGTGCCACCTGCTCATGGATGACGTGGTCAGTGCG 463

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGlu-CysGlnGluGlySerAlaCysProAl 202

Db        464 GATAAC--------------TATACACTGGACCTGTGGGCTGGGCAGCAGCTGCTGTGG 508

Qy        202 aAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGl 222

Db        509 AAGGGCTCCTTCAAG-CCCAGCGAG-----------------CAT-------------- 535

Qy        222 uAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLe 242

Db        536 --------------------------------GTGAAACCCAGGGCCCCAGGAAACCT 561

Qy        242 uGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspTh 262

Db        562 GACAGTT--------------------CACACCAATGTCTCCGACACTCTGCTGCTGAC 600

Qy        262 rTrpSerThrProHisSer--------------TyrPheSerLeuThrPheGlyValGl 277

Db        601 CTGGAGCAACCCGTATCCCCCTGACAATTACCTGTATAATCATCTCACCTATGCAGTCAA 660

Qy        277 nValGlnGlyLysAsnAsn--------------------------------ArgGluLy 286

Db        661 CATTTGGAGTGAAAACGACCCGGCAGATTTCAGAATCTATAACGTGACCTACCTAGAACC 720

Qy        286 sLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHisLysAspAlaLy 306

Db        721 CTCCCTCCGCATCGCAGCCAGCACCCTGAAGTCTGGGATT------------TCCTACAG 768

Qy        306 sIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAla----- 324

Db        769 GGCACGGGTGAGGGCCTGGGCTCAGTGCTATAACACCACCTGGAGTGAGTGGAGCCCCAG 828

Qy        325 ------------------------------------------------------------Se 325

Db        829 CACCAAGTGGCACAACTCCTACAGGGAGCCCTTCGAGCAGCACCTCCTGCTGGGCGTCAG 888

Qy        325 rValSerCys 328

Db        889 CGTTTCCTGC 898

RESULT 9
US-10-511-937-2802
; Sequence 2802, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
;  APPLICANT: EXPRESSION DIAGNOSTICS, INC.
;  APPLICANT:  Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
```

```
;  APPLICANT:  Prentice, James
;  APPLICANT:  Morris, MacDonald
;  APPLICANT:  Rosenberg, Steven
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
;  TITLE OF INVENTION:  AND MONITORING TRANSPLANT REJECTION
;  FILE REFERENCE: 506612000104
;  CURRENT APPLICATION NUMBER: US/10/511,937
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: PCT/US2003/012946
;  PRIOR FILING DATE: 2003-04-24
;  PRIOR APPLICATION NUMBER: US 10/131,831
;  PRIOR FILING DATE: 2002-04-24
;  PRIOR APPLICATION NUMBER: US 10/325,899
;  PRIOR FILING DATE: 2002-12-20
;  NUMBER OF SEQ ID NOS: 3117
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2802
;   LENGTH: 3597
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-511-937-2802

Alignment Scores:
Pred. No.:              0.471          Length:          3597
Score:                  99.50          Matches:           56
Percent Similarity:     34.4%          Conservative:      28
Best Local Similarity:  23.0%          Mismatches:        72
Query Match:            5.7%           Indels:            89
DB:                     6              Gaps:              11

US-10-821-670A-56 (1-328) x US-10-511-937-2802 (1-3597)

Qy        135 AsnTyrSerGlyArgPheThrCysTrpTrpLeu------------ThrAlaIleSerThr 150
              :::|||              ||||||   |||             |||      ||||||
Db        284 GACTACATGAGCATCTCTACTTGCGAGTGGAAGATGAATGGTCCCACCAATTGCAGCACC 343

Qy        151 AspLeuLysPheThrValLys--------------SerSerArgGlySerSerAspPro 165
              :::|||:::        :::               |||         :::      |||
Db        344 GAGCTCCGCCTGTTGTACCAGCTGGTTTTTCTGCTCTCCGAAGCCCACACGTGTATCCCT 403

Qy        166 Gln---------GlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              :::         |||      |||             |||    :::   |||
Db        404 GAGAACAACGGAGGCGCGGGGTGCGTGTGCCACCTGCTCATGGATGACGTGGTCAGTGCG 463

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGlu-CysGlnGluGlySerAlaCysProAl 202
              ||||||               ||||||:::::: |||      |||||||:::|||
Db        464 GATAAC--------------TATACACTGGACCTGTGGGCTGGGCAGCAGCTGCTGTGG 508

Qy        202 aAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGl 222
                  |||   |||   |||                  |||
Db        509 AAGGGCTCCTTCAAG-CCCAGCGAG-----------------CAT-------------- 535

Qy        222 uAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLe 242
                                        :::||||||      |||   |||||
Db        536 --------------------------------GTGAAACCCAGGGCCCCAGGAAACCT 561

Qy        242 uGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspTh 262
              |   :::                    |||      ||||||                ||
Db        562 GACAGTT-------------------CACACCAATGTCTCCGACACTCTGCTGCTGAC 600

Qy        262 rTrpSerThrProHisSer--------------TyrPheSerLeuThrPheGlyValGl 277
              |||||||   |||:::              |||      ||||||:::   |||
Db        601 CTGGAGCAACCCGTATCCCCCTGACAATTACCTGTATAATCATCTCACCTATGCAGTCAA 660

Qy        277 nValGlnGlyLysAsnAsn--------------------------------ArgGluLy 286
               :::      :::|||:::                                   |||
Db        661 CATTTGGAGTGAAAACGACCCGGCAGATTTCAGAATCTATAACGTGACCTACCTAGAACC 720

Qy        286 sLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHisLysAspAlaLy 306
                  |||::::::                 :::   :::                ::
Db        721 CTCCCTCCGCATCGCAGCCAGCACCCTGAAGTCTGGGATT------------TCCTACAG 768

Qy        306 sIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAla----- 324
```

```
              :   ||||||:::|||      :::   |||:::::::::||||||   |||:::
Db        769 GGCACGGGTGAGGGCCTGGGCTCAGTGCTATAACACCACCTGGAGTGAGTGGAGCCCCAG 828

Qy        325 ------------------------------------------------------------Se 325
                                                                           ||
Db        829 CACCAAGTGGCACAACTCCTACAGGGAGCCCTTCGAGCAGCACCTCCTGCTGGGCGTCAG 888

Qy        325 rValSerCys 328
              |||||||||
Db        889 CGTTTCCTGC 898

RESULT 10
US-11-313-450-1
; Sequence 1, Application US/11313450
; Publication No. US20060110778A1
; GENERAL INFORMATION:
;  APPLICANT: Adorante, Joeseph S.
;  APPLICANT:  Ehring, George R.
;  TITLE OF INVENTION: High-Throughput Screens For Identifying
;  TITLE OF INVENTION:  Selective Persistent Sodium Channels Channel Blockers
;  FILE REFERENCE: 17407 CIP (AP)
;  CURRENT APPLICATION NUMBER: US/11/313,450
;  CURRENT FILING DATE:  2005-12-19
;  PRIOR APPLICATION NUMBER: 09/989797
;  PRIOR FILING DATE: 2001-11-20
;  PRIOR APPLICATION NUMBER: 60/252771
;  PRIOR FILING DATE: 2000-11-22
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 5997
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-313-450-1

Alignment Scores:
Pred. No.:              1.12           Length:          5997
Score:                  99.00          Matches:           46
Percent Similarity:     35.2%          Conservative:      22
Best Local Similarity:  23.8%          Mismatches:        88
Query Match:            5.6%           Indels:            37
DB:                     7              Gaps:              6

US-10-821-670A-56 (1-328) x US-11-313-450-1 (1-5997)

Qy         36 AspTrpHisProAspAlaProGlyGluMet-ValValLeuThrCysAsnThrProGluGl 55
              ||||||   |||      |||      ::: :::   |||      ::::::
Db       2898 GATTGGAAACCTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTCTGAGCTCATTTAGTGC 2957

Qy         55 uAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLe 75
               |||::::::      |||   |||   :::                          ||
Db       2958 AGACAACCTTGCAGCCACTGATGATGATAATGAAATG--------------AATAATCT 3002

Qy         75 uThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGl 95
              |   |||   |||                    |||          |||      ||
Db       3003 CCAAATTGCTGTGGATAGGATGCACAAAGGAGTAGCTTATGTGAAAAGAAAAATATATGA 3062

Qy         95 uValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAs 115
              |   :::      ||||||:::          |||      |||   |||      ||
Db       3063 ATTTATTCAACAGTCCTTCATTAGGAAACAAAAGATTTTAGATGAAATTAAACCACTTGA 3122

Qy        115 pIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAs 135
              |   |||      :::|||:::|||                        |||   :::   ::
Db       3123 TGATCTAAACAACAAGAAAGACAGT--------------------TGTATGTCCAATCA 3161

Qy        135 nTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheTh 155
              :                          |||   |||      ||||||   :::
Db       3162 T--------------------------ACAACAGAAATTGGGAAAGATCTTGACTATCT 3194

Qy        155 rValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThr-- 174
                                         |||      |||   |||   |||      |||
Db       3195 T--------------------AAAGATGTAAATGGAACTACAAGTGGTATAGGAACTGG 3233
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Qy        175 -LeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrValGluCy 194
Db       3234 CAGCAGTGTTGAAAAATACATTATTGATGAAAGTGATTACATGTCATTCATAAACAAC-- 3291

Qy        194 sGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValValValAs 214
Db       3292 ------------------CCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGAGAATC 3332

Qy        214 pAlaIleHisLysLeuLysTyrGluAsnTyrThrSer 226
Db       3333 TGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGT 3369
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RESULT 11
US-11-263-326-90
; Sequence 90, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulley, John C
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT APPLICATION NUMBER: US/11/263,326
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US 10/482,834
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 90
; LENGTH: 8370
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-263-326-90

Alignment Scores:

Pred. No.:	1.83	Length:	8370
Score:	99.00	Matches:	46
Percent Similarity:	35.2%	Conservative:	22
Best Local Similarity:	23.8%	Mismatches:	88
Query Match:	5.6%	Indels:	37
DB:	7	Gaps:	6

US-10-821-670A-56 (1-328) x US-11-263-326-90 (1-8370)

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Qy         36 AspTrpHisProAspAlaProGlyGluMet-ValValLeuThrCysAsnThrProGluGl 55
Db       3186 GATTGGAAACCTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTCTGAGCTCATTTAGTGC 3245

Qy         55 uAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLe 75
Db       3246 AGACAACCTTGCAGCCACTGATGATGATAATGAAATG--------------AATAATCT 3290

Qy         75 uThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGl 95
Db       3291 CCAAATTGCTGTGGATAGGATGCACAAAGGAGTAGCTTATGTGAAAAGAAAAATATATGA 3350

Qy         95 uValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAs 115
Db       3351 ATTTATTCAACAGTCCTTCATTAGGAAACAAAAGATTTTAGATGAAATTAAACCACTTGA 3410

Qy        115 pIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAs 135
Db       3411 TGATCTAAACAACAAGAAAGACAGT--------------------TGTATGTCCAATCA 3449

Qy        135 nTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheTh 155
Db       3450 T--------------------------ACAACAGAAATTGGGAAAGATCTTGACTATCT 3482

Qy        155 rValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThr-- 174
Db       3483 T--------------------AAAGATGTAAATGGAACTACAAGTGGTATAGGAACTGG 3521

Qy        175 -LeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrValGluCy 194
Db       3522 CAGCAGTGTTGAAAAATACATTATTGATGAAAGTGATTACATGTCATTCATAAACAAC-- 3579

Qy        194 sGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValValValAs 214
Db       3580 ------------------CCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGAGAATC 3620

Qy        214 pAlaIleHisLysLeuLysTyrGluAsnTyrThrSer 226
Db       3621 TGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGT 3657
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RESULT 12
US-11-263-326-95
; Sequence 95, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulley, John C
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT APPLICATION NUMBER: US/11/263,326
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US 10/482,834
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 95
; LENGTH: 8377
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-263-326-95

Alignment Scores:

Pred. No.:	1.83	Length:	8377
Score:	99.00	Matches:	46
Percent Similarity:	35.2%	Conservative:	22
Best Local Similarity:	23.8%	Mismatches:	88
Query Match:	5.6%	Indels:	37
DB:	7	Gaps:	6

US-10-821-670A-56 (1-328) x US-11-263-326-95 (1-8377)

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Qy         36 AspTrpHisProAspAlaProGlyGluMet-ValValLeuThrCysAsnThrProGluGl 55
Db       3197 GATTGGAAACCTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTCTGAGCTCATTTAGTGC 3256

Qy         55 uAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLe 75
Db       3257 AGACAACCTTGCAGCCACTGATGATGATAATGAAATG--------------AATAATCT 3301

Qy         75 uThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGl 95
Db       3302 CCAAATTGCTGTGGATAGGATGCACAAAGGAGTAGCTTATGTGAAAAGAAAAATATATGA 3361

Qy         95 uValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAs 115
Db       3362 ATTTATTCAACAGTCCTTCATTAGGAAACAAAAGATTTTAGATGAAATTAAACCACTTGA 3421

Qy        115 pIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAs 135
Db       3422 TGATCTAAACAACAAGAAAGACAGT--------------------TGTATGTCCAATCA 3460

Qy        135 nTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheTh 155
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OM nucleic - nucleic search, using sw model

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Title: US-10-821-670A-55
Perfect score: 985
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Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	985	100.0	985	2	AR595967	AR595967 Sequence
c	2	985	100.0	985	2	AR595968	AR595968 Sequence
	3	985	100.0	987	2	AR595950	AR595950 Sequence
c	4	985	100.0	987	2	AR595951	AR595951 Sequence
	5	981.8	99.7	990	2	AX076200	AX076200 Sequence
	6	981.8	99.7	990	2	AX076482	AX076482 Sequence
	7	981.8	99.7	1006	14	FCIL12P40	Y07762 Felis catus
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	12	980.2	99.5	2193	2	AR242435	AR242435 Sequence
	13	980.2	99.5	2193	2	AR280203	AR280203 Sequence
	14	980.2	99.5	2193	2	AR322418	AR322418 Sequence
	15	977	99.2	990	14	FCU83184	U83184 Felis catus
	16	919	93.3	921	2	AR242436	AR242436 Sequence
	17	919	93.3	921	2	AR280204	AR280204 Sequence
	18	919	93.3	921	2	AR322419	AR322419 Sequence
	19	917.4	93.1	921	2	AR242437	AR242437 Sequence
	20	917.4	93.1	921	2	AR280205	AR280205 Sequence
	21	917.4	93.1	921	2	AR322420	AR322420 Sequence
	22	917.4	93.1	921	2	AR595948	AR595948 Sequence
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	24	917.4	93.1	1533	2	AR595959	AR595959 Sequence
c	25	917.4	93.1	1533	2	AR595960	AR595960 Sequence
	26	884.2	89.8	990	2	AR151071	AR151071 Sequence
	27	884.2	89.8	990	2	BD014663	BD014663 Process f
	28	884.2	89.8	990	2	E15017	E15017 Canine mRNA
	29	884.2	89.8	990	2	AR316470	AR316470 Sequence
	30	884.2	89.8	2267	2	AR596011	AR596011 Sequence
c	31	884.2	89.8	2267	2	AR596012	AR596012 Sequence
	32	881	89.4	987	2	AR595969	AR595969 Sequence
c	33	881	89.4	987	2	AR595970	AR595970 Sequence
	34	881	89.4	1015	14	CFU49100	U49100 Canis famil
	35	881	89.4	1599	2	AR595971	AR595971 Sequence
c	36	881	89.4	1599	2	AR595972	AR595972 Sequence
	37	873	88.6	990	2	BD014653	BD014653 Process f
	38	869.8	88.3	990	2	AR151061	AR151061 Sequence
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	40	863.2	87.6	2154	2	BD171281	BD171281 Novel can
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	42	824.6	83.7	921	2	AR595965	AR595965 Sequence
c	43	824.6	83.7	921	2	AR595966	AR595966 Sequence
	44	823	83.6	1533	2	AR595973	AR595973 Sequence
c	45	823	83.6	1533	2	AR595974	AR595974 Sequence

ALIGNMENTS

RESULT 1
AR595967
LOCUS AR595967 985 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 55 from patent US 6818444.
ACCESSION AR595967
VERSION AR595967.1 GI:56646948
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 985)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 55 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .985
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 100.0%; Score 985; DB 2; Length 985;
Best Local Similarity 100.0%; Pred. No. 4.3e-288;
Matches 985; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

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Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
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Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
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Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985
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RESULT 2
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LOCUS       AR595968                985 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 57 from patent US 6818444.
ACCESSION   AR595968
VERSION     AR595968.1  GI:56646949
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 985)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 57 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .985
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN
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Query Match             100.0%;  Score 985;  DB 2;  Length 985;
Best Local Similarity   100.0%;  Pred. No. 4.3e-288;
Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
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Db         25 AGCAACTGGGCATCCGTGTCCTGCA 1
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RESULT 3
AR595950
LOCUS       AR595950                 987 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 29 from patent US 6818444.
ACCESSION   AR595950
VERSION     AR595950.1  GI:56646931
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 29 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 985;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-288;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 4
AR595951/c
LOCUS       AR595951                 987 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 31 from patent US 6818444.
ACCESSION   AR595951
VERSION     AR595951.1  GI:56646932
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 31 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .987
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                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 985;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-288;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGCA 3


RESULT 5
AX076200
LOCUS       AX076200                990 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 1 from Patent WO0104155.
ACCESSION   AX076200
VERSION     AX076200.1  GI:12710825
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 1 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="feline IL-12 p40"
ORIGIN

  Query Match             99.7%;  Score 981.8;  DB 2;  Length 990;
  Best Local Similarity   99.8%;  Pred. No. 4.1e-287;
  Matches  983;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
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Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
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Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
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Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
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Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 6
AX076482
LOCUS       AX076482                990 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 8 from Patent WO0104280.
ACCESSION   AX076482
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VERSION     AX076482.1  GI:12711034
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 8 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
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ORIGIN

  Query Match             99.7%;  Score 981.8;  DB 2;  Length 990;
  Best Local Similarity   99.8%;  Pred. No. 4.1e-287;
  Matches  983;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
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Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
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Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
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Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
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Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
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Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
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Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 7
FCIL12P40
LOCUS       FCIL12P40               1006 bp    mRNA    linear   MAM 18-APR-2005
DEFINITION  Felis catus mRNA for interleukin-12 p40 chain.
ACCESSION   Y07762
VERSION     Y07762.1  GI:2102664
KEYWORDS    interleukin-12 p40.
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1
  AUTHORS   Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
  TITLE     Molecular cloning of cat interleukin-12
  JOURNAL   Immunogenetics 45 (6), 462-463 (1997)
   PUBMED   9089110
REFERENCE   2  (bases 1 to 1006)
  AUTHORS   Schijns,V.E.C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
            Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
            Utrecht, NETHERLANDS
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9685"
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                     /tissue_type="peripheral blood"
     gene            1. .1006
                     /gene="IL-12.p40"
     CDS             1. .990
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                     /protein_id="CAA69068.1"
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                     GSSDPQEVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPAAEESLPIEVVVDAIHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFGV
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ORIGIN
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  Query Match             99.7%;  Score 981.8;  DB 14;  Length 1006;
  Best Local Similarity   99.8%;  Pred. No. 4.1e-287;
  Matches  983;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Db        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
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Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
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Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
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Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
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Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985
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RESULT 8
AR595956
LOCUS       AR595956               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 38 from patent US 6818444.
ACCESSION   AR595956
VERSION     AR595956.1  GI:56646937
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 38 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
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ORIGIN

  Query Match             99.7%;  Score 981.8;  DB 2;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 4.6e-287;
  Matches  983;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
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Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
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Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
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Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
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Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 9
AR595957/c
LOCUS       AR595957               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 40 from patent US 6818444.
ACCESSION   AR595957
VERSION     AR595957.1  GI:56646938
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 40 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             99.7%;  Score 981.8;  DB 2;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 4.6e-287;
  Matches  983;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
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Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
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Db       1359 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 1300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
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Db       1239 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db       1179 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 1120

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Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
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Db        999 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 940

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
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Db        879 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 820

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
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Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 760

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        759 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 640

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
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Db        639 AGCAACTGGGCATCCGTGTCCTGCA 615


RESULT 10
AX076209
LOCUS       AX076209               4522 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 10 from Patent WO0104155.
ACCESSION   AX076209
VERSION     AX076209.1  GI:12710834
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 10 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .4522
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Plasmid pMol-fil12p40"
ORIGIN

  Query Match             99.7%;  Score 981.8;  DB 2;  Length 4522;
  Best Local Similarity   99.8%;  Pred. No. 5.9e-287;
  Matches  983;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
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Db       3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Db       3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Db       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Db       3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Db       3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Db       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Db       3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Db       3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Db       3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Db       3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Db       3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Db       3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Db       3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Db       3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Db       3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985

Db       4007 AGCAACTGGGCATCCGTGTCCTGCA 4031


RESULT 11
AX076476
LOCUS       AX076476               4522 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 2 from Patent WO0104280.
ACCESSION   AX076476
VERSION     AX076476.1  GI:12711028
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 2 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .4522
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="IL-12p40"
ORIGIN

  Query Match             99.7%;  Score 981.8;  DB 2;  Length 4522;
  Best Local Similarity   99.8%;  Pred. No. 5.9e-287;
  Matches  983;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Db       3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Db       3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Db       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Db       3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Db       3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Db       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Db       3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Db       3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Db       3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Db       3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Db       3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
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Db       3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
                |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
                |||||||||||||||||||||||||
Db       4007 AGCAACTGGGCATCCGTGTCCTGCA 4031


RESULT 12
AR242435
LOCUS       AR242435               2193 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 5 from patent US 6472509.
ACCESSION   AR242435
VERSION     AR242435.1  GI:27288852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2193)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 5 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .2193
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match            99.5%;  Score 980.2;  DB 2;  Length 2193;
  Best Local Similarity  99.7%;  Pred. No. 1.5e-286;
  Matches  982;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              |||||||||||||| |||||||||||||||| |||||||||||||||||||| |||
Db         64 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTACCTGGTTTTGCTGGCACCTCCTCTC 123

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 183

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 243

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 303

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 363

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 423

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Db        424 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 483

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 543

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 603

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 663

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 723

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 783

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 843

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 903

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 963

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 1023

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
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Db       1024 AGCAACTGGGCATCCGTGTCCTGCA 1048


RESULT 13
AR280203
LOCUS       AR280203               2193 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 5 from patent US 6518045.
ACCESSION   AR280203
VERSION     AR280203.1  GI:29715593
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2193)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 5 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .2193
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                     /mol_type="mRNA"
ORIGIN

  Query Match            99.5%;  Score 980.2;  DB 2;  Length 2193;
  Best Local Similarity  99.7%;  Pred. No. 1.5e-286;
  Matches  982;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
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Db         64 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTACCTGGTTTTGCTGGCACCTCCTCTC 123
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Qy          61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Db         124 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 183

Qy         121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         184 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 243

Qy         181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         244 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 303

Qy         241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         304 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 363

Qy         301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         364 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 423

Qy         361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Db         424 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 483

Qy         421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db         484 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 543

Qy         481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Db         544 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 603

Qy         541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         604 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 663

Qy         601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         664 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 723

Qy         661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         724 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 783

Qy         721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
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Db         784 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 843

Qy         781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
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Db         844 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 903

Qy         841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         904 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 963

Qy         901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
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Db         964 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 1023

Qy         961 AGCAACTGGGCATCCGTGTCCTGCA 985
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Db        1024 AGCAACTGGGCATCCGTGTCCTGCA 1048
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RESULT 14
AR322418
LOCUS       AR322418               2193 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 5 from patent US 6566097.
ACCESSION   AR322418
VERSION     AR322418.1  GI:33708171
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2193)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 5 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .2193
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ORIGIN

  Query Match             99.5%;  Score 980.2;  DB 2;  Length 2193;
  Best Local Similarity   99.7%;  Pred. No. 1.5e-286;
  Matches  982;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy           1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
               |||||||||||||| |||||||||||||||||| |||||||||||||||||||||| |||
Db          64 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTACCTGGTTTTGCTGGCACCTCCTCTC 123

Qy          61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         124 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 183

Qy         121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
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Qy         301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
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Qy         481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Db         544 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 603

Qy         541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Qy         601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
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Qy         661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Qy         721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
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Qy         781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
```

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Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
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Db       1024 AGCAACTGGGCATCCGTGTCCTGCA 1048


RESULT 15
FCU83184
LOCUS       FCU83184                990 bp    mRNA    linear   MAM 16-JUL-1999
DEFINITION  Felis catus interleukin-12 p40 subunit (IL-12) mRNA, complete cds.
ACCESSION   U83184
VERSION     U83184.1  GI:2735050
KEYWORDS    .
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Nucleotide and predicted peptide sequence of feline interleukin-12
            (IL-12)
  JOURNAL   DNA Seq. 8 (1-2), 77-82 (1997)
   PUBMED   9522125
REFERENCE   2  (bases 1 to 990)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal
            Veterinary Medicine, University of Zurich, Winterthurerstrasse 260,
            Zurich, ZH 8057, Switzerland
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
     CDS             1. .990
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                     /codon_start=1
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                     GSSDPQGVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPAAEESLPIEVVVDAIHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFGV
                     QVQGKNNREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSNWASVSCS"
ORIGIN

  Query Match             99.2%;  Score 977;  DB 14;  Length 990;
  Best Local Similarity   99.5%;  Pred. No. 1.2e-285;
  Matches  980;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||||||||||||| | || ||||||||||||||||||||||||
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Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

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Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
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Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
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Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
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Job time : 4059.16 secs
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 10, 2006, 03:13:22 ; Search time 727.626 Seconds
(without alignments)
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Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	985	100.0	985	6	ABK98962	Abk98962 Feline in
	2	985	100.0	985	6	ABK98961	Abk98961 Feline in
	3	985	100.0	985	14	ADV34707	Adv34707 Feline N-
c	4	985	100.0	985	14	ADV34709	Adv34709 Feline N-
	5	985	100.0	987	6	ABK98944	Abk98944 Feline in
c	6	985	100.0	987	6	ABK98945	Abk98945 Feline in
	7	985	100.0	987	14	ADV34682	Adv34682 Feline si
c	8	985	100.0	987	14	ADV34684	Adv34684 Feline si
	9	981.8	99.7	990	4	AAF26082	Aaf26082 Feline IL
	10	981.8	99.7	990	4	AAF26085	Aaf26085 Feline IL
	11	981.8	99.7	1599	6	ABK98950	Abk98950 Feline in
c	12	981.8	99.7	1599	6	ABK98951	Abk98951 Feline in
	13	981.8	99.7	1599	14	ADV34691	Adv34691 Feline si
c	14	981.8	99.7	1599	14	ADV34693	Adv34693 Feline si
	15	981.8	99.7	4522	4	AAF26076	Aaf26076 Feline IL
	16	981.8	99.7	4522	4	AAF26094	Aaf26094 Plasmid p
	17	980.2	99.5	2193	2	AAV56625	Aav56625 Feline FL
	18	919	93.3	921	2	AAV56626	Aav56626 Feline FL
	19	917.4	93.1	921	2	AAV56627	Aav56627 Feline FL
	20	917.4	93.1	921	6	ABK98942	Abk98942 Feline in
c	21	917.4	93.1	921	6	ABK98943	Abk98943 Feline in
c	22	917.4	93.1	921	14	ADV34681	Adv34681 Feline si
	23	917.4	93.1	921	14	ADV34679	Adv34679 Feline si
c	24	917.4	93.1	1533	6	ABK98954	Abk98954 Feline in
	25	917.4	93.1	1533	6	ABK98953	Abk98953 Feline in
c	26	917.4	93.1	1533	14	ADV34697	Adv34697 Feline si
	27	917.4	93.1	1533	14	ADV34695	Adv34695 Feline si
	28	884.2	89.8	990	2	AAV13817	Aav13817 Canine IL
	29	884.2	89.8	990	2	AAX03162	Aax03162 Nucleic a
	30	884.2	89.8	990	2	AAX35625	Aax35625 Nucleic a
	31	884.2	89.8	990	4	AAI64388	Aai64388 Canine co
c	32	884.2	89.8	2267	6	ABK99006	Abk99006 Canine in
	33	884.2	89.8	2267	6	ABK99005	Abk99005 Canine in
	34	884.2	89.8	2267	14	ADV34757	Adv34757 Canine si
c	35	884.2	89.8	2267	14	ADV34759	Adv34759 Canine si
	36	881	89.4	987	6	ABK98963	Abk98963 Canine in
c	37	881	89.4	987	6	ABK98964	Abk98964 Canine in
c	38	881	89.4	987	14	ADV34712	Adv34712 Canine si
	39	881	89.4	987	14	ADV34710	Adv34710 Canine si
	40	881	89.4	1015	13	ADT04849	Adt04849 Canine in
	41	881	89.4	1599	6	ABK98965	Abk98965 Canine in
c	42	881	89.4	1599	6	ABK98966	Abk98966 Canine in
c	43	881	89.4	1599	14	ADV34715	Adv34715 Canine si
	44	881	89.4	1599	14	ADV34713	Adv34713 Canine si
	45	873	88.6	990	2	AAV13816	Aav13816 Canine IL

ALIGNMENTS

RESULT 1
ABK98962/c
ID ABK98962 standard; cDNA; 985 BP.
XX
AC ABK98962;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p40-N985 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Example 3; Page 75-76; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,

```
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 985 BP; 207 A; 245 C; 250 G; 283 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 985;  DB 6;  Length 985;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-298;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
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Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
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Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
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Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGCA 1


RESULT 2
ABK98961
ID   ABK98961 standard; cDNA; 985 BP.
XX
AC   ABK98961;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p40-N985 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69311.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 3; Page 73-74; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 985 BP; 283 A; 250 C; 245 G; 207 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 985;  DB 6;  Length 985;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-298;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
```

```
Qy          61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy         301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy         361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy         421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy         481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy         541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy         601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy         661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy         721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy         781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy         841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy         901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy         961 AGCAACTGGGCATCCGTGTCCTGCA 985
               |||||||||||||||||||||||||
Db         961 AGCAACTGGGCATCCGTGTCCTGCA 985
```

```
RESULT 3
ADV34707
ID   ADV34707 standard; cDNA; 985 BP.
XX
AC   ADV34707;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline N-terminal IL-12p40 protein encoding cDNA, nFeIL-12p40-N985.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .984
FT                   /*tag=  a
FT                   /product= "PCaIL-12P40-N328 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34708.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 55; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline N-terminal single chain IL-12p40 protein
CC   encoding cDNA.
XX
SQ   Sequence 985 BP; 283 A; 250 C; 245 G; 207 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 985;  DB 14;  Length 985;
  Best Local Similarity  100.0%;  Pred. No. 6.4e-298;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy           1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy          61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
```

```
Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985
```

RESULT 4
ADV34709/c
ID ADV34709 standard; DNA; 985 BP.
XX
AC ADV34709;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline N-terminal IL-12p40 protein complementary DNA, nFeIL-12p40-N985.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Felis catus.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 3; SEQ ID NO 57; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline N-terminal single chain IL-12p40
CC complementary DNA.
XX
SQ Sequence 985 BP; 207 A; 245 C; 250 G; 283 T; 0 U; 0 Other;

Query Match 100.0%; Score 985; DB 14; Length 985;
Best Local Similarity 100.0%; Pred. No. 6.4e-298;
Matches 985; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
                |||||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGCA 1
```

RESULT 5
ABK98944
ID ABK98944 standard; cDNA; 987 BP.
XX
AC ABK98944;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p40-987 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69303.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 1; Page 51-53; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 987 BP; 283 A; 250 C; 246 G; 208 T; 0 U; 0 Other;

  Query Match   100.0%; Score 985; DB 6; Length 987;
  Best Local Similarity   100.0%; Pred. No. 6.4e-298;
  Matches 985; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
```

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Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 6
ABK98945/c
ID   ABK98945 standard; cDNA; 987 BP.
XX
AC   ABK98945;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p40-987 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 3; Page 54; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 987 BP; 208 A; 246 C; 250 G; 283 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 985;  DB 6;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-298;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGCA 3


RESULT 7
ADV34682
ID   ADV34682 standard; cDNA; 987 BP.
XX
AC   ADV34682;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12p40 full-length cDNA, nFeIL-12p40 987.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
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FH   Key             Location/Qualifiers
FT   CDS             1. .987
FT                   /*tag=  a
FT                   /product= "PFeIL-12p40 329 protein "
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34683.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 23; SEQ ID NO 29; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12p40 subunit protein
CC   encoding full-length cDNA.
XX
SQ   Sequence 987 BP; 283 A; 250 C; 246 G; 208 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 985;  DB 14;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-298;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 8
ADV34684/c
ID   ADV34684 standard; DNA; 987 BP.
XX
AC   ADV34684;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12p40 complementary DNA, nFeIL-12p40 987.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
```

```
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 31; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12p40 subunit full-length
CC   complementary DNA.
XX
SQ   Sequence 987 BP; 208 A; 246 C; 250 G; 283 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 985;  DB 14;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-298;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGCA 3


RESULT 9
AAF26082
ID   AAF26082 standard; DNA; 990 BP.
XX
AC   AAF26082;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p40 encoding DNA SEQ ID 8.
XX
KW   Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW   interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS   Felis sp.
XX
PN   WO200104280-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002262.
XX
PR   08-JUL-1999;   99CH-00001258.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
XX
PI   Leutenegger C,  Schroff M,  Wittig B,  Lutz H;
XX
DR   WPI; 2001-147190/15.
XX
PT   Vaccine for treating or preventing lentivirus infection in cats, contains
PT   nucleic acid sequence encoding viral protein under control of eukaryotic
PT   promoter.
XX
PS   Claim 14; Page 36; 37pp; German.
XX
CC   This invention describes a novel vaccine (A) for prevention or treatment
CC   of lentivirus infection in felines which comprises an immunizing nucleic
CC   acid sequence (I) that contains, or comprises, at least part of a gene
CC   encoding a protein (II) of the virus, under control of a eukaryotic
CC   promoter functional in the relevant animal. (II) is especially the
CC   envelope (env) protein. The invention also describes (1) vaccine (A)
CC   containing an immunizing protein, or fragment, from a lentivirus plus at
CC   least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC   lentivirus protein, or fragment, especially derived from feline immune
CC   deficiency virus (FIV), by expressing the corresponding nucleic acid
CC   sequence in a host cell. The products of the invention have antiviral
CC   activity. The vaccine (A) and related protein-based vaccines, are
CC   particularly used to treat or prevent lentivirus infections in domestic
CC   cats, especially feline immune deficiency virus (FIV). Vaccination with
CC   (A) allows differentiation between vaccinated and infected animals, from
CC   the antibody status. The vaccines may be formulated with an adjuvant
CC   (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC   immune response, particularly a Th1 response
XX
SQ   Sequence 990 BP; 283 A; 249 C; 248 G; 210 T; 0 U; 0 Other;
```

```
  Query Match           99.7%;  Score 981.8;  DB 4;  Length 990;
  Best Local Similarity  99.8%;  Pred. No. 6.5e-297;
  Matches  983;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985
```

```
RESULT 10
AAF26085
ID   AAF26085 standard; DNA; 990 BP.
XX
AC   AAF26085;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p40 encoding DNA.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS   Felis sp.
XX
PN   WO200104155-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002263.
XX
PR   08-JUL-1999;   99CH-00001259.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Lutz H,  Leutenegger C,  Pedersen N,  Schroff M,  Wittig B;
XX
DR   WPI; 2001-147178/15.
XX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs.
XX
PS   Claim 3; Page 30; 35pp; German.
XX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
CC   following: (i) as immunostimulant, for preventative or therapeutic use;
CC   and (ii) treating tumors and autoimmune diseases, or diseases associated
CC   with a Th1 defect, especially pre-existing infections by feline immune
CC   deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ   Sequence 990 BP; 283 A; 249 C; 248 G; 210 T; 0 U; 0 Other;
```

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  Query Match           99.7%;  Score 981.8;  DB 4;  Length 990;
  Best Local Similarity  99.8%;  Pred. No. 6.5e-297;
  Matches  983;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
```

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Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 11
ABK98950
ID   ABK98950 standard; cDNA; 1599 BP.
XX
AC   ABK98950;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1599 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69306.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 58-60; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

  Query Match             99.7%;  Score 981.8;  DB 6;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 8.5e-297;
  Matches  983;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985
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RESULT 12
ABK98951/c
ID   ABK98951 standard; cDNA; 1599 BP.
XX
AC   ABK98951;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1599 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 61-62; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

  Query Match             99.7%;  Score 981.8;  DB 6;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 8.5e-297;
  Matches  983;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1599 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 1540

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 1420

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1359 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 1300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1299 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 1240

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1179 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 1120

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1119 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 1060

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        999 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 940

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        939 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 880

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        879 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 820

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 760

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        759 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 640

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        639 AGCAACTGGGCATCCGTGTCCTGCA 615


RESULT 13
ADV34691
ID   ADV34691 standard; cDNA; 1599 BP.
XX
AC   ADV34691;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1599
FT                   /*tag=  a
FT                   /product= "PFeIL-12p533 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34692.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 38; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

  Query Match             99.7%;  Score 981.8;  DB 14;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 8.5e-297;
  Matches  983;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
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Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 14
ADV34693/c
ID   ADV34693 standard; DNA; 1599 BP.
XX
AC   ADV34693;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 complementary DNA, nFeIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 40; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 complementary DNA.
XX
SQ   Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

  Query Match             99.7%;  Score 981.8;  DB 14;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 8.5e-297;
  Matches  983;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1599 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 1540

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 1420

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1359 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 1300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1299 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 1240

Qy        361 AAAGAATCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1179 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 1120

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       1119 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 1060

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        999 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 940

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        939 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 880

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        879 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 820

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 760

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        759 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 640

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        639 AGCAACTGGGCATCCGTGTCCTGCA 615


RESULT 15
AAF26076
ID   AAF26076 standard; DNA; 4522 BP.
XX
AC   AAF26076;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p40 encoding DNA SEQ ID 2.
XX
KW   Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW   interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS   Felis sp.
XX
PN   WO200104280-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002262.
XX
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PR 08-JUL-1999; 99CH-00001258.
XX
PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA (UYZU-) UNIV ZUERICH.
XX
PI Leutenegger C, Schroff M, Wittig B, Lutz H;
XX
DR WPI; 2001-147190/15.
XX
PT Vaccine for treating or preventing lentivirus infection in cats, contains
PT nucleic acid sequence encoding viral protein under control of eukaryotic
PT promoter.
XX
PS Disclosure; Page 29-31; 37pp; German.
XX
CC This invention describes a novel vaccine (A) for prevention or treatment
CC of lentivirus infection in felines which comprises an immunizing nucleic
CC acid sequence (I) that contains, or comprises, at least part of a gene
CC encoding a protein (II) of the virus, under control of a eukaryotic
CC promoter functional in the relevant animal. (II) is especially the
CC envelope (env) protein. The invention also describes (1) vaccine (A)
CC containing an immunizing protein, or fragment, from a lentivirus plus at
CC least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC lentivirus protein, or fragment, especially derived from feline immune
CC deficiency virus (FIV), by expressing the corresponding nucleic acid
CC sequence in a host cell. The products of the invention have antiviral
CC activity. The vaccine (A) and related protein-based vaccines, are
CC particularly used to treat or prevent lentivirus infections in domestic
CC cats, especially feline immune deficiency virus (FIV). Vaccination with
CC (A) allows differentiation between vaccinated and infected animals, from
CC the antibody status. The vaccines may be formulated with an adjuvant
CC (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC immune response, particularly a Th1 response
XX
SQ Sequence 4522 BP; 1180 A; 1126 C; 1106 G; 1110 T; 0 U; 0 Other;

Query Match 99.7%; Score 981.8; DB 4; Length 4522;
Best Local Similarity 99.8%; Pred. No. 1.6e-296;
Matches 983; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
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Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Db       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db       3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
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Db       3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Db       3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
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Db       3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
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Db       3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
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Search completed: June 10, 2006, 04:50:52
Job time : 729.626 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 10, 2006, 03:16:38 ; Search time 5752.33 Seconds
(without alignments)
9575.336 Million cell updates/sec

Title: US-10-821-670A-55
Perfect score: 985
Sequence: 1 atgcatcctcagcagttggt.....ctgggcatccgtgtcctgca 985

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
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10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	581.6	59.0	756	5	CK130264	CK130264 AGENCOURT
	2	579.6	58.8	735	5	CD559605	CD559605 AGENCOURT
	3	570	57.9	747	5	CD559607	CD559607 AGENCOURT
	4	568.6	57.7	772	5	CD559604	CD559604 AGENCOURT
	5	512.8	52.1	745	5	CD559602	CD559602 AGENCOURT
	6	508.6	51.6	1839	6	AK162981	AK162981 Mus muscu
c	7	507.2	51.5	785	5	CD559448	CD559448 AGENCOURT
c	8	506	51.4	772	5	CD559450	CD559450 AGENCOURT
c	9	501	50.9	736	5	CD559453	CD559453 AGENCOURT
c	10	499.4	50.7	762	5	CD559451	CD559451 AGENCOURT
	11	497.6	50.5	2908	6	AK155593	AK155593 Mus muscu
c	12	477	48.4	754	5	CD559452	CD559452 AGENCOURT
c	13	471.4	47.9	766	5	CD559449	CD559449 AGENCOURT
c	14	435.6	44.2	725	5	CD559454	CD559454 AGENCOURT
	15	418.8	42.5	724	5	CD559603	CD559603 AGENCOURT
	16	401.4	40.8	1042	5	CD559606	CD559606 AGENCOURT
	17	355.4	36.1	649	5	CJ134671	CJ134671
	18	265.8	27.0	475	7	BF704417	BF704417 MI-P-E6-a
	19	249.8	25.4	417	8	CO949904	CO949904 UMC-pd12c
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	21	220.4	22.4	423	4	BY218447	BY218447 BY218447
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	24	207.4	21.1	346	4	BY164658	BY164658 BY164658
	25	202.8	20.6	355	4	BY221814	BY221814 BY221814
	26	199.8	20.3	700	12	CE093997	CE093997 tigr-gss-
	27	181.8	18.5	252	10	DV799576	DV799576 est_t_tru
	28	180.4	18.3	535	11	AZ441303	AZ441303 1M0232M24
c	29	169.8	17.2	569	11	AZ853726	AZ853726 2M0157M01
	30	148.2	15.0	666	4	BY749553	BY749553 BY749553
c	31	95.2	9.7	668	14	AG079702	AG079702 Pan trogl
	32	76	7.7	672	13	DU179885	DU179885 109855349
	33	73.4	7.5	704	13	CZ422673	CZ422673 1018376 R
	34	65.8	6.7	850	3	BU291084	BU291084 603603708
c	35	63.6	6.5	324	11	AQ981401	AQ981401 RPCI-23-3
	36	53.8	5.5	645	13	CL344654	CL344654 RPCI44_27
	37	47.8	4.9	657	13	CL344592	CL344592 RPCI44_27
c	38	47.2	4.8	872	12	CC581475	CC581475 CH240_376
c	39	42.8	4.3	581	11	AQ394113	AQ394113 CITBI-E1-
c	40	42.2	4.3	801	2	BI661062	BI661062 603304362
c	41	41.2	4.2	772	11	BZ070797	BZ070797 ljr96a09.
c	42	40.4	4.1	919	12	CG071974	CG071974 PUFYL33TB
	43	40.2	4.1	642	4	CA351258	CA351258 622276 NC
	44	40.2	4.1	862	12	CG277764	CG277764 OG5BA27TC
	45	39.8	4.0	401	4	BW814962	BW814962 BW814962

ALIGNMENTS

RESULT 1
CK130264
LOCUS CK130264 756 bp mRNA linear EST 02-DEC-2003
DEFINITION AGENCOURT_14496566 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971871 5', mRNA sequence.
ACCESSION CK130264
VERSION CK130264.1 GI:38622200
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 756)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: h column: 02
High quality sequence start: 5
High quality sequence stop: 731.
FEATURES Location/Qualifiers
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/tissue_type="mixed"
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/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:

loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 59.0%; Score 581.6; DB 5; Length 756;
Best Local Similarity 88.6%; Pred. No. 1.1e-158;
Matches 642; Conservative 0; Mismatches 80; Indels 3; Gaps 1;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              |||  ||  |||||||||||||||| | ||||||||||||||||| ||||||  ||||||||
Db         34 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 93

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||| ||||| | |||||||| ||||| ||||| ||| | || |||
Db         94 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 153

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||| |||||||||||||||||||||  | || ||||||||||||  |||||||||
Db        154 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 213

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||  |||||||||||||| ||| |||||||||| ||||| ||||||||||||||||||
Db        214 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 273

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              || |||| |||||||||||||||| |||||||| |||||||||||||||||| |||||||||
Db        274 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 333

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              |||| ||| | |||||||||||||||||||||||||||||||||||| |||| ||| |||
Db        334 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 393

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||| |||||||||||| |||||||| ||| ||||| ||||||||||||||||||||
Db        394 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 453

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db        454 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 513

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Db        574 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 630

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
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Db        631 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 690

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              || |||||||||||||||||||||||||||||||||||||||| |||| ||||||||||||
Db        691 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCNAACCTGACCCACCCAAG 750

Qy        721 AACCT 725
              ||| |
Db        751 AACTT 755
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RESULT 2
CD559605
LOCUS CD559605 735 bp mRNA linear EST 26-NOV-2003
DEFINITION AGENCOURT_14496534 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971870 5', mRNA sequence.
ACCESSION CD559605
VERSION CD559605.2 GI:38558937
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 735)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585673.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: h column: 01
High quality sequence stop: 709.
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/mol_type="mRNA"
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/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 58.8%; Score 579.6; DB 5; Length 735;
Best Local Similarity 88.6%; Pred. No. 4.2e-158;
Matches 640; Conservative 0; Mismatches 79; Indels 3; Gaps 1;

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Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Db         77 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 136
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Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
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Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Db        197 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 256

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
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Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Qy        721 AA 722
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Db        734 AA 735
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RESULT 3
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LOCUS       CD559607                747 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14497061 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971868 5', mRNA sequence.
ACCESSION   CD559607
VERSION     CD559607.2  GI:38558941
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 747)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585675.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: g  column: 11
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                      /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                      loxP-HindIII; Clones from this library have been
                      PCR-amplified using gene-specific primers to contain the
                      complete open reading frame (based on known gene sequences
                      available from NCBI's RefSeq). Template for PCR is cDNA
                      derived from either pooled cytoplasmic polyA RNA from 30
                      cells lines or pooled total RNA from 10 different tissues
                      (from BD Biosciences/Clontech and Washington University).
                      PCR products are directionally cloned into the loxP sites
                      of the pDNR-Dual vector. Library constructed by Dr.
                      Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                      Expression Laboratory, Research Technology Program, SAIC
                      Frederick, NCI-Frederick, Frederick, MD 21702). For
                      information on which gene each clone represents, please
                      visit our anonymous ftp site at
                      ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                      a Note: this is a NIH_MGC Library."
ORIGIN
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  Query Match             57.9%;  Score 570;  DB 5;  Length 747;
  Best Local Similarity   88.4%;  Pred. No. 2.8e-155;
  Matches  631;  Conservative    0;  Mismatches   80;  Indels    3;  Gaps    1;

Qy          8 CTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCA 67
              | |||||||||||||| | |||||||||||||||| |||||| |||||||| ||||||
Db         36 CCCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTCGTGGCCA 95

Qy         68 TATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCG 127
              |||||||||| ||||| | |||||||| ||||| ||||| ||| | || |||||||| |
Db         96 TATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCTG 155

Qy        128 GAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCTG 187
              |||||||||||||||||||||  | || ||||||||||||  ||||||||||||  |
Db        156 GAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTGG 215

Qy        188 ACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTG 247
              |||||||||||| ||| |||||||| ||||| ||||||||||||||||||| ||||
Db        216 ACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTTG 275

Qy        248 CAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCC 307
              |||||||||||||||| |||||||| |||||||||||||||| ||||||||| |||| |
Db        276 GAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTGC 335

Qy        308 TGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAAT 367
              || | |||||||||||||||||||||||||||||||||||| |||| ||| |||||||||
Db        336 TGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAAC 395

Qy        368 CCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCT 427
              |||||||||||| |||||||| ||| ||||| ||||||||||||||||||||||||||||
Db        396 CCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCT 455

Qy        428 GGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCT 487
              |||||||||| |||||||||| ||||||| ||||| |||||||||||||||||||||| |
Db        456 GGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTT 515

Qy        488 CTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGG 547
              |||||||||||||||||| || ||||| || |||||||| |||||||  ||||||| ||
Db        516 CTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGG 575
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Qy        548 ACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTG 607
              |||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||||| ||||
Db        576 ACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTG 632

Qy        608 CCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAA 667
              | |||||||| || |||||||| ||| |||||||     |||||||||| |||| ||||
Db        633 CTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATTGCGTTCACAAGCTCCAGTATGAAA 692

Qy        668 ACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGA 721
              |||||||| |||||||||||||||||||||||||||||||| |||||||||| |
Db        693 ACTACACCCGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAAA 746
```

RESULT 4
CD559604
LOCUS CD559604 772 bp mRNA linear EST 26-NOV-2003
DEFINITION AGENCOURT_14496598 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971872 5', mRNA sequence.
ACCESSION CD559604
VERSION CD559604.2 GI:38558934
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 772)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585672.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: h column: 03
High quality sequence start: 13
High quality sequence stop: 750.

FEATURES Location/Qualifiers
source 1. .772
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971872"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 57.7%; Score 568.6; DB 5; Length 772;
Best Local Similarity 87.9%; Pred. No. 7.2e-155;
Matches 632; Conservative 0; Mismatches 84; Indels 3; Gaps 1;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||| ||  ||||||||||||||| | |||||||||||||||| |||||| ||||||||
Db         38 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 97

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||| ||||| | |||||||| ||||| ||||| ||| | || |||
Db         98 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 157

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||| |||||||||||||||||||||||  | || ||||||||||||  |||||||||
Db        158 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 217

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||  |||||||||||||| ||||||||||||||| |||| ||||||||||||||||||
Db        218 ACCTTGGACCAGAGCAGTGAGGTCCTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 277

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              || |||| |||||||||||||| |||||||| |||||||||||||||| |||||||||
Db        278 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 337

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              |||| ||| | |||||||||||||||||||||||||||||||||| |||| ||| |||
Db        338 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 397

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||| |||||||||| |||||||| ||| ||||| |||||||||||||||||||||||
Db        398 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 457

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              |||||||||||||||| |||||||| ||||||| ||||| ||||||||||||||||||
Db        458 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 517

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||| |||||||||||||||||| || ||||| || |||||||| |||||||  |||
Db        518 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 577

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||| |||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||
Db        578 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 634

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
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Db        635 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 694

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAA 719
              || |||||||||||||||||||||||||||||||||||||||| | |  |   || ||
Db        695 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAACCTGACCAACCCAAA 753
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RESULT 5
CD559602
LOCUS CD559602 745 bp mRNA linear EST 26-NOV-2003
DEFINITION AGENCOURT_14496684 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971874 5', mRNA sequence.
ACCESSION CD559602
VERSION CD559602.2 GI:38558930
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 745)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585670.

```
           Contact: Daniela S. Gerhard, Ph.D.
           Office of Cancer Genomics
           National Cancer Institute / NIH
           Bldg. 31 Rm10A07 Bethesda, MD 20892
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: IRBK2  row: h  column: 05
           High quality sequence start: 2
           High quality sequence stop: 644.
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971874"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             52.1%;  Score 512.8;  DB 5;  Length 745;
  Best Local Similarity   86.6%;  Pred. No. 1.7e-138;
  Matches  589;  Conservative    0;  Mismatches   87;  Indels    4;  Gaps    2;

Qy          8 CTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCA 67
              | |||||||||||||| | ||||||||||||||||| |||||| |||||||| ||||||
Db         13 CCCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTCGTGGCCA 72

Qy         68 TATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCG 127
              |||||||||| ||||| | |||||||| ||||| ||||| ||| | || |||||||| |
Db         73 TATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCTG 132

Qy        128 GAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCTG 187
              |||||||||||||||||||||   | || ||||||||||||  ||||||||||||   |
Db        133 GAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTGG 192

Qy        188 ACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTG 247
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Db        193 ACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTTG 252

Qy        248 CAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCC 307
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Db        253 GAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTGC 312

Qy        308 TGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAAT 367
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Db        313 TGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAAC 372

Qy        368 CCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCT 427
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Db        373 CCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCT 432

Qy        428 GGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCT 487
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Db        433 GGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTT 492

Qy        488 CTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGG 547
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Db        493 CTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGG 552

Qy        548 ACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTG 607
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Db        553 ACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTG 609

Qy        608 CCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAA 667
              | ||||||||  ||  ||||||||  |||  |||||||  ||    ||||||||||  ||    |||
Db        610 CTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGC-CGTCACAAGCTCATGTTGAAAA 668

Qy        668 ACTACACCAGCAGCTTCTTC 687
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Db        669 TACACCACGGCTTCTTTCTC 688


RESULT 6
AK162981
LOCUS       AK162981               1839 bp    mRNA    linear   HTC 21-SEP-2005
DEFINITION  Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched
            library, clone:A430014H12 product:interleukin 12b, full insert
            sequence.
ACCESSION   AK162981
VERSION     AK162981.1  GI:74188061
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
            Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
            Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
            Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
            Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
```

Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

CONSRTM RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409 (6821), 685-690 (2001)

PUBMED 11217851

REFERENCE 5

AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420 (6915), 563-573 (2002)

PUBMED 12466851

REFERENCE 6

AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE The transcriptional landscape of the mammalian genome

JOURNAL Science 309 (5740), 1559-1563 (2005)

PUBMED 16141072

REFERENCE 7

AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.

CONSRTM RIKEN Genome Exploration Research Group

TITLE Antisense transcription in the mammalian transcriptome

JOURNAL Science 309 (5740), 1564-1566 (2005)

PUBMED 16141073

REFERENCE 8 (bases 1 to 1839)

AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

source 1. .1839
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/mol_type="mRNA"
/strain="C57BL/6J"
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ORIGIN

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Matches 731; Conservative 0; Mismatches 239; Indels 39; Gaps 4;

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RESULT 7
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DEFINITION AGENCOURT_14496712 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971874 5', mRNA sequence.
ACCESSION CD559448
VERSION CD559448.2 GI:38453466
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 785)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585516.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: h column: 05
High quality sequence stop: 696.

FEATURES Location/Qualifiers
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/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 51.5%; Score 507.2; DB 5; Length 785;
Best Local Similarity 85.8%; Pred. No. 7.5e-137;
Matches 587; Conservative 0; Mismatches 93; Indels 4; Gaps 2;

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RESULT 8
CD559450/c

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ACCESSION   CD559450
VERSION     CD559450.2  GI:38453469
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Hominidae; Homo.
REFERENCE   1  (bases 1 to 772)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585518.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
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                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN
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              |||||||||| ||| ||| |  |||||||||||||||||| |||| | |||| |||  ||||
Db        234 AAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGCAAAAATGC 175

Qy        915 CAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATC 974
              ||  ||  ||||||  |||   ||||||||||||||||||||| |||||| | ||||||||
Db        174 CAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAATGGGCATC 115

Qy        975 CGTGTCCTGCA 985
              ||| ||||||
Db        114 TGTGCCCTGCA 104


RESULT 9
CD559453/c
LOCUS       CD559453                736 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14497154 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971869 5', mRNA sequence.
ACCESSION   CD559453
VERSION     CD559453.2  GI:38453475
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 736)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585521.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: g  column: 12
            High quality sequence stop: 683.
FEATURES             Location/Qualifiers
     source          1. .736
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971869"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN
```

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  Query Match           50.9%;  Score 501;  DB 5;  Length 736;
  Best Local Similarity  87.2%;  Pred. No. 4.8e-135;
  Matches  573;  Conservative    0;  Mismatches   80;  Indels    4;  Gaps    2;

Qy        329 GAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAA 388
              | | |||||||||||||||| |||| ||| ||||||||| |||||||||||| ||||||||
Db        732 GGAATTGGTCCACTGATAT-TTAAAGGACCAGAAAGAACCCAAAAATAAGACCTTTCTAA 674

Qy        389 AATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTA 448
              |||  ||||| ||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        673 GATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGACAATCAGTA 614

Qy        449 CCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTT 508
              | |||||||  ||||| |||||||||||||||||||||| |||||||||||||||||||| |
Db        613 CTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGT 554

Qy        509 GTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGT 568
              | ||||| || |||||||| |||||||  |||||| |||||||| ||| |||    |||
Db        553 GCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAACAAGGAGTAT---GAGT 497

Qy        569 ACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTG 628
              || |||||||||| ||||||| |||||||||||| ||||| |||||||| || |||||||
Db        496 ACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCTGAGGAGAGTCTGCCCATTG 437

Qy        629 AAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCA 688
              | ||| |||||||  ||  |||||||||||||||| ||||||||||||||||||||||||||
Db        436 AGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCA 377

Qy        689 TCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATT 748
              |||||||||||||||||| |||||||||||||| |||| ||||||||||||||| ||||
Db        376 TCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATT 317

Qy        749 CTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACT 808
              ||||||| ||||| || |||||||| |||||||||||||||| || ||||||||||||
Db        316 CTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACATTCCTACT 257

Qy        809 TCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGAC 868
              ||||| | |||||  |||| |||||||||||||||| ||| ||||||||||||| |||
Db        256 TCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGCAAGAGAGAAAAGAAAGATAGAG 197

Qy        869 TCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGC 928
              ||| |  |||||||||||||||||| |||| | |||| |||  ||||||  ||  ||||||
Db        196 TCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGCAAAAATGCCAGCATTAGCGTGC 137

Qy        929 AAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCA 985
              |||  |||||||||||||||||||| |||||| | |||||||| ||| ||||||
Db        136 GGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAATGGGCATCTGTGCCCTGCA 80


RESULT 10
CD559451/c
LOCUS       CD559451                762 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496580 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971871 5', mRNA sequence.
ACCESSION   CD559451
VERSION     CD559451.2  GI:38453471
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585519.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
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            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: IRBK2  row: h  column: 02
           High quality sequence start: 38
           High quality sequence stop: 761.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971871"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             50.7%;  Score 499.4;  DB 5;  Length 762;
  Best Local Similarity   87.1%;  Pred. No. 1.4e-134;
  Matches  572;  Conservative    0;  Mismatches   81;  Indels    4;  Gaps    2;

Qy        329 GAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAA 388
              | | ||||||||||||||| |||| ||| ||||||||| |||||||||||| || |||||
Db        753 GGAATTGGTCCACTGATAT-TTAAAGGACCAGAAAGAACCCAAAAATAAGACCTCTCTAA 695

Qy        389 AATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTA 448
              ||| ||||| |||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        694 GATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGACAATCAGTA 635

Qy        449 CCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTT 508
              | ||||||| ||||| |||||||||||||||||||| |||||||||||||||||||| |
Db        634 CTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGT 575

Qy        509 GTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGT 568
              | ||||| || |||||||| |||||||  ||||||| |||||||| ||| |||    |||
Db        574 GCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAACAAGGAGTAT---GAGT 518

Qy        569 ACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTG 628
              || |||||||||| ||||||| |||||||||||| ||||| |||||||| || |||||||
Db        517 ACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCTGAGGAGAGTCTGCCCATTG 458

Qy        629 AAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCA 688
              | ||| ||||||| ||  |||||||||||||||| ||||||||||||||||||||||||
Db        457 AGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCA 398

Qy        689 TCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATT 748
              |||||||||||||||||| |||||||||||||| |||| |||||||||||||| ||||
Db        397 TCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATT 338

Qy        749 CTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACT 808
              ||||||| ||||| || |||||||| |||||||||||||||| || ||||||||||||
Db        337 CTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACATTCCTACT 278

Qy        809 TCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGAC 868
              ||||| | |||||  |||| |||||||||||||||| ||| |||||||||||||| |||
Db        277 TCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGCAAGAGAGAAAAGAAAGATAGAG 218

Qy        869 TCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGC 928
              ||| |  |||||||||||||||||| |||| | |||| ||| ||||||  ||  ||||||
Db        217 TCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGCAAAAATGCCAGCATTAGCGTGC 158

Qy        929 AAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCA 985
              |||   |||||||||||||||||||| |||||| | |||||||| ||| ||||||
Db        157 GGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAATGGGCATCTGTGCCCTGCA 101
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RESULT 11
AK155593

LOCUS	AK155593 2908 bp mRNA linear HTC 21-SEP-2005
DEFINITION	Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F730005O03 product:interleukin 12b, full insert sequence.
ACCESSION	AK155593
VERSION	AK155593.1 GI:74212721
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE	1
AUTHORS	Carninci,P. and Hayashizaki,Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
PUBMED	10349636
REFERENCE	2
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
PUBMED	11042159
REFERENCE	3
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
PUBMED	11076861
REFERENCE	4
AUTHORS	Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
CONSRTM	RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium

TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
PUBMED 11217851
REFERENCE 5
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
CONSRTM FANTOM Consortium
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420 (6915), 563-573 (2002)
PUBMED 12466851
REFERENCE 6
AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.
CONSRTM FANTOM Consortium
TITLE The transcriptional landscape of the mammalian genome
JOURNAL Science 309 (5740), 1559-1563 (2005)
PUBMED 16141072
REFERENCE 7
AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.
CONSRTM RIKEN Genome Exploration Research Group
TITLE Antisense transcription in the mammalian transcriptome
JOURNAL Science 309 (5740), 1564-1566 (2005)
PUBMED 16141073
REFERENCE 8 (bases 1 to 2908)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
FEATURES Location/Qualifiers
source 1. .2908
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:F730005O03"
/db_xref="taxon:10090"
/clone="F730005O03"
/cell_type="B6-derived CD11 +ve dendritic cells"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
misc_feature 1. .2908
/note="interleukin 12b (MGD|MGI:96540 GB|M86671, evidence: BLASTN, 99%, match=1807)
putative"
ORIGIN

Query Match 50.5%; Score 497.6; DB 6; Length 2908;
Best Local Similarity 72.4%; Pred. No. 8.1e-134;
Matches 731; Conservative 0; Mismatches 239; Indels 40; Gaps 5;

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Db        461 ATGTGTCCTCAGAAGCTAACCATCTCCTGGTTTGCCATCGTTTTGCTGGTGTCTCCACTC 520

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Db        521 ATGGCCATGTGGGAGCTGGAGAAAGACGTTTATGTTGTAGAGGTGGACTGGACTCCCGAT 580

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
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Db        581 GCCCCTGGAGAAACAGTGAACCTCACCTGTGACACGCCTGAAGAAGATGACATCACCTGG 640

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Db        641 ACCTCAGACCAGAGACATGGAGTCATAGGCTCTGGAAAGACCCTGACCATCACTGTCAAA 700

Qy        241 GAATTTGCAGATGCTGGCCAG-TATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTC 299
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Db        701 GAGTTTCTAGATGCTGGCCAGCTACACCTGCCACAAAGGAGGCGAGACTCTGAGCCACTC 760

Qy        300 GTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACA 359
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Db        761 ACATCTGCTGCTCCACAAGAAGGAAAATGGAATTTGGTCCACTGAAATTTTA-------- 812

Qy        360 GAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTT 419
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Db        813 -AAAAATTTCAAAAACAAGACTTTCCTGAAGTGTGAAGCACCAAATTACTCCGGACGGTT 871

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Db        872 CACGTGCTCATGGCTGGTGCAAAGAAACATGGACTTGAAGTTCAACATCAAGAGCAGTAG 931

Qy        480 AGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGT 539
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Db        932 CAGTTCCCCTGACTCTCGGGCAGTGACATGTGGAATGGCGTCTCTGTCTGCAGAGAAGGT 991

Qy        540 CAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTG 599
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Db        992 CACACTGGACCAAAGGGACTATGAGAAGTATTCAGTGTCCTGCCAGGAGGATGTCACCTG 1051

Qy        600 CCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAA 659
              |||  |||||||||||| ||| |||||||| | | | |||| ||    ||  ||  ||
Db       1052 CCCAACTGCCGAGGAGACCCTGCCCATTGAACTGGCGTTGGAAGCACGGCAGCAGAATAA 1111

Qy        660 GTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAA 719
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Db       1112 ATATGAGAACTACAGCACCAGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAA 1171

Qy        720 GAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCC 779
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Db       1172 GAACTTGCAGATGAAGCCTTTGAAGAACTC---ACAGGTGGAGGTCAGCTGGGAGTACCC 1228

Qy        780 TGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGG 839
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Db       1229 TGACTCCTGGAGCACTCCCCATTCCTACTTCTCCCTCAAGTTCTTTGTTCGAATCCAGCG 1288

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Db       1289 CAAGAAAGAAAAGATGAAGGAGACAGAGGAGGGGTGTAACCAGAAAGGTGCGTTCCTCGT 1348

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Db       1349 AGAGAAGACATCTACCGAAGTCCAATG---CAAAGGCGGGAATGTCTGCGTGCAAGCTCA 1405

Qy        936 AGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCA 985
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Db       1406 GGATCGCTATTACAATTCCTCATGCAGCAAGTGGGCATGTGTTCCCTGCA 1455


RESULT 12
CD559452/c
LOCUS       CD559452                754 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496548 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971870 5', mRNA sequence.
ACCESSION   CD559452
VERSION     CD559452.2  GI:38453473
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.

REFERENCE   1  (bases 1 to 754)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585520.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 01
            High quality sequence start: 130
            High quality sequence stop: 572.
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                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
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                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match           48.4%;  Score 477;  DB 5;  Length 754;
  Best Local Similarity   84.9%;  Pred. No. 5.3e-128;
  Matches  558;  Conservative    0;  Mismatches   95;  Indels    4;  Gaps    2;

Qy        329 GAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAA 388
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Db        752 GAATTTGGTCCAATGATAT-TTAAAGGACCAGAAAGAACCCAAAAATAAGACCTTTCTAA 694

Qy        389 AATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTA 448
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Db        693 GATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGACAATCAGTA 634

Qy        449 CCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTT 508
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Db        633 CTGATTTGACATTCAGTGTCAAGAGCAGCAGAGGCTTTTTTGACCCCCAAGGGGTGACGT 574

Qy        509 GTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGT 568
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Db        573 GCGGAGCTGCTACACTCTTTGCAGAGAGAGTCAGAGGGGACAACAAGGAGTAT---GAGT 517

Qy        569 ACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTG 628
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Db        516 ACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGGTGAGGAGAGTTTGCCCATTG 457

Qy        629 AAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCA 688
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Db        456 AGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACCAGCAGGTTTTTCA 397

Qy        689 TCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATT 748
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Db        396 TCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATT 337

Qy        749 CTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACT 808
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Db        336 CTTGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACATTCCTAAT 277

Qy        809 TCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGAC 868
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Db        276 TTTCCCTGACATTTTGCGTTCAGGTTCAGGGCAAGAGCAAGAGAGAAAAGAAAGATAGAG 217

Qy        869 TCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGC 928
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Db        216 TTTTCACGGACAAGACCTTAGCCACGGTCATTTGCCGCAAAAATGCCAGCATTAGCGTGC 157

Qy        929 AAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCA 985
                |||   ||||| |||||||||||||  |||||| | |||||||  ||| ||||||
Db        156 GGGCCCAGGACCGGTACTATAGCTCATTTTGGAGCGAATGGGCATTTGTGCCCTGCA 100


RESULT 13
CD559449/c
LOCUS       CD559449                766 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496649 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971873 5', mRNA sequence.
ACCESSION   CD559449
VERSION     CD559449.2  GI:38453467
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 766)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585517.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 04
            High quality sequence stop: 641.
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                     /clone="IMAGE:6971873"
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                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match           47.9%;  Score 471.4;  DB 5;  Length 766;
  Best Local Similarity  85.8%;  Pred. No. 2.4e-126;
  Matches  536;  Conservative    0;  Mismatches   86;  Indels    3;  Gaps    1;

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db        654 ACCTGGTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 595

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Db        594 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 535

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Db        534 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 478

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
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Db        477 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 418

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Db        417 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 358

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
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Db        357 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 298

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
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Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              ||| | |||||||| ||| ||||||
Db        117 AGCGAATGGGCATCTGTGCCCTGCA 93


RESULT 14
CD559454/c
LOCUS       CD559454                725 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14497089 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971868 5', mRNA sequence.
ACCESSION   CD559454
VERSION     CD559454.2  GI:38453478
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
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REFERENCE   1  (bases 1 to 725)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585522.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: g  column: 11
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            High quality sequence stop: 573.
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                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match            44.2%;  Score 435.6;  DB 5;  Length 725;
  Best Local Similarity  84.0%;  Pred. No. 7.4e-116;
  Matches  516;  Conservative    0;  Mismatches   94;  Indels    4;  Gaps    2;

Qy        372 AAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTG 431
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Db        714 AAAAATAAAGCTTTTTAAGATGGGGGCCAAGAAGTATTTGGGAAGTTTCCCTCGCTGTCG 655

Qy        432 GCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGA 491
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Db        654 GCTGACGACAATCAGTACTGA-TTGAACTTCAGTGTCAAAAGCAGCAGAGGTTCCTCTGA 596

Qy        492 CCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAA 551
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Db        595 CCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAA 536

Qy        552 CAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGA 611
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Db        535 CAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCTGA 479

Qy        612 GGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTA 671
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Db        478 GGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTA 419

Qy        672 CACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACT 731
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PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 42.5%; Score 418.8; DB 5; Length 724;
Best Local Similarity 89.6%; Pred. No. 6.3e-111;
Matches 450; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

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Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 10, 2006, 04:51:14 ; Search time 212.629 Seconds
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

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Maximum DB seq length: 2000000000

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	2	985	100.0	985	3	US-09-917-265A-57	Sequence 57, Appl
	3	985	100.0	987	3	US-09-917-265A-29	Sequence 29, Appl
c	4	985	100.0	987	3	US-09-917-265A-31	Sequence 31, Appl
	5	981.8	99.7	1599	3	US-09-917-265A-38	Sequence 38, Appl
c	6	981.8	99.7	1599	3	US-09-917-265A-40	Sequence 40, Appl
	7	980.2	99.5	2193	3	US-09-011-143-5	Sequence 5, Appli
	8	980.2	99.5	2193	3	US-09-302-495-5	Sequence 5, Appli
	9	980.2	99.5	2193	3	US-10-079-616-5	Sequence 5, Appli
	10	919	93.3	921	3	US-09-011-143-6	Sequence 6, Appli
	11	919	93.3	921	3	US-09-302-495-6	Sequence 6, Appli
	12	919	93.3	921	3	US-10-079-616-6	Sequence 6, Appli
	13	917.4	93.1	921	3	US-09-011-143-7	Sequence 7, Appli
	14	917.4	93.1	921	3	US-09-302-495-7	Sequence 7, Appli
	15	917.4	93.1	921	3	US-10-079-616-7	Sequence 7, Appli
	16	917.4	93.1	921	3	US-09-917-265A-26	Sequence 26, Appl
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	18	917.4	93.1	1533	3	US-09-917-265A-43	Sequence 43, Appl
c	19	917.4	93.1	1533	3	US-09-917-265A-45	Sequence 45, Appl
	20	884.2	89.8	990	3	US-09-079-984A-11	Sequence 11, Appl
	21	884.2	89.8	990	3	US-09-390-729-11	Sequence 11, Appl
	22	884.2	89.8	2267	3	US-09-917-265A-107	Sequence 107, App
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	24	881	89.4	987	3	US-09-917-265A-58	Sequence 58, Appl
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	29	869.8	88.3	990	3	US-09-390-729-1	Sequence 1, Appli
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	36	778.6	79.0	1018	2	US-08-184-009-194	Sequence 194, App
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	43	778.6	79.0	1623	2	US-08-751-767A-9	Sequence 9, Appli
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ALIGNMENTS

RESULT 1
US-09-917-265A-55
; Sequence 55, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
; LENGTH: 985
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(984)
US-09-917-265A-55

Query Match 100.0%; Score 985; DB 3; Length 985;
Best Local Similarity 100.0%; Pred. No. 3.7e-310;
Matches 985; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
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RESULT 2
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; Sequence 57, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 985
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265A-57

Query Match 100.0%; Score 985; DB 3; Length 985;
Best Local Similarity 100.0%; Pred. No. 3.7e-310;
Matches 985; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 29, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
US-09-917-265A-29

  Query Match             100.0%;  Score 985;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-310;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
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Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 4
US-09-917-265A-31/c
; Sequence 31, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-31

  Query Match             100.0%;  Score 985;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-310;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
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Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGCA 3
```

RESULT 5
US-09-917-265A-38
; Sequence 38, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1599)
US-09-917-265A-38

Query Match 99.7%; Score 981.8; DB 3; Length 1599;
Best Local Similarity 99.8%; Pred. No. 5.6e-309;
Matches 983; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985
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RESULT 6
US-09-917-265A-40/c
; Sequence 40, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-40

  Query Match             99.7%;  Score 981.8;  DB 3;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 5.6e-309;
  Matches  983;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1599 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 1540

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 1420

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1359 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 1300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1299 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 1240

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1179 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 1120

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1119 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 1060

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        999 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 940

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        939 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 880

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        879 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 820

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 760

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        759 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 640

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        639 AGCAACTGGGCATCCGTGTCCTGCA 615


RESULT 7
US-09-011-143-5
; Sequence 5, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2193 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-5

  Query Match             99.5%;  Score 980.2;  DB 3;  Length 2193;
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  Best Local Similarity   99.7%;  Pred. No. 2.3e-308;
  Matches  982;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||| |||||||||||||||| |||||||||||||||||||||| |||
Db         64 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTACCTGGTTTTGCTGGCACCTCCTCTC 123

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 183

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 243

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 303

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 363

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 423

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 483

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 543

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 603

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 663

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 723

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 783

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 843

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 903

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 963

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 1023

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
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Db       1024 AGCAACTGGGCATCCGTGTCCTGCA 1048

RESULT 8
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US-09-302-495-5
; Sequence 5, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2193 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-302-495-5

  Query Match           99.5%;  Score 980.2;  DB 3;  Length 2193;
  Best Local Similarity   99.7%;  Pred. No. 2.3e-308;
  Matches  982;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||| |||||||||||||||| |||||||||||||||||||||| |||
Db         64 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTACCTGGTTTTGCTGGCACCTCCTCTC 123

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 183

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 243

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 303

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
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Db        304 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 363

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
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Db        364 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 423

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 483

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 543

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 603

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 663

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 723

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 783

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
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Db        784 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 843

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
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Db        844 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 903

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Db        904 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 963

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
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Db        964 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 1023

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db       1024 AGCAACTGGGCATCCGTGTCCTGCA 1048


RESULT 9
US-10-079-616-5
; Sequence 5, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2193 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-079-616-5

  Query Match             99.5%;  Score 980.2;  DB 3;  Length 2193;
  Best Local Similarity   99.7%;  Pred. No. 2.3e-308;
  Matches  982;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
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Db         64 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTACCTGGTTTTGCTGGCACCTCCTCTC 123

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Db        124 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 183

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 243

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
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Db        304 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 363

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
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Db        364 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 423

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db        484 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 543

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 603

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Db        604 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 663
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Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
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Db        664 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 723

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
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Db        784 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 843

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 903

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Db        904 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 963

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
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Db        964 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 1023

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
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Db       1024 AGCAACTGGGCATCCGTGTCCTGCA 1048
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RESULT 10
US-09-011-143-6
; Sequence 6, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  921 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-6

  Query Match             93.3%;  Score 919;  DB 3;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-288;
  Matches  919;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
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Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
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Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
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Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCA 985
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Db        901 TGGGCATCCGTGTCCTGCA 919


RESULT 11
US-09-302-495-6
; Sequence 6, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-302-495-6

  Query Match             93.3%;  Score 919;  DB 3;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-288;
  Matches  919;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
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Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
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Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
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Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
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Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
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Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
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Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

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Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
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Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
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Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCA 985
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Db        901 TGGGCATCCGTGTCCTGCA 919


RESULT 12
US-10-079-616-6
; Sequence 6, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
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;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-079-616-6

  Query Match             93.3%;  Score 919;  DB 3;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-288;
  Matches  919;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
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Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
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Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
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Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
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Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
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Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
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Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
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Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCA 985
              ||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCA 919


RESULT 13
US-09-011-143-7
; Sequence 7, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  921 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
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;    MOLECULE TYPE:  cDNA
US-09-011-143-7

  Query Match            93.1%;  Score 917.4;  DB 3;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 3.9e-288;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
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Db           1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

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Qy         187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
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Db         121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
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Db         181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
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Db         241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

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Qy         427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
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Db         361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

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Db         421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy         547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
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Db         481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy         607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
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Db         541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy         667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy         727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
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Db         661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

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Db         721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy         847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
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Db         781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy         907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
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Db         841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy         967 TGGGCATCCGTGTCCTGCA 985
               ||||||||||||||||||
Db         901 TGGGCATCCGTGTCCTGCA 919


RESULT 14
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US-09-302-495-7
; Sequence 7, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 7:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-302-495-7

  Query Match            93.1%;  Score 917.4;  DB 3;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 3.9e-288;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
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Db          61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
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Qy         307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
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Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
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Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
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RESULT 15
US-10-079-616-7
; Sequence 7, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 7:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-079-616-7

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  Best Local Similarity   99.9%;  Pred. No. 3.9e-288;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
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Db        901 TGGGCATCCGTGTCCTGCA 919
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Job time : 213.629 secs

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OM nucleic - nucleic search, using sw model

Run on: June 10, 2006, 07:19:28 ; Search time 1122.97 Seconds
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Perfect score: 985
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Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

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Maximum Match 100%
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16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	3	985	100.0	985	9	US-10-821-670-55	Sequence 55, Appl
c	4	985	100.0	985	9	US-10-821-670-57	Sequence 57, Appl
	5	985	100.0	987	3	US-09-917-265-29	Sequence 29, Appl
c	6	985	100.0	987	3	US-09-917-265-31	Sequence 31, Appl
	7	985	100.0	987	9	US-10-821-670-29	Sequence 29, Appl
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	10	981.8	99.7	1599	3	US-09-917-265-38	Sequence 38, Appl
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c	35	881	89.4	1599	3	US-09-917-265-63	Sequence 63, Appl
	36	881	89.4	1599	9	US-10-821-670-61	Sequence 61, Appl
c	37	881	89.4	1599	9	US-10-821-670-63	Sequence 63, Appl
	38	824.6	83.7	921	3	US-09-917-265-52	Sequence 52, Appl
c	39	824.6	83.7	921	3	US-09-917-265-54	Sequence 54, Appl
	40	824.6	83.7	921	9	US-10-821-670-52	Sequence 52, Appl
c	41	824.6	83.7	921	9	US-10-821-670-54	Sequence 54, Appl
	42	823	83.6	1533	3	US-09-917-265-66	Sequence 66, Appl
c	43	823	83.6	1533	3	US-09-917-265-68	Sequence 68, Appl
	44	823	83.6	1533	9	US-10-821-670-66	Sequence 66, Appl
c	45	823	83.6	1533	9	US-10-821-670-68	Sequence 68, Appl

ALIGNMENTS

RESULT 1
US-09-917-265-55
; Sequence 55, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 985
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(984)
; OTHER INFORMATION:
US-09-917-265-55

Query Match 100.0%; Score 985; DB 3; Length 985;
Best Local Similarity 100.0%; Pred. No. 1.4e-307;
Matches 985; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
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Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

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Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

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RESULT 2
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; Sequence 57, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1

; SEQ ID NO 57
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-57

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Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26
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Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGCA 1
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RESULT 3
US-10-821-670-55
; Sequence 55, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
; LENGTH: 985
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(984)
US-10-821-670-55

Query Match 100.0%; Score 985; DB 9; Length 985;
Best Local Similarity 100.0%; Pred. No. 1.4e-307;
Matches 985; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985
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RESULT 4
US-10-821-670-57/c
; Sequence 57, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 985
; TYPE: DNA
; ORGANISM: Felis catus
US-10-821-670-57

Query Match 100.0%; Score 985; DB 9; Length 985;
Best Local Similarity 100.0%; Pred. No. 1.4e-307;
Matches 985; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746
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Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGCA 1
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RESULT 5
US-09-917-265-29
; Sequence 29, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
;   OTHER INFORMATION:
US-09-917-265-29

  Query Match             100.0%;  Score 985;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-307;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
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Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 6
US-09-917-265-31/c
; Sequence 31, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-31

  Query Match             100.0%;  Score 985;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-307;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGCA 3


RESULT 7
US-10-821-670-29
; Sequence 29, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
US-10-821-670-29

  Query Match             100.0%;  Score 985;  DB 9;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-307;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985
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RESULT 8
US-10-821-670-31/c
; Sequence 31, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-31
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  Query Match           100.0%;  Score 985;  DB 9;  Length 987;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-307;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGCA 3
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RESULT 9
US-10-041-672C-1
; Sequence 1, Application US/10041672C
; Publication No. US20030157059A1
; GENERAL INFORMATION:
;  APPLICANT: Mologen Forschungs-, Entwicklungs- und Vetriebs GmbH
;  APPLICANT:  Universitat Zurich
;  TITLE OF INVENTION: FELINE INTERLEUKIN-12 AS IMMUNOSTIMULANT
;  FILE REFERENCE: NHL-NP-36
;  CURRENT APPLICATION NUMBER: US/10/041,672C
;  CURRENT FILING DATE:  2002-01-08
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 990
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: feline IL-12 p40
US-10-041-672C-1

  Query Match             99.7%;  Score 981.8;  DB 7;  Length 990;
  Best Local Similarity   99.8%;  Pred. No. 1.6e-306;
  Matches  983;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 10
US-09-917-265-38
; Sequence 38, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
US-09-917-265-38

  Query Match             99.7%;  Score 981.8;  DB 3;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 2.1e-306;
  Matches  983;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
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Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985
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RESULT 11
US-09-917-265-40/c
; Sequence 40, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265-40

Query Match 99.7%; Score 981.8; DB 3; Length 1599;
Best Local Similarity 99.8%; Pred. No. 2.1e-306;
Matches 983; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1599 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 1540

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 1420

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1359 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 1300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1299 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 1240

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1179 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 1120

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1119 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 1060

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        999 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 940

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        939 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 880

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        879 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 820

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 760

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        759 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 640

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        639 AGCAACTGGGCATCCGTGTCCTGCA 615
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RESULT 12
US-10-821-670-38
; Sequence 38, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.

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;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-10-821-670-38

  Query Match            99.7%;  Score 981.8;  DB 9;  Length 1599;
  Best Local Similarity  99.8%;  Pred. No. 2.1e-306;
  Matches  983;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 13
US-10-821-670-40/c
; Sequence 40, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-40

  Query Match            99.7%;  Score 981.8;  DB 9;  Length 1599;
  Best Local Similarity  99.8%;  Pred. No. 2.1e-306;
  Matches  983;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1599 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 1540

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 1420

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1359 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 1300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1299 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 1240

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180
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Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1179 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 1120

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       1119 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 1060

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        999 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 940

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        939 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 880

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        879 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 820

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 760

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Db        759 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 640

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        639 AGCAACTGGGCATCCGTGTCCTGCA 615
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RESULT 14
US-10-041-672C-10
; Sequence 10, Application US/10041672C
; Publication No. US20030157059A1
; GENERAL INFORMATION:
; APPLICANT: Mologen Forschungs-, Entwicklungs- und Vetriebs GmbH
; APPLICANT: Universitat Zurich
; TITLE OF INVENTION: FELINE INTERLEUKIN-12 AS IMMUNOSTIMULANT
; FILE REFERENCE: NHL-NP-36
; CURRENT APPLICATION NUMBER: US/10/041,672C
; CURRENT FILING DATE: 2002-01-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 4522
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pMol-fil12p40
US-10-041-672C-10

Query Match 99.7%; Score 981.8; DB 7; Length 4522;
Best Local Similarity 99.8%; Pred. No. 3.6e-306;
Matches 983; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166
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Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Db       3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
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Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Db       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Db       3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Db       3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db       3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
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RESULT 15
US-10-079-616-5
; Sequence 5, Application US/10079616
; Publication No. US20020107366A1
; GENERAL INFORMATION:
; APPLICANT: IMAMURA, Takayuki
; MAEDA, Hiroaki
; FUJIYASU, Takeshi
; IMAGAWA, Yoshitaka
; TOKIYOSHI, Sachio
; TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN

```
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 5:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 2193 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-079-616-5

  Query Match             99.5%;  Score 980.2;  DB 6;  Length 2193;
  Best Local Similarity   99.7%;  Pred. No. 8.1e-306;
  Matches  982;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||| |||||||||||||||||| |||||||||||||||||||||| |||
Db         64 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTACCTGGTTTTGCTGGCACCTCCTCTC 123

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Db        124 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 183

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
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Db        184 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 243

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 303

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
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Db        364 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 423

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Db        424 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 483

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db        484 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 543

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 603

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 663

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 723

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Db        724 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 783

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 843

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
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Db        844 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 903

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 963

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 1023

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
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Db       1024 AGCAACTGGGCATCCGTGTCCTGCA 1048


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OM nucleic - nucleic search, using sw model

Run on: June 10, 2006, 15:46:40 ; Search time 17.0752 Seconds
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Perfect score: 985
Sequence: 1 atgcatcctcagcagttggt.....ctgggcatccgtgtcctgca 985

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 253354 seqs, 63461778 residues

Total number of hits satisfying chosen parameters: 506708

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	36.8	3.7	3401	6	US-10-196-749-411	Sequence 411, App
	2	34.8	3.5	3166	7	US-11-293-697-739	Sequence 739, App
c	3	34.4	3.5	1438	6	US-10-953-349-20792	Sequence 20792, A
	4	34.4	3.5	2268	7	US-11-217-529-1612	Sequence 1612, Ap
	5	33.8	3.4	1948	6	US-10-508-063A-4	Sequence 4, Appli
	6	33.2	3.4	2513	7	US-11-293-697-145	Sequence 145, App
	7	32.4	3.3	2152	6	US-10-953-349-38921	Sequence 38921, A
	8	32	3.2	620	6	US-10-953-349-32903	Sequence 32903, A
	9	32	3.2	2024	7	US-11-293-697-1253	Sequence 1253, Ap
	10	31.8	3.2	1404	6	US-10-471-571A-5411	Sequence 5411, Ap
c	11	31.8	3.2	1906	6	US-10-953-349-22720	Sequence 22720, A
c	12	31.4	3.2	1636	6	US-10-953-349-22635	Sequence 22635, A
c	13	31.4	3.2	6051	7	US-11-313-450-9	Sequence 9, Appli
	14	31.2	3.2	1286	7	US-11-145-307A-72	Sequence 72, Appl
	15	31	3.1	2843	7	US-11-293-697-1498	Sequence 1498, Ap
c	16	30.8	3.1	992	6	US-10-953-349-31065	Sequence 31065, A
	17	30.8	3.1	2640	6	US-10-527-411-29	Sequence 29, Appl
	18	30.8	3.1	3930	7	US-11-217-529-76026	Sequence 76026, A
	19	30.6	3.1	2619	7	US-11-302-678-18	Sequence 18, Appl
	20	30.6	3.1	3232	7	US-11-302-678-16	Sequence 16, Appl
c	21	30.4	3.1	296	7	US-11-301-554-517	Sequence 517, App
	22	30.4	3.1	444	7	US-11-217-529-79558	Sequence 79558, A
c	23	30.4	3.1	1467	7	US-11-217-529-79610	Sequence 79610, A
c	24	30.4	3.1	2249	7	US-11-293-697-442	Sequence 442, App
c	25	30.4	3.1	3294	7	US-11-293-697-1397	Sequence 1397, Ap
c	26	30.2	3.1	924	7	US-11-217-529-1898	Sequence 1898, Ap
	27	30.2	3.1	1848	6	US-10-519-335-5	Sequence 5, Appli
	28	30.2	3.1	1878	6	US-10-519-335-3	Sequence 3, Appli
	29	30.2	3.1	1932	6	US-10-519-335-1	Sequence 1, Appli
	30	30	3.0	1376	6	US-10-527-411-71	Sequence 71, Appl
	31	30	3.0	1376	6	US-10-527-411-73	Sequence 73, Appl
	32	30	3.0	1376	6	US-10-527-411-75	Sequence 75, Appl
	33	30	3.0	1376	6	US-10-527-411-77	Sequence 77, Appl
	34	30	3.0	1385	6	US-10-527-411-69	Sequence 69, Appl
	35	30	3.0	2600	6	US-10-527-411-33	Sequence 33, Appl
	36	30	3.0	2600	6	US-10-527-411-35	Sequence 35, Appl
	37	30	3.0	2600	6	US-10-527-411-37	Sequence 37, Appl
	38	30	3.0	2609	6	US-10-527-411-31	Sequence 31, Appl
	39	30	3.0	2625	6	US-10-527-411-150	Sequence 150, App
	40	30	3.0	2625	6	US-10-527-411-164	Sequence 164, App
	41	30	3.0	2625	6	US-10-527-411-166	Sequence 166, App
	42	30	3.0	2625	6	US-10-527-411-168	Sequence 168, App
	43	30	3.0	2637	6	US-10-527-411-156	Sequence 156, App
	44	30	3.0	2643	6	US-10-527-411-61	Sequence 61, Appl
	45	30	3.0	2667	6	US-10-527-411-160	Sequence 160, App

ALIGNMENTS

RESULT 1
US-10-196-749-411
; Sequence 411, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 411
; LENGTH: 3401
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-196-749-411

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  Query Match             3.7%;  Score 36.8;  DB 6;  Length 3401;
  Best Local Similarity   46.5%;  Pred. No. 0.1;
  Matches  119;  Conservative    0;  Mismatches  137;  Indels    0;  Gaps    0;

Qy        540 CAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTG 599
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Db        130 CACCGTCTACTACGTGCACAACATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAG 189

Qy        600 CCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAA 659
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Db        190 CCTGACGGGCTACCGCACCTACCGCTGTGCCCACCCCCTGGCCACACTCTTCAAGATCCT 249

Qy        660 GTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAA 719
              |         ||||| ||||    || || ||   | | |||||     | || |||
Db        250 GGCGTCCTTCTACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCATGTACACACTGTG 309

Qy        720 GAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCC 779
              |    ||| || |    |  | || || |    |  || |    |  |   |||   |
Db        310 GTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTTGAGTCGATCCGTGAGGAGAGCAG 369

Qy        780 TGACACCTGGAGCACC 795
              ||| |   | | ||
Db        370 CTACAGCGACATCCCC 385


RESULT 2
US-11-293-697-739
; Sequence 739, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 739
;   LENGTH: 3166
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-739

  Query Match             3.5%;  Score 34.8;  DB 7;  Length 3166;
  Best Local Similarity   49.5%;  Pred. No. 0.42;
  Matches   90;  Conservative    0;  Mismatches   92;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
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Db       1418 GGACAGAGAGGTCAGAAATGAATATAACATCACCATCACCGTGACCGACTTGGGGACACC 1477

Qy        597 CTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCT 656
              | | | |    |||||  | | | || || |    |||   |  | | |    ||   |
Db       1478 CAGGCTGAAAACCGAGCACAACATAACCGTGCTGGTCTCCGACGTCAATGACAACGCCCC 1537

Qy        657 CAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACC 716
              ||  | |    |   | ||  || | | ||| || | || | || ||  || | ||  |
Db       1538 CATCTTCACCCAAACCTCCTACACCCTGTTCGTCCGCGAGAACAACAGCCCCGCCCTGCA 1597

Qy        717 CA 718
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Db       1598 CA 1599


RESULT 3
US-10-953-349-20792/c
; Sequence 20792, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20792
;   LENGTH: 1438
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-20792

  Query Match             3.5%;  Score 34.4;  DB 6;  Length 1438;
  Best Local Similarity   50.0%;  Pred. No. 0.35;
  Matches   86;  Conservative    0;  Mismatches   86;  Indels    0;  Gaps    0;

Qy        243 ATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTT 302
              ||  ||| |||   || | ||  |||     | | |||   |      ||| ||  | |
Db       1331 ATAGGCACATGGAAGCAATTACTCCTTCACCATATGAGAACAACACTGGAGTCAAGCATG 1272

Qy        303 CCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAA 362
                |||| || ||| |    |||  ||   |    ||| || | || || | | ||   ||
Db       1271 GATCCTAATCCACTAGTTCGAAACTGTGTTAAACTCCTCTCAAATTTTCATGCAATCTAA 1212

Qy        363 AGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGA 414
                ||   |||| |||||| | |    | | | ||   ||| |   ||
Db       1211 CTGTAACACTGATAACATCTTTTTTACCCCTTATGTAATACTTTACTGCTGA 1160


RESULT 4
US-11-217-529-1612
; Sequence 1612, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1612
;   LENGTH: 2268
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-1612

  Query Match             3.5%;  Score 34.4;  DB 7;  Length 2268;
  Best Local Similarity   59.0%;  Pred. No. 0.46;
  Matches   59;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy        150 CAATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGG 209
              ||||||  ||||||||| ||||||      |||  | | |    | ||   ||  |   |
Db       1869 CAATACCCCTGAAGAAAATGACACTGAGGGGAAGTATAATACAATCAAGAAAAGCTCGGA 1928

Qy        210 CTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCA 249
                | || | || |||  | ||   |  ||||||||||  ||
Db       1929 TTATGATGAATCTCATATCACGAATATCAAAGAATTACCA 1968


RESULT 5
US-10-508-063A-4
; Sequence 4, Application US/10508063A
; Publication No. US20060088832A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: Deutsches Krebsforschungszentrum
;  APPLICANT:  ANGEL, Peter
;  APPLICANT:  FURSTENBERGER, Gerhard
;  APPLICANT:  BREITENBACH, Ute
;  APPLICANT:  RICHTER, Harmut
;  APPLICANT:  HESS, Jochen
;  APPLICANT:  TUCKERMAN, Jan
;  TITLE OF INVENTION: TAP-70, A NOVEL MARKER FOR EPITHELIAL TUMORS
;  FILE REFERENCE: 31304-701.831
;  CURRENT APPLICATION NUMBER: US/10/508,063A
;  CURRENT FILING DATE:  2004-09-16
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 1948
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-508-063A-4

  Query Match             3.4%;  Score 33.8;  DB 6;  Length 1948;
  Best Local Similarity   52.4%;  Pred. No. 0.65;
  Matches   99;  Conservative    0;  Mismatches   87;  Indels    3;  Gaps    1;

Qy        495 CCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAG 554
              | ||| ||  | | | | ||    ||   ||| |  | |  || || ||      | |
Db       1111 CAAAGTGGCCAATGGGGCAGAGATGAAGATCTTGGGTGTGTGGGACACAGAAATTAGCCT 1170

Qy        555 GGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGA 614
              ||   | |  |||   |  |  |||| || || || ||  ||| ||   || |  ||||
Db       1171 GGGCAAGACAAAGCTGAAGGCCGAGTTTCTGGTGGCCAACGCCAGC---GCAGAAGAGGC 1227

Qy        615 GAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACAC 674
               |   |   ||  || ||| ||  ||||   | |  |  |||  | | |||| ||  |||
Db       1228 TATTATTGGCACAGACGTCTTGCAGGACCACAATGCCGTGCTGGACTTCGAACACCGCAC 1287

Qy        675 CAGCAGCTT 683
              | ||| | |
Db       1288 CTGCACCCT 1296


RESULT 6
US-11-293-697-145
; Sequence 145, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 145
;   LENGTH: 2513
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-145

  Query Match             3.4%;  Score 33.2;  DB 7;  Length 2513;
  Best Local Similarity   52.1%;  Pred. No. 1.2;
  Matches   74;  Conservative    0;  Mismatches   68;  Indels    0;  Gaps    0;

Qy        627 TGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTT 686
              |||| | |   |||| |||     |  |  |  |||| | |||| || | |     || |
Db        973 TGAAATGGCCCTGGATGCTGAGTTCCTGGACGTGTACAAGAACTGCAACGGGGTGGTCAT 1032

Qy        687 CATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAA 746
               ||   ||||| | ||| | |   |   |||  || | |  | | |||    ||||
Db       1033 GATGTTCGACATTACCAAGCAGTGGACCTTCAATTACATTCTCCGGGAGCTTCCAAAAGT 1092

Qy        747 TTCTCGGCATGTGGAAGTGAGC 768
                |    || |||  |||| ||
Db       1093 GCCCACCCACGTGCCAGTGTGC 1114


RESULT 7
US-10-953-349-38921
; Sequence 38921, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38921
;   LENGTH: 2152
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-38921

  Query Match             3.3%;  Score 32.4;  DB 6;  Length 2152;
  Best Local Similarity   47.9%;  Pred. No. 1.9;
  Matches   93;  Conservative    0;  Mismatches  101;  Indels    0;  Gaps    0;

Qy        524 TCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTC 583
              |||| || ||| || ||||        | |  | |  | | |||| | || |  ||| |
Db        475 TCTCGGCCGAGGAGATCAGCTCCATGATCCTGAACAAGATGAAGGAGACGGCCGAGGCTT 534

Qy        584 AGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACG 643
              |    ||||   ||  |  |   || |  |  | | | ||      |  ||   |    |
Db        535 ACCTCGGCACCACCATCAAGAACGCTGTCGTCACCGTCCCGGCCTACTTCAACGACTCCC 594

Qy        644 CTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCA 703
                ||       |||| |||    |  || |  | || ||  | ||| |  ||||||||
Db        595 AGCGCCAGGCCACCAAGGACGCCGGCGTCATCTCCGGCCTCAACGTCATGCGCATCATCA 654

Qy        704 AACCGGACCCACCC 717
              |   |  | |  ||
Db        655 ACGAGCCCACCGCC 668


RESULT 8
US-10-953-349-32903
; Sequence 32903, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32903
;   LENGTH: 620
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-32903

  Query Match             3.2%;  Score 32;  DB 6;  Length 620;
  Best Local Similarity   47.1%;  Pred. No. 1.2;
  Matches   98;  Conservative    0;  Mismatches  110;  Indels    0;  Gaps    0;

Qy        574 GTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTC 633
              |||||||       | |    ||    || |||||| | |  |   |  ||   |   ||
Db         90 GTGGAGTTGGCAAAAGCTCATGAGATCCAGGCTGCTGTGCTGTTGCACCCTTCTTTTGTT 149

Qy        634 GTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGG 693
                || |||| |||  |  || |||||| || ||  |  | |  | |        ||
```

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Db        150 ACCGTTGACGATATCAAAGAGGTCAAGTGCGCAATTTCTATCCTCGGAGCTGAGATTGAC 209

Qy        694 GACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGG 753

Db        210 AAAATGTCCCCACCGGAGCTAATCAAGCAGTTCGAGCAGGTCCTTTCTTTGAACTCAGGG 269

Qy        754 CATGTGGAAGTGAGCTGGGAATACCCTG 781

Db        270 GTTGGCCACTTCGTCAAGATCTTCCCTG 297


RESULT 9
US-11-293-697-1253
; Sequence 1253, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1253
;   LENGTH: 2024
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1253

  Query Match             3.2%;  Score 32;  DB 7;  Length 2024;
  Best Local Similarity   50.7%;  Pred. No. 2.5;
  Matches   77;  Conservative    0;  Mismatches   75;  Indels    0;  Gaps    0;

Qy        210 CTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTG 269

Db        496 CTCTGTTGAAAGTTTGTTTCACCAGCAAATACTTTCTTCTTGTGCCAAAAGCTATAACTT 555

Qy        270 TCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGG 329

Db        556 TGATCAATATAGGAAGGTCTTTACTCATTCATCATTGCTTAATCAACAAGAGGAAATAGA 615

Qy        330 AATTTGGTCCACTGATATCTTAAGGGAACAGA 361

Db        616 TATTTGGGGAAAACATCACATATATGATAAAA 647


RESULT 10
US-10-471-571A-5411
; Sequence 5411, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 5411
;   LENGTH: 1404
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-5411

  Query Match             3.2%;  Score 31.8;  DB 6;  Length 1404;
  Best Local Similarity   57.6%;  Pred. No. 2.3;
  Matches   57;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy        328 GGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTA 387

Db         11 GTAATTTTTTAAATGTAGAGTTAATAGGTACTAAAATAATAACAATGGAAGACTTTTATA 70

Qy        388 AAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Db         71 AAATGAAGGAAGAAGAATTTTTCTTAAAATCTAAGCTAC 109


RESULT 11
US-10-953-349-22720/c
; Sequence 22720, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22720
;   LENGTH: 1906
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-22720

  Query Match             3.2%;  Score 31.8;  DB 6;  Length 1906;
  Best Local Similarity   61.4%;  Pred. No. 2.8;
  Matches   51;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy        226 ACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAG 285

Db        918 ACTATCCAAGTCACTGACATTGCAGTTCCCATTATTTAACGCAGTCATATCTATAGAGGA 859

Qy        286 GTTCTGAGCCATTCGTTCCTCCT 308

Db        858 ATTTTGAGCCAATGCTTCCTCCT 836


RESULT 12
US-10-953-349-22635/c
; Sequence 22635, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22635
;   LENGTH: 1636
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-22635

  Query Match             3.2%;  Score 31.4;  DB 6;  Length 1636;
  Best Local Similarity   46.9%;  Pred. No. 3.4;
  Matches   98;  Conservative    0;  Mismatches  111;  Indels    0;  Gaps    0;

Qy        650 ACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGG 709

Db       1479 ACACAGTCATGGACTTTTCATATCCATCTCACTCTTGCATGCGGATGATACACCTAATGG 1420

Qy        710 ACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCT 769

Db       1419 ACTGTCCCTTCAGCATTAAATCAAAAGCTTTGTTGATCTCTGAGAATGGAACTGTGTGAG 1360

Qy        770 GGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTAC 829
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Db       1359 TGATGAATTTGTCCACTTCTAGCTCCCCACTCATGTACTTCTCGACAACAGATGGAAGAT 1300

Qy        830 AGGTCCAGGGCAAGAACAACAGAGAAAAG 858
              ||| |  ||   | |      | |||||
Db       1299 CGGTGCGTGGTTTGTAGTTGCCATAAAAG 1271


RESULT 13
US-11-313-450-9/c
; Sequence 9, Application US/11313450
; Publication No. US20060110778A1
; GENERAL INFORMATION:
;  APPLICANT: Adorante, Joeseph S.
;  APPLICANT:  Ehring, George R.
;  TITLE OF INVENTION: High-Throughput Screens For Identifying
;  TITLE OF INVENTION:  Selective Persistent Sodium Channels Channel Blockers
;  FILE REFERENCE: 17407 CIP (AP)
;  CURRENT APPLICATION NUMBER: US/11/313,450
;  CURRENT FILING DATE:  2005-12-19
;  PRIOR APPLICATION NUMBER: 09/989797
;  PRIOR FILING DATE: 2001-11-20
;  PRIOR APPLICATION NUMBER: 60/252771
;  PRIOR FILING DATE: 2000-11-22
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 6051
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-313-450-9

  Query Match             3.2%;  Score 31.4;  DB 7;  Length 6051;
  Best Local Similarity   59.6%;  Pred. No. 7.6;
  Matches   53;  Conservative    0;  Mismatches   36;  Indels    0;  Gaps    0;

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              |||| | ||  || ||   || ||||||    ||||   || ||| | |||| || |||
Db       5636 AACTTCTCCTCCATCTGGATCTTCAGGGCGTCCATCTCCCCAGACTCCCCCAGGACCCTT 5577

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCA 755
                  ||||| ||   | ||  ||   |||
Db       5576 TTGGTGAAGGCAAAGAGAATGTCCATGCA 5548


RESULT 14
US-11-145-307A-72
; Sequence 72, Application US/11145307A
; Publication No. US20060094035A1
; GENERAL INFORMATION:
;  APPLICANT: Arcturus Bioscience, Inc.
;  APPLICANT:  Erlander, Mark G.
;  APPLICANT:  Ma, Xiao-Jun
;  TITLE OF INVENTION: Identification of Tumors
;  FILE REFERENCE: 022041-002020US
;  CURRENT APPLICATION NUMBER: US/11/145,307A
;  CURRENT FILING DATE:  2005-06-03
;  PRIOR APPLICATION NUMBER: US 60/577,084
;  PRIOR FILING DATE: 2004-06-04
;  NUMBER OF SEQ ID NOS: 268
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72
;   LENGTH: 1286
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-145-307A-72

  Query Match             3.2%;  Score 31.2;  DB 7;  Length 1286;
  Best Local Similarity   50.7%;  Pred. No. 3.4;
  Matches   75;  Conservative    0;  Mismatches   73;  Indels    0;  Gaps    0;

Qy        534 GAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAG 593
              | ||||    |||||  |   ||| |   || ||| ||   ||||    | ||    | |
Db        632 GCAGGTGGAGGTGGAGGAGGAGGAGTTCCAGGAGTTCATCCTGGACACACTGGTCCTCTG 691

Qy        594 TGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAA 653
                  || ||||   |||  |||   ||   | || ||| | | |   |  || ||
Db        692 CCTGCAGGAGGATGCCACCGAGGCCCTGGGCAGCAATGTGGTGCTTGTCCTGAAGCAGAA 751

Qy        654 GCTCAAGTACGAAAACTACACCAGCAGC 681
              ||||     ||  ||| | | || | ||
Db        752 GCTCCTCAGCGCCAACCAGAACATCCGC 779


RESULT 15
US-11-293-697-1498
; Sequence 1498, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1498
;   LENGTH: 2843
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1498

  Query Match             3.1%;  Score 31;  DB 7;  Length 2843;
  Best Local Similarity   48.6%;  Pred. No. 6.4;
  Matches   85;  Conservative    0;  Mismatches   90;  Indels    0;  Gaps    0;

Qy        563 AGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTAC 622
              ||  |||| ||| | ||    || |       |||  ||||||  ||  | ||||| |
Db       1858 AGGTGTACGCAGAGAAGAAGGAGAATTCACCAGCCCCCCCGGCACCCATGCAGAGCATCT 1917

Qy        623 CCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCT 682
              |||  |   ||  || |   |  | | || ||      |  ||  || |  || ||
Db       1918 CCAGCGGCATCAGGGAGACAGTGAGCCCCCAGGACATCGTGCAGGACGCCATCCACAACT 1977

Qy        683 TCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCC 737
              ||| | |   ||     | |  || | |   ||| | ||  |   |  | |||
Db       1978 TCTCCCCCGCCTACCAGCACTACACGCAGCAGGCCACGCACGAGGCGCCCAGGCC 2032


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OM nucleic - nucleic search, using sw model

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Title: US-10-821-670A-55
Perfect score: 985
Sequence: 1 atgcatcctcagcagttggt.....ctgggcatccgtgtcctgca 985

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 6366136 seqs, 31973710525 residues

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SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	3	985	100.0	987	2	AR595950	AR595950 Sequence
c	4	985	100.0	987	2	AR595951	AR595951 Sequence
	5	928	94.2	2193	2	AR242435	AR242435 Sequence
	6	928	94.2	2193	2	AR280203	AR280203 Sequence
	7	928	94.2	2193	2	AR322418	AR322418 Sequence
	8	919	93.3	921	2	AR242436	AR242436 Sequence
	9	919	93.3	921	2	AR280204	AR280204 Sequence
	10	919	93.3	921	2	AR322419	AR322419 Sequence
	11	903	91.7	1006	14	FCIL12P40	Y07762 Felis catus
	12	903	91.7	1599	2	AR595956	AR595956 Sequence
c	13	903	91.7	1599	2	AR595957	AR595957 Sequence
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	15	884	89.7	990	2	AX076482	AX076482 Sequence
	16	884	89.7	4522	2	AX076209	AX076209 Sequence
	17	884	89.7	4522	2	AX076476	AX076476 Sequence
	18	868	88.1	921	2	AR242437	AR242437 Sequence
	19	868	88.1	921	2	AR280205	AR280205 Sequence
	20	868	88.1	921	2	AR322420	AR322420 Sequence
	21	868	88.1	921	2	AR595948	AR595948 Sequence
c	22	868	88.1	921	2	AR595949	AR595949 Sequence
	23	868	88.1	1533	2	AR595959	AR595959 Sequence
c	24	868	88.1	1533	2	AR595960	AR595960 Sequence
	25	829	84.2	990	14	FCU83184	U83184 Felis catus
	26	382	38.8	431	14	AF054607	AF054607 Felis cat
	27	83	8.4	990	2	AX154603	AX154603 Sequence
	28	66	6.7	921	2	AR595965	AR595965 Sequence
c	29	66	6.7	921	2	AR595966	AR595966 Sequence
	30	66	6.7	924	2	BD171282	BD171282 Novel can
	31	66	6.7	987	2	AR595969	AR595969 Sequence
c	32	66	6.7	987	2	AR595970	AR595970 Sequence
	33	66	6.7	990	2	AR151061	AR151061 Sequence
	34	66	6.7	990	2	AR151071	AR151071 Sequence
	35	66	6.7	990	2	BD014653	BD014653 Process f
	36	66	6.7	990	2	BD014663	BD014663 Process f
	37	66	6.7	990	2	E15017	E15017 Canine mRNA
	38	66	6.7	990	2	AR316460	AR316460 Sequence
	39	66	6.7	990	2	AR316470	AR316470 Sequence
	40	66	6.7	1533	2	AR595973	AR595973 Sequence
c	41	66	6.7	1533	2	AR595974	AR595974 Sequence
	42	66	6.7	1599	2	AR595971	AR595971 Sequence
c	43	66	6.7	1599	2	AR595972	AR595972 Sequence
	44	66	6.7	2154	2	BD171281	BD171281 Novel can
	45	66	6.7	2267	2	AR596011	AR596011 Sequence
c	46	66	6.7	2267	2	AR596012	AR596012 Sequence
	47	65	6.6	984	2	AX154600	AX154600 Sequence
	48	63	6.4	588	14	AF349536	AF349536 Canis fam
	49	63	6.4	1015	14	CFU49100	U49100 Canis famil
	50	61	6.2	621	7	BV242752	BV242752 S234P6134
	51	61	6.2	984	2	AX154598	AX154598 Sequence
	52	60	6.1	984	2	AX154599	AX154599 Sequence
	53	53	5.4	975	2	AX154602	AX154602 Sequence
	54	51	5.2	452	14	AF333121	AF333121 Canis fam
	55	51	5.2	821	6	RNU16674	U16674 Rattus norv
	56	51	5.2	1008	6	AF133197	AF133197 Rattus no
	57	49	5.0	1425	6	AF421395	AF421395 Sigmodon
	58	44	4.5	224	14	DQ152965	DQ152965 Ovis arie
	59	44	4.5	525	14	CEU10160	U10160 Cervus elap
	60	44	4.5	906	2	BD021808	BD021808 Natural k
	61	44	4.5	906	2	BD021809	BD021809 Natural k
	62	44	4.5	969	2	AX154601	AX154601 Sequence
	63	44	4.5	984	14	AF004024	AF004024 Ovis arie
	64	44	4.5	984	14	AF209435	AF209435 Ovis arie
	65	44	4.5	987	2	AR008950	AR008950 Sequence
	66	44	4.5	987	2	BD007070	BD007070 IL-12 gen
	67	44	4.5	987	2	BD007076	BD007076 Gene expr
	68	44	4.5	987	2	BD105974	BD105974 Animal mo
	69	44	4.5	987	2	BD136034	BD136034 Interfero
	70	44	4.5	987	2	CQ803342	CQ803342 Sequence
	71	44	4.5	987	2	CS131491	CS131491 Sequence
	72	44	4.5	987	2	I28591	I28591 Sequence 1
	73	44	4.5	987	2	AR533404	AR533404 Sequence
	74	44	4.5	987	2	AX154633	AX154633 Sequence
	75	44	4.5	993	14	AY603406	AY603406 Capra hir
	76	44	4.5	993	14	CEU57752	U57752 Cervus elap
	77	44	4.5	1005	5	AY234218	AY234218 Papio anu
	78	44	4.5	1005	5	CTU19834	U19834 Cercocebus
	79	44	4.5	1007	5	AF180563	AF180563 Homo sapi
	80	44	4.5	1008	14	AB246273	AB246273 Bubalus c
	81	44	4.5	1008	14	AB246353	AB246353 Bubalus b
	82	44	4.5	1008	14	AB246358	AB246358 Bubalus b
	83	44	4.5	1012	14	AF007576	AF007576 Capra hir
	84	44	4.5	1012	14	AY198121	AY198121 Bubalus b
	85	44	4.5	1012	14	BTU11815	U11815 Bos taurus
	86	44	4.5	1018	2	AR052857	AR052857 Sequence
	87	44	4.5	1018	2	AR288169	AR288169 Sequence
	88	44	4.5	1018	2	AR567156	AR567156 Sequence
	89	44	4.5	1019	2	E35794	E35794 Process for
	90	44	4.5	1029	2	CQ829448	CQ829448 Sequence
	91	44	4.5	1046	5	BC074723	BC074723 Homo sapi

92	44	4.5	1073	5	BC067498	BC067498 Homo sapi
93	44	4.5	1073	5	BC067499	BC067499 Homo sapi
94	44	4.5	1073	5	BC067500	BC067500 Homo sapi
95	44	4.5	1073	5	BC067501	BC067501 Homo sapi
96	44	4.5	1073	5	BC067502	BC067502 Homo sapi
97	44	4.5	1080	5	MMU19841	U19841 Macaca mula
98	44	4.5	1389	2	AR393788	AR393788 Sequence
99	44	4.5	1389	2	AX084106	AX084106 Sequence
100	44	4.5	1397	2	BD165800	BD165800 Antibody
101	44	4.5	1399	2	AR091391	AR091391 Sequence
102	44	4.5	1399	5	HUMCLMF40	M65272 Human cytot
103	44	4.5	1560	2	AR091395	AR091395 Sequence
104	44	4.5	1623	2	AR091394	AR091394 Sequence
105	44	4.5	1870	2	A92079	A92079 Sequence 3
106	44	4.5	1870	2	AR230691	AR230691 Sequence
107	44	4.5	2307	2	CQ715179	CQ715179 Sequence
108	44	4.5	2318	2	AR228993	AR228993 Sequence
109	44	4.5	2318	5	HUMNKSFP40	M65290 Human natur
110	44	4.5	2362	2	AR082684	AR082684 Sequence
111	44	4.5	2362	2	AR122960	AR122960 Sequence
112	44	4.5	2362	2	I28325	I28325 Sequence 1
113	44	4.5	2362	2	AR309636	AR309636 Sequence
114	44	4.5	2362	2	I89770	I89770 Sequence 1
115	44	4.5	5686	2	BD136048	BD136048 Interfero
116	44	4.5	6139	2	AR091393	AR091393 Sequence
117	39	4.0	993	14	AB107654	AB107654 Lama glam
118	39	4.0	15648	5	AF512686	AF512686 Homo sapi
119	39	4.0	18340	5	AY008847	AY008847 Homo sapi
120	39	4.0	108511	5	AC011418	AC011418 Homo sapi
121	38	3.9	446	14	AF091134	AF091134 Canis fam
122	37	3.8	508	6	AF097507	AF097507 Cavia por
123	37	3.8	999	6	AB025724	AB025724 Cavia por
c 124	35	3.6	681	7	BV440664	BV440664 S237P6324
125	35	3.6	972	8	AY191829	AY191829 Synthetic
126	35	3.6	975	2	AX154597	AX154597 Sequence
127	35	3.6	2090	14	SSU08317	U08317 Sus scrofa
128	32	3.2	1058	14	ECIL12P40	Y11129 Equus cabal
129	32	3.2	1626	8	AF401989	AF401989 Synthetic
c 130	30	3.0	30	2	AX027245	AX027245 Sequence
131	30	3.0	73	2	AR439759	AR439759 Sequence
132	30	3.0	73	2	AX268996	AX268996 Sequence
133	30	3.0	200	5	AY591921	AY591921 Macaca fa
134	30	3.0	600	2	E26663	E26663 Improved me
135	30	3.0	932	14	AY686641S1	AY686641 Equus cab
136	30	3.0	1061	2	AR069654	AR069654 Sequence
137	30	3.0	1143	6	AF128214	AF128214 Mus muscu
138	30	3.0	1143	6	AF128215	AF128215 Mus muscu
139	30	3.0	1381	6	BC103608	BC103608 Mus muscu
140	30	3.0	1381	6	BC103609	BC103609 Mus muscu
141	30	3.0	1381	6	BC103610	BC103610 Mus muscu
142	30	3.0	1381	6	BC103614	BC103614 Mus muscu
143	30	3.0	1409	2	AR393787	AR393787 Sequence
144	30	3.0	1409	2	AX084105	AX084105 Sequence
145	30	3.0	1472	2	AR393786	AR393786 Sequence
146	30	3.0	1472	2	AX084104	AX084104 Sequence
147	30	3.0	1569	2	AR393796	AR393796 Sequence
148	30	3.0	1569	2	AX084114	AX084114 Sequence
149	30	3.0	1582	14	AY686641S2	AY686644 Equus cab
150	30	3.0	1669	8	AF411293	AF411293 Synthetic
151	30	3.0	1840	6	MUSIL40A	M86671 Mus musculu
152	30	3.0	2013	2	AR393795	AR393795 Sequence
153	30	3.0	2013	2	AX084113	AX084113 Sequence
154	30	3.0	2438	2	CQ812173	CQ812173 Sequence
155	30	3.0	2709	2	AR393797	AR393797 Sequence
156	30	3.0	2709	2	AX084115	AX084115 Sequence
157	30	3.0	5252	2	CQ803341	CQ803341 Sequence
158	30	3.0	5966	2	BD136050	BD136050 Interfero
159	30	3.0	9049	2	CQ803350	CQ803350 Sequence
160	30	3.0	10633	2	CQ803349	CQ803349 Sequence
161	30	3.0	11746	2	CQ803348	CQ803348 Sequence
162	30	3.0	38246	2	CQ803351	CQ803351 Sequence
163	30	3.0	285389	12	AC096348	AC096348 Rattus no
164	29	2.9	528	6	AF082494	AF082494 Marmota m
165	29	2.9	984	6	AF288519	AF288519 Marmota m
166	29	2.9	984	6	MMIL12P40	X97019 M.monax mRN
167	29	2.9	1000	6	S82420S3	S82422 interleukin
168	29	2.9	76047	6	AL669944	AL669944 Mouse DNA
169	29	2.9	110000	12	AC073744_2	Continuation (3 of
170	29	2.9	110000	12	AC073744_3	Continuation (4 of
171	29	2.9	189236	6	AL607030	AL607030 Mouse DNA
c 172	29	2.9	268294	12	AC020885	AC020885 Mus muscu
173	29	2.9	287927	12	AC079530	AC079530 Mus muscu
174	28	2.8	28	2	AR595991	AR595991 Sequence
175	28	2.8	37	2	AR595993	AR595993 Sequence
176	28	2.8	2276	6	AB085792	AB085792 Mesocrice
c 177	25	2.5	25	2	AR595992	AR595992 Sequence
c 178	24	2.4	26	2	E26678	E26678 Improved me
179	24	2.4	30	2	BD014607	BD014607 Process f
180	24	2.4	30	2	BD174647	BD174647 Process f
181	24	2.4	39	2	AR151073	AR151073 Sequence
182	24	2.4	39	2	BD014665	BD014665 Process f
183	24	2.4	39	2	E15027	E15027 PCR primer
184	24	2.4	39	2	AR316472	AR316472 Sequence
185	24	2.4	540	2	E32843	E32843 Canine inte
186	24	2.4	540	2	AR361993	AR361993 Sequence
187	24	2.4	987	2	BD007077	BD007077 Gene expr
188	24	2.4	987	2	BD007078	BD007078 Gene expr
189	24	2.4	987	2	BD136035	BD136035 Interfero
190	24	2.4	987	2	BD136036	BD136036 Interfero
191	23	2.3	500	6	S82420S4	S82423 interleukin
192	23	2.3	37305	5	HS344F5	AL031712 Human DNA
c 193	23	2.3	110000	12	AC073744_3	Continuation (4 of
194	23	2.3	142974	12	AC152028	AC152028 Dasypus n
195	23	2.3	195680	5	AC120498	AC120498 Homo sapi
196	23	2.3	265786	5	AE006466	AE006466 Homo sapi
197	23	2.3	268294	12	AC020885	AC020885 Mus muscu
198	22	2.2	399	2	CS211342	CS211342 Sequence
199	22	2.2	399	2	CS214984	CS214984 Sequence
200	22	2.2	399	6	AF046211	AF046211 Mesocrice

ALIGNMENTS

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RESULT 1
AR595967
LOCUS       AR595967                985 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 55 from patent US 6818444.
ACCESSION   AR595967
VERSION     AR595967.1  GI:56646948
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 985)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 55 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .985
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 985;  DB 2;  Length 985;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
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Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
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Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
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Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
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Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
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Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
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Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
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Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
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Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 2
AR595968/c
LOCUS       AR595968                985 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 57 from patent US 6818444.
ACCESSION   AR595968
VERSION     AR595968.1  GI:56646949
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 985)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 57 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .985
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 985;  DB 2;  Length 985;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

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Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
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Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
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Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
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Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
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Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86
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Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
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Db         25 AGCAACTGGGCATCCGTGTCCTGCA 1


RESULT 3
AR595950
LOCUS       AR595950                 987 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 29 from patent US 6818444.
ACCESSION   AR595950
VERSION     AR595950.1  GI:56646931
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 29 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 985;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
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Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
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Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
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Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 4
AR595951/c
LOCUS       AR595951                 987 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 31 from patent US 6818444.
ACCESSION   AR595951
VERSION     AR595951.1  GI:56646932
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 31 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 985;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
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Db         27 AGCAACTGGGCATCCGTGTCCTGCA 3
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RESULT 5
AR242435
LOCUS       AR242435               2193 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 5 from patent US 6472509.
ACCESSION   AR242435
VERSION     AR242435.1  GI:27288852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2193)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 5 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
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  Query Match             94.2%;  Score 928;  DB 2;  Length 2193;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  928;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         58 CTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCT 117
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Db        121 CTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCT 180

Qy        118 GATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACC 177
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACC 240

Qy        178 TGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTC 237
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTC 300

Qy        238 AAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCAT 297
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCAT 360

Qy        298 TCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAA 357
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Db        361 TCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAA 420

Qy        358 CAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGT 417
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGT 480

Qy        418 TTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGC 477
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGC 540

Qy        478 AGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAG 537
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAG 600

Qy        538 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 597
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 660

Qy        598 TGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTC 657
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Db        661 TGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTC 720

Qy        658 AAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCC 717
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCC 780

Qy        718 AAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATAC 777
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATAC 840

Qy        778 CCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAG 837
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Db        841 CCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAG 900

Qy        838 GGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTC 897
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTC 960

Qy        898 GTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCC 957
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Db        961 GTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCC 1020

Qy        958 TGGAGCAACTGGGCATCCGTGTCCTGCA 985
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RESULT 6
AR280203
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LOCUS       AR280203                2193 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 5 from patent US 6518045.
ACCESSION   AR280203
VERSION     AR280203.1  GI:29715593
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2193)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 5 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .2193
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ORIGIN

  Query Match             94.2%;  Score 928;  DB 2;  Length 2193;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  928;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         58 CTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCT 117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCT 180

Qy        118 GATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACC 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACC 240

Qy        178 TGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTC 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTC 300

Qy        238 AAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCAT 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCAT 360

Qy        298 TCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAA 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAA 420

Qy        358 CAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGT 417
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Db        421 CAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGT 480

Qy        418 TTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGC 477
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Db        481 TTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGC 540

Qy        478 AGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAG 537
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Db        541 AGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAG 600

Qy        538 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 597
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Db        601 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 660

Qy        598 TGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTC 657
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Qy        658 AAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCC 717
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Db        721 AAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCC 780

Qy        718 AAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATAC 777
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Db        781 AAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATAC 840

Qy        778 CCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAG 837
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Db        841 CCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAG 900

Qy        838 GGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTC 897
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTC 960

Qy        898 GTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCC 957
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCC 1020

Qy        958 TGGAGCAACTGGGCATCCGTGTCCTGCA 985
              ||||||||||||||||||||||||||||
Db       1021 TGGAGCAACTGGGCATCCGTGTCCTGCA 1048


RESULT 7
AR322418
LOCUS       AR322418                2193 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 5 from patent US 6566097.
ACCESSION   AR322418
VERSION     AR322418.1  GI:33708171
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2193)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 5 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .2193
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             94.2%;  Score 928;  DB 2;  Length 2193;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  928;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         58 CTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCT 117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCT 180

Qy        118 GATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACC 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACC 240

Qy        178 TGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTC 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTC 300

Qy        238 AAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCAT 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCAT 360

Qy        298 TCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAA 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAA 420

Qy        358 CAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGT 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGT 480

Qy        418 TTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGC 477
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGC 540

Qy        478 AGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAG 537
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Db        541 AGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAG 600

Qy        538 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 597
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Db        601 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 660

Qy        598 TGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTC 657
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Db        661 TGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTC 720

Qy        658 AAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCC 717
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Db        721 AAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCC 780

Qy        718 AAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATAC 777
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATAC 840

Qy        778 CCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAG 837
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Db        841 CCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAG 900

Qy        838 GGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTC 897
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTC 960

Qy        898 GTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCC 957
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCC 1020

Qy        958 TGGAGCAACTGGGCATCCGTGTCCTGCA 985
              ||||||||||||||||||||||||||||
Db       1021 TGGAGCAACTGGGCATCCGTGTCCTGCA 1048


RESULT 8
AR242436
LOCUS       AR242436                921 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 6 from patent US 6472509.
ACCESSION   AR242436
VERSION     AR242436.1  GI:27288853
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 6 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN


  Query Match             93.3%;  Score 919;  DB 2;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  919;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCA 985
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Db        901 TGGGCATCCGTGTCCTGCA 919


RESULT 9
AR280204
LOCUS       AR280204                921 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 6 from patent US 6518045.
ACCESSION   AR280204
VERSION     AR280204.1  GI:29715594
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 6 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
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    source          1. .921
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ORIGIN

  Query Match             93.3%;  Score 919;  DB 2;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  919;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
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Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
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Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCA 985
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Db        901 TGGGCATCCGTGTCCTGCA 919
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RESULT 10
AR322419
LOCUS       AR322419                921 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 6 from patent US 6566097.
ACCESSION   AR322419
VERSION     AR322419.1  GI:33708172
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 6 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
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ORIGIN

  Query Match             93.3%;  Score 919;  DB 2;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  919;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
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Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
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Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
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Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
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Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
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Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
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Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
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Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCA 985
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Db        901 TGGGCATCCGTGTCCTGCA 919


RESULT 11
FCIL12P40
LOCUS       FCIL12P40                1006 bp    mRNA    linear   MAM 18-APR-2005
DEFINITION  Felis catus mRNA for interleukin-12 p40 chain.
ACCESSION   Y07762
VERSION     Y07762.1  GI:2102664
KEYWORDS    interleukin-12 p40.
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1
  AUTHORS   Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
  TITLE     Molecular cloning of cat interleukin-12
  JOURNAL   Immunogenetics 45 (6), 462-463 (1997)
   PUBMED   9089110
REFERENCE   2  (bases 1 to 1006)
  AUTHORS   Schijns,V.E.C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
            Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
            Utrecht, NETHERLANDS
FEATURES             Location/Qualifiers
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  Query Match             91.7%;  Score 903;  DB 14;  Length 1006;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  953;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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RESULT 12
AR595956
LOCUS       AR595956                 1599 bp    DNA     linear   PAT 15-DEC-2004
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DEFINITION  Sequence 38 from patent US 6818444.
ACCESSION   AR595956
VERSION     AR595956.1  GI:56646937
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 38 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
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  Query Match             91.7%;  Score 903;  DB 2;  Length 1599;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  953;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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RESULT 13
AR595957/c
LOCUS       AR595957               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 40 from patent US 6818444.
ACCESSION   AR595957
VERSION     AR595957.1  GI:56646938
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 40 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             91.7%;  Score 903;  DB 2;  Length 1599;
  Best Local Similarity   99.9%;  Pred. No. 0;
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Qy        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571
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RESULT 14
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DEFINITION Sequence 1 from Patent WO0104155.
ACCESSION AX076200
VERSION AX076200.1 GI:12710825
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
TITLE Feline interleukin-12 as an immune stimulant
JOURNAL Patent: WO 0104155-A 1 18-JAN-2001;
Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
CALIFORNIA (US)
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ORIGIN

Query Match 89.7%; Score 884; DB 2; Length 990;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 934; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAG 935
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RESULT 15
AX076482
LOCUS AX076482 990 bp DNA linear PAT 06-FEB-2001
DEFINITION Sequence 8 from Patent WO0104280.
ACCESSION AX076482
VERSION AX076482.1 GI:12711034
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
TITLE Vaccine against lentiviral infections, such as the feline immune deficiency virus of the cat
JOURNAL Patent: WO 0104280-A 8 18-JAN-2001;
Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
Universitaet Zuerich (CH)
FEATURES Location/Qualifiers
source 1. .990
/organism="synthetic construct"
/mol_type="unassigned DNA"

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                     /db_xref="taxon:32630"
                     /note="Sequence coding for SEQ ID NO 2, IL-12 p40"
ORIGIN

  Query Match             89.7%;  Score 884;  DB 2;  Length 990;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  934;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
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Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
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Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
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Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
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Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
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Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
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Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
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Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAG 935
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RESULT 16
AX076209
LOCUS       AX076209                4522 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 10 from Patent WO0104155.
ACCESSION   AX076209
VERSION     AX076209.1  GI:12710834
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 10 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .4522
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Plasmid pMol-fil12p40"
ORIGIN

  Query Match             89.7%;  Score 884;  DB 2;  Length 4522;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  934;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Db       3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

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Db       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Db       3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
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Db       3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
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Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Db       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db       3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Db       3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Db       3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
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Db       3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706
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Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
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Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Db       3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAG 935
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Db       3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAG 3981


RESULT 17
AX076476
LOCUS       AX076476               4522 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 2 from Patent WO0104280.
ACCESSION   AX076476
VERSION     AX076476.1  GI:12711028
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 2 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="IL-12p40"
ORIGIN

  Query Match             89.7%;  Score 884;  DB 2;  Length 4522;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  934;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
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Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
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Db       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Db       3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

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Db       3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
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Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Db       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db       3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Db       3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
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Db       3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
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Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
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Db       3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

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RESULT 18
AR242437
LOCUS       AR242437               921 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 7 from patent US 6472509.
ACCESSION   AR242437
VERSION     AR242437.1  GI:27288854
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 7 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             88.1%;  Score 868;  DB 2;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
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Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
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Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
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Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
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Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
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Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
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Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
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Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
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Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
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Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
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Qy        967 TGGGCATCCGTGTCCTGCA 985
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Db        901 TGGGCATCCGTGTCCTGCA 919


RESULT 19
AR280205
LOCUS       AR280205                 921 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 7 from patent US 6518045.
ACCESSION   AR280205
VERSION     AR280205.1  GI:29715595
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 7 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
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ORIGIN

  Query Match             88.1%;  Score 868;  DB 2;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
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Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCA 985
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Db        901 TGGGCATCCGTGTCCTGCA 919


RESULT 20
AR322420
LOCUS       AR322420                 921 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 7 from patent US 6566097.
ACCESSION   AR322420
VERSION     AR322420.1  GI:33708173
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 7 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             88.1%;  Score 868;  DB 2;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCA 985
              ||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCA 919


RESULT 21
AR595948
LOCUS       AR595948                 921 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 26 from patent US 6818444.
ACCESSION   AR595948
VERSION     AR595948.1  GI:56646929
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 26 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             88.1%;  Score 868;  DB 2;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
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Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCA 985
              ||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCA 919


RESULT 22
AR595949/c
LOCUS       AR595949                921 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 28 from patent US 6818444.
ACCESSION   AR595949
VERSION     AR595949.1  GI:56646930
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 28 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
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ORIGIN

  Query Match             88.1%;  Score 868;  DB 2;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        967 TGGGCATCCGTGTCCTGCA 985
              ||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCA 3


RESULT 23
AR595959
LOCUS       AR595959                1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 43 from patent US 6818444.
ACCESSION   AR595959
VERSION     AR595959.1  GI:56646940
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
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  JOURNAL   Patent: US 6818444-A 43 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             88.1%;  Score 868;  DB 2;  Length 1533;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy         367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy         427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy         487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
               |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy         547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy         607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy         667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy         727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy         787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy         847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy         907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy         967 TGGGCATCCGTGTCCTGCA 985
               ||||||||||||||||||
Db         901 TGGGCATCCGTGTCCTGCA 919


RESULT 24
AR595960/c
LOCUS       AR595960               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 45 from patent US 6818444.
ACCESSION   AR595960
VERSION     AR595960.1  GI:56646941
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 45 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             88.1%;  Score 868;  DB 2;  Length 1533;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy         367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy         427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy         487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
               |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy         547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy         607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy         667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874
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Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        967 TGGGCATCCGTGTCCTGCA 985
              ||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCA 615
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RESULT 25
FCU83184
LOCUS       FCU83184                990 bp    mRNA    linear   MAM 16-JUL-1999
DEFINITION  Felis catus interleukin-12 p40 subunit (IL-12) mRNA, complete cds.
ACCESSION   U83184
VERSION     U83184.1  GI:2735050
KEYWORDS    .
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Nucleotide and predicted peptide sequence of feline interleukin-12
            (IL-12)
  JOURNAL   DNA Seq. 8 (1-2), 77-82 (1997)
   PUBMED   9522125
REFERENCE   2  (bases 1 to 990)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal
            Veterinary Medicine, University of Zurich, Winterthurerstrasse 260,
            Zurich, ZH 8057, Switzerland
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="Felis catus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
     CDS             1. .990
                     /note="cytokine"
                     /codon_start=1
                     /product="interleukin-12 p40 subunit"
                     /protein_id="AAB93835.1"
                     /db_xref="GI:2735051"
                     /translation="MHPQQLVIAWFSLVLLAPPLMAIWELEKNVYVVELDWHPDAPGE
                     MVVLTCDTPEEDDITWTSDQSSEVLGSGKTLTIQVKEFADAGQYTCHKGGEVLSHSFL
                     LIHKKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFTVKSSR
                     GSSDPQGVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPAAEESLPIEVVVDAIHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFGV
                     QVQGKNNREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSNWASVSCS"
ORIGIN

  Query Match           84.2%;  Score 829;  DB 14;  Length 990;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  829;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        157 CCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGT 216
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 CCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGT 216
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Qy        217 AAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAA 276
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        217 AAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAA 276

Qy        277 GGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGG 336
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        277 GGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGG 336

Qy        337 TCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAG 396
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        337 TCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAG 396

Qy        397 GCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTG 456
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        397 GCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTG 456

Qy        457 AAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCA 516
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        457 AAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCA 516

Qy        517 GCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTG 576
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        517 GCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTG 576

Qy        577 GAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTG 636
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        577 GAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTG 636

Qy        637 GTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGAC 696
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        637 GTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGAC 696

Qy        697 ATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCAT 756
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        697 ATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCAT 756

Qy        757 GTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTA 816
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        757 GTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTA 816

Qy        817 ACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTG 876
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        817 ACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTG 876

Qy        877 GACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGA 936
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        877 GACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGA 936

Qy        937 GACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCA 985
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        937 GACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCA 985
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RESULT 26
AF054607
LOCUS       AF054607                431 bp    mRNA    linear   MAM 26-JUL-2000
DEFINITION  Felis catus interleukin 12 p40 subunit mRNA, partial cds.
ACCESSION   AF054607
VERSION     AF054607.1  GI:3126822
KEYWORDS    .
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1  (bases 1 to 431)
  AUTHORS   Harley,R., Helps,C.R., Harbour,D.A., Gruffydd-Jones,T.J. and
            Day,M.J.
  TITLE     Cytokine mRNA expression in lesions in cats with chronic
            gingivostomatitis
  JOURNAL   Clin. Diagn. Lab. Immunol. 6 (4), 471-478 (1999)
   PUBMED   10391845
```

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REFERENCE   2  (bases 1 to 431)
  AUTHORS   Harley,R., Helps,C.R., Gruffydd-Jones,T.J., Day,M.J. and
            Harbour,D.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-1998) Clinical Veterinary Science, University of
            Bristol, Langford House, Langford, Bristol BS40 7DU, U.K.
FEATURES             Location/Qualifiers
     source          1. .431
                     /organism="Felis catus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
                     /cell_line="FL4"
                     /cell_type="T cell"
                     /note="persistant FIV infection"
     CDS             <1. .>431
                     /codon_start=1
                     /product="interleukin 12 p40 subunit"
                     /protein_id="AAC15980.1"
                     /db_xref="GI:3126823"
                     /translation="CHKGXEVLSHSXVLIXEKEDGIWSTDILREQKESKNKIFLKCEA
                     KNYSGRFTCWWLTAISTDLKFTVKSSRGSSDPQGVTCGAATLSAEKVRVDNRDYKKYT
                     VECQEGSACPAAEESLPIEVVVDAIHKLKYENYTSSFFIRD"
ORIGIN

  Query Match             38.8%;  Score 382;  DB 14;  Length 431;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-200;
  Matches  382;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        317 AAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATA 376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         50 AAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATA 109

Qy        377 AGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGA 436
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        110 AGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGA 169

Qy        437 CGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCC 496
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 CGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCC 229

Qy        497 AAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGG 556
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 AAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGG 289

Qy        557 ATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGA 616
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 ATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGA 349

Qy        617 GCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCA 676
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 GCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCA 409

Qy        677 GCAGCTTCTTCATCAGGGACAT 698
              |||||||||||||||||||||
Db        410 GCAGCTTCTTCATCAGGGACAT 431


RESULT 27
AX154603
LOCUS       AX154603                990 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 7 from Patent WO0140257.
ACCESSION   AX154603
VERSION     AX154603.1  GI:14536186
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 7 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match             8.4%;  Score 83;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 5.7e-34;
  Matches   83;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        865 AGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGC 924
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 AGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGC 924

Qy        925 GTGCAAGCCAGAGACCGCTACTA 947
              |||||||||||||||||||||||
Db        925 GTGCAAGCCAGAGACCGCTACTA 947


RESULT 28
AR595965
LOCUS       AR595965                921 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 52 from patent US 6818444.
ACCESSION   AR595965
VERSION     AR595965.1  GI:56646946
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 52 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy        597 CTGCCC 602
              ||||||
Db        531 CTGCCC 536


RESULT 29
AR595966/c
LOCUS       AR595966                921 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 54 from patent US 6818444.
ACCESSION   AR595966
VERSION     AR595966.1  GI:56646947
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 54 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="genomic DNA"
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ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy        597 CTGCCC 602
              ||||||
Db        391 CTGCCC 386


RESULT 30
BD171282
LOCUS       BD171282                924 bp    DNA     linear   PAT 18-FEB-2003
DEFINITION  Novel canine cytokine protein.
ACCESSION   BD171282
VERSION     BD171282.1  GI:28412572
KEYWORDS    JP 2002241398-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 924)
  AUTHORS   Imamura,T., Maeda,H., Tokiyoshi,Y. and Eda,Y.
  TITLE     Novel canine cytokine protein
  JOURNAL   Patent: JP 2002241398-A 2 28-AUG-2002;
            CHEMO SERO THERAPEUT RES INST
COMMENT     OS   Canine splenocyte
            PN   JP 2002241398-A/2
            PD   28-AUG-2002
            PF   03-JUN-1997 JP 1997161936
            PI   TAKAYUKI IMAMURA,HIROAKI MAEDA,YUKIO TOKIYOSHI,YASUYUKI EDA PC
              C07K14/52,A61K38/00,A61K39/395,C07K16/24,C12N5/10,C12N15/09, PC
            C12P21/02//
            PC   C12P21/08,(C12P21/02,C12R1:91),A61K37/02,C12N5/00,C12N15/00 CC
              Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES            Location/Qualifiers
     source         1. .924
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"
ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 924;
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  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 533

Qy        597 CTGCCC 602
              ||||||
Db        534 CTGCCC 539


RESULT 31
AR595969
LOCUS       AR595969                987 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 58 from patent US 6818444.
ACCESSION   AR595969
VERSION     AR595969.1  GI:56646950
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 58 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES            Location/Qualifiers
     source         1. .987
                    /organism="unknown"
                    /mol_type="genomic DNA"
ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 32
AR595970/c
LOCUS       AR595970                987 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 60 from patent US 6818444.
ACCESSION   AR595970
VERSION     AR595970.1  GI:56646951
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 60 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES            Location/Qualifiers
     source         1. .987
                    /organism="unknown"
                    /mol_type="genomic DNA"
ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy        597 CTGCCC 602
              ||||||
Db        391 CTGCCC 386


RESULT 33
AR151061
LOCUS       AR151061                990 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 1 from patent US 6231850.
ACCESSION   AR151061
VERSION     AR151061.1  GI:15117111
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12
  JOURNAL   Patent: US 6231850-A 1 15-MAY-2001;
FEATURES            Location/Qualifiers
     source         1. .990
                    /organism="unknown"
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                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 34
AR151071
LOCUS       AR151071                990 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 11 from patent US 6231850.
ACCESSION   AR151071
VERSION     AR151071.1  GI:15117121
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12
  JOURNAL   Patent: US 6231850-A 11 15-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 35
BD014653
LOCUS       BD014653                990 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy.
ACCESSION   BD014653
VERSION     BD014653.1  GI:22555436
KEYWORDS    JP 2001161378-A/1.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F.
  TITLE     Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy
  JOURNAL   Patent: JP 2001161378-A 1 19-JUN-2001;
            TORAY INDUSTRIES INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 2001161378-A/1
            PD   19-JUN-2001
            PF   26-SEP-2000 JP 2000292946
            PI   FUMIYOSHI OKANO
            PC   C12N15/09,A61K38/00,A61P17/00,A61P17/00,A61P31/04,A61P31/04,
            PC   A61P35/00,
            PC   A61P37/00,C07K1/18,C07K1/22,C07K14/54,C12P21/02//(C12P21/02,
            PC   C12R1:91),
            PC   (C12P21/02,C12R1:93),C12N15/00,A61K37/02
            CC   Process for producing highly pure protein, interleukin 12,  CC
                 protein
            CC   inhibiting interleukin-12 activity, remedies for mammalian  CC
                 immunopathy and
            CC   method of treating immunopathy
            FH   Key             Location/Qualifiers
            FT   CDS             (1). .(987)
            FT   mat_peptide     (67). .(987).
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="Canis sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9616"
ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 36
BD014663
LOCUS       BD014663                990 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy.
ACCESSION   BD014663
VERSION     BD014663.1  GI:22555446
KEYWORDS    JP 2001161378-A/11.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F.
  TITLE     Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy
  JOURNAL   Patent: JP 2001161378-A 11 19-JUN-2001;
            TORAY INDUSTRIES INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 2001161378-A/11
            PD   19-JUN-2001
            PF   26-SEP-2000 JP 2000292946
            PI   FUMIYOSHI OKANO
            PC   C12N15/09,A61K38/00,A61P17/00,A61P17/00,A61P31/04,A61P31/04,
            PC   A61P35/00,
            PC   A61P37/00,C07K1/18,C07K1/22,C07K14/54,C12P21/02//(C12P21/02,
            PC   C12R1:91),
            PC   (C12P21/02,C12R1:93),C12N15/00,A61K37/02
            CC   Process for producing highly pure protein, interleukin 12,  CC
                 protein
            CC   inhibiting interleukin-12 activity, remedies for mammalian  CC
                 immunopathy and
            CC   method of treating immunopathy
            FH   Key             Location/Qualifiers
            FT   CDS             (1). .(987)
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           FT   mat_peptide     (67). .(987).
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="Canis sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9616"
ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 37
E15017
LOCUS       E15017                    990 bp    DNA     linear   PAT 28-JUL-1999
DEFINITION  Canine mRNA for interleukin 12 40kDa subunit,complete cds.
ACCESSION   E15017
VERSION     E15017.1  GI:5709700
KEYWORDS    JP 1998036397-A/1.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F.
  TITLE     CANINE INTERLEUKIN 12 AND ITS PRODUCTION
  JOURNAL   Patent: JP 1998036397-A 1 10-FEB-1998;
            TORAY IND INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 1998036397-A/1
            PD   10-FEB-1998
            PF   08-NOV-1996 JP 1996296789
            PR   08-NOV-1995 JP 95P   289729, 23-MAY-1996 JP 96P   128104 PI
            OKANO FUMIYOSHI
            PC   C07K14/54,C07H21/04,C12N5/10,C12N15/09,C12P21/02,(C12N5/10, PC
              C12R1:91),
            PC   (C12P21/02,C12R1:91);
            CC   strandedness: Double;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .990
            FT                   /organism='Canis sp.'
            FT                   /tissue_type='liver'
            FT   CDS             1. .990
            FT                   /product='interleukin 12 40kDa subunit'.
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="Canis sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9616"
ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 38
AR316460
LOCUS       AR316460                  990 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 1 from patent US 6562334.
ACCESSION   AR316460
VERSION     AR316460.1  GI:33695288
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12 administration as an immune disease treatment
  JOURNAL   Patent: US 6562334-A 1 13-MAY-2003;
            Toray Industries, Inc.;;
            JPX;
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 39
AR316470
LOCUS       AR316470                  990 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 11 from patent US 6562334.
ACCESSION   AR316470
VERSION     AR316470.1  GI:33695298
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12 administration as an immune disease treatment
  JOURNAL   Patent: US 6562334-A 11 13-MAY-2003;
            Toray Industries, Inc.;;
            JPX;
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602
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RESULT 40
AR595973
LOCUS       AR595973               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 66 from patent US 6818444.
ACCESSION   AR595973
VERSION     AR595973.1  GI:56646954
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 66 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy        597 CTGCCC 602
              ||||||
Db        531 CTGCCC 536


RESULT 41
AR595974/c
LOCUS       AR595974               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 68 from patent US 6818444.
ACCESSION   AR595974
VERSION     AR595974.1  GI:56646955
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 68 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy        597 CTGCCC 602
              ||||||
Db       1003 CTGCCC 998


RESULT 42
AR595971
LOCUS       AR595971               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 61 from patent US 6818444.
ACCESSION   AR595971
VERSION     AR595971.1  GI:56646952
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 61 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 43
AR595972/c
LOCUS       AR595972               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 63 from patent US 6818444.
ACCESSION   AR595972
VERSION     AR595972.1  GI:56646953
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 63 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy        597 CTGCCC 602
              ||||||
Db       1003 CTGCCC 998


RESULT 44
BD171281
LOCUS       BD171281               2154 bp    DNA     linear   PAT 18-FEB-2003
DEFINITION  Novel canine cytokine protein.
ACCESSION   BD171281
VERSION     BD171281.1  GI:28412571
KEYWORDS    JP 2002241398-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
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REFERENCE   1  (bases 1 to 2154)
  AUTHORS   Imamura,T., Maeda,H., Tokiyoshi,Y. and Eda,Y.
  TITLE     Novel canine cytokine protein
  JOURNAL   Patent: JP 2002241398-A 1 28-AUG-2002;
            CHEMO SERO THERAPEUT RES INST
COMMENT     OS   Canine splenocyte
            PN   JP 2002241398-A/1
            PD   28-AUG-2002
            PF   03-JUN-1997 JP 1997161936
            PI   TAKAYUKI IMAMURA,HIROAKI MAEDA,YUKIO TOKIYOSHI,YASUYUKI EDA PC
              C07K14/52,A61K38/00,A61K39/395,C07K16/24,C12N5/10,C12N15/09, PC
            C12P21/02//
            PC   C12P21/08,(C12P21/02,C12R1:91),A61K37/02,C12N5/00,C12N15/00 CC
              Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES                Location/Qualifiers
     source             1. .2154
                        /organism="unidentified"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32644"
ORIGIN

  Query Match              6.7%;  Score 66;  DB 2;  Length 2154;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 650

Qy        597 CTGCCC 602
              ||||||
Db        651 CTGCCC 656


RESULT 45
AR596011
LOCUS       AR596011                2267 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 107 from patent US 6818444.
ACCESSION   AR596011
VERSION     AR596011.1  GI:56646992
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2267)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 107 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES                Location/Qualifiers
     source             1. .2267
                        /organism="unknown"
                        /mol_type="genomic DNA"
ORIGIN

  Query Match              6.7%;  Score 66;  DB 2;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 749

Qy        597 CTGCCC 602
              ||||||
Db        750 CTGCCC 755


RESULT 46
AR596012/c
LOCUS       AR596012                2267 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 109 from patent US 6818444.
ACCESSION   AR596012
VERSION     AR596012.1  GI:56646993
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2267)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 109 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES                Location/Qualifiers
     source             1. .2267
                        /organism="unknown"
                        /mol_type="genomic DNA"
ORIGIN

  Query Match              6.7%;  Score 66;  DB 2;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1578 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1519

Qy        597 CTGCCC 602
              ||||||
Db       1518 CTGCCC 1513


RESULT 47
AX154600
LOCUS       AX154600                 984 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 4 from Patent WO0140257.
ACCESSION   AX154600
VERSION     AX154600.1  GI:14536183
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 4 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES                Location/Qualifiers
     source             1. .984
                        /organism="synthetic construct"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:32630"
                        /note="Synthetic Sequence"
ORIGIN

  Query Match              6.6%;  Score 65;  DB 2;  Length 984;
  Best Local Similarity   100.0%;  Pred. No. 5.7e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        451 GATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGT 510
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGT 510

Qy        511 GGAGC 515
              |||||
Db        511 GGAGC 515


RESULT 48
AF349536
LOCUS       AF349536                 588 bp    mRNA    linear   MAM 17-MAY-2001
DEFINITION  Canis familiaris interleukin-12 subunit p40 mRNA, partial cds.
ACCESSION   AF349536
VERSION     AF349536.1  GI:14133584
```

```
KEYWORDS    .
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 588)
  AUTHORS   Fonfara,S., Groene,A., Koenig,M. and Baumgaertner,W.
  TITLE     Sequence of canine interleukin-12-p40 mRNA in DH82-cells
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 588)
  AUTHORS   Fonfara,S., Groene,A., Koenig,M. and Baumgaertner,W.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-FEB-2001) Institute of Pathology,
            Justus-Liebig-University, Frankfurter Str. 96, Giessen 35392,
            Germany
FEATURES             Location/Qualifiers
     source          1. .588
                     /organism="Canis familiaris"
                     /mol_type="mRNA"
                     /db_xref="taxon:9615"
                     /cell_line="DH82"
     CDS             <1. .>588
                     /codon_start=3
                     /product="interleukin-12 subunit p40"
                     /protein_id="AAK54070.1"
                     /db_xref="GI:14133585"
                     /translation="QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVV
                     LTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIH
                     KKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFS
                     DPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGS"
ORIGIN

  Query Match             6.4%;  Score 63;  DB 14;  Length 588;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-23;
  Matches   63;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         88 GTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACC 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 GTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACC 140

Qy        148 TGC 150
              |||
Db        141 TGC 143


RESULT 49
CFU49100
LOCUS       CFU49100                1015 bp    mRNA    linear   MAM 13-MAR-1996
DEFINITION  Canis familiaris interleukin-12 p40 subunit mRNA, complete cds.
ACCESSION   U49100
VERSION     U49100.1  GI:1223907
KEYWORDS    .
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 1015)
  AUTHORS   Belke-Louis,G.F. and Buettner,M.
  TITLE     Cloning and sequence analysis of the p35 and p40 subunits of canine
            interleukin-12
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1015)
  AUTHORS   Belke-Louis,G.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-FEB-1996) Georg F. Belke-Louis, Institute of Med.
            Microbiology, Veterinaerstr. 13, Muenchen, D-80539, Germany
FEATURES             Location/Qualifiers
     source          1. .1015
                     /organism="Canis familiaris"
                     /mol_type="mRNA"
                     /db_xref="taxon:9615"
     CDS             1. .990
                     /codon_start=1
                     /product="interleukin-12 p40 subunit"
                     /protein_id="AAA92059.1"
                     /db_xref="GI:1223908"
                     /translation="MHPQQLVISWFSLVLLASSLMTIWELEKDVYVVELDWHPDAPGE
                     MVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLL
                     LIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSR
                     GFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHK
                     LKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCV
                     QAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSDWASVSCS"
ORIGIN

  Query Match             6.4%;  Score 63;  DB 14;  Length 1015;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-23;
  Matches   63;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         88 GTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACC 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 GTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACC 147

Qy        148 TGC 150
              |||
Db        148 TGC 150


RESULT 50
BV242752
LOCUS       BV242752                621 bp    DNA     linear   STS 19-JAN-2005
DEFINITION  S234P6134RD4.T0 EnglishShepherd Canis familiaris STS genomic,
            sequence tagged site.
ACCESSION   BV242752
VERSION     BV242752.1  GI:57305294
KEYWORDS    STS.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 621)
  AUTHORS   Lindblad-Toh,K.
  TITLE     The genome sequence of Canis familiaris
  JOURNAL   Unpublished (2004)
COMMENT
            Contact: Kerstin Lindblad-Toh
            Whitehead Institute for Biomedical Research, Center for Genome
            Research
            320 Charles Street, Cambridge, MA 02141, USA
            Tel: 6172521477
            Fax: 6172580903
            Email: kersli@genome.wi.mit.edu
            Primer A: No sequence submitted
            Primer B: No sequence submitted
            STS size: 621
            Protocol:
            WGS-discovery (WGS):
            Paired-end low-coverage whole genome shotgun reads were generated
            from 9 breeds
            (German Shepherd, Rottweiler, Bedlington Terrier, Beagle, Labrador
            Retriever, English
            Shepherd, Italian Greyhound, Alaskan Malamute and the Portuguese
            Water Dog -100,000 each)
            and five other canids (Chinese, Alaskan, Indian and Spanish Gray
            Wolf as well as the
            Californian Coyote).
            The WGS reads were placed uniquely on the CanFam1.0 boxer assembly
            and SNP detection was
            carried out by SSAHA-SNP. 863872 reads were annotated as STSs and
            485941 SNPs were
            annotated with alleles from the boxer and the breed or canid from
            which the particular
            read came. The validation rate for these SNPs was estimated at
            approximately 98%.
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            WGA-discovery (WGA) of Boxer/Poodle SNPs:
            A second set of SNPs was generated using a similar methodology
            except that the contigs
            from the 1.5x poodle assembly (Kirkness 2003) were used instead of
            WGS reads. Since this
            sequence lacked base quality scores, arbitrary quality scores of
            phred 40 were assigned
            before the poddle seqeunce was placed uniquely on the CanFam1.0
            boxer assembly and SNP
            detection was carried out by SSAHA-SNP. 1637780 SNPs were annotated
            with alleles from the
            boxer and the poodle. The validation rate for these SNPs was
            estimated at approximately TBD%.
            Internal-WGA-discovery (I-WGA):
            A third set of SNPs were discovered by comparing reads in the WGA
            assembly. SNPs were
            defined as mismatch positions that had a base quality of >= 30 on
            both reads in a region
            that aligned without gaps, and with at most one additional mismatch
            in the ten flanking
            bases. For each allele, at least one additional read had to confirm
            it. 731476 SNPs were
            annotated with alleles between the two boxer alleles. The
            validation rate for these SNPs
            was estimated at approximately TBD%.
FEATURES             Location/Qualifiers
     source          1. .621
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /strain="EnglishShepherd"
                     /db_xref="taxon:9615"
                     /map="+ 4 22-568 54361767-54362313"
                     /clone_lib="EnglishShepherd"
     STS             <1. .>621
ORIGIN

  Query Match             6.2%;  Score 61;  DB 7;  Length 621;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-21;
  Matches   61;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        873 CGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGC 932
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 CGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGC 328

Qy        933 C 933
              |
Db        329 C 329


RESULT 51
AX154598
LOCUS       AX154598                984 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 2 from Patent WO0140257.
ACCESSION   AX154598
VERSION     AX154598.1  GI:14536181
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 2 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .984
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match             6.2%;  Score 61;  DB 2;  Length 984;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-22;
  Matches   61;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        673 ACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTG 732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        673 ACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTG 732

Qy        733 A 733
              |
Db        733 A 733


RESULT 52
AX154599
LOCUS       AX154599                984 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 3 from Patent WO0140257.
ACCESSION   AX154599
VERSION     AX154599.1  GI:14536182
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 3 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .984
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match             6.1%;  Score 60;  DB 2;  Length 984;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-21;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAAC 723
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAAC 723


RESULT 53
AX154602
LOCUS       AX154602                975 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 6 from Patent WO0140257.
ACCESSION   AX154602
VERSION     AX154602.1  GI:14536185
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 6 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .975
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match             5.4%;  Score 53;  DB 2;  Length 975;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-17;
  Matches   53;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        895 GTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTA 947
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        874 GTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTA 926


RESULT 54
AF333121
LOCUS       AF333121                 452 bp    mRNA    linear   MAM 06-FEB-2001
DEFINITION  Canis familiaris interleukin 12 subunit p40 mRNA, partial cds.
ACCESSION   AF333121
VERSION     AF333121.1  GI:12667429
KEYWORDS    .
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 452)
  AUTHORS   Markus,S. and Baumgaertner,W.
  TITLE     Expression of canine interleukin-12 subunit p40 mRNA in a
            continuous macrophage cell line
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 452)
  AUTHORS   Markus,S. and Baumgaertner,W.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-JAN-2001) Department of Veterinary Pathology,
            Justus-Liebig-University of Giessen, Frankfurter Strasse 96,
            Giessen 35392, Germany
FEATURES             Location/Qualifiers
     source          1. .452
                     /organism="Canis familiaris"
                     /mol_type="mRNA"
                     /db_xref="taxon:9615"
                     /cell_line="DH 82"
                     /cell_type="macrophage"
                     /note="amplified using primer pair p77s/p34as"
     CDS             <1. .>452
                     /codon_start=2
                     /product="interleukin 12 subunit p40"
                     /protein_id="AAK01441.1"
                     /db_xref="GI:12667430"
                     /translation="TCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHK
                     GGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAIST
                     DLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGS"
ORIGIN

  Query Match             5.2%;  Score 51;  DB 14;  Length 452;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-16;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGA 587
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGA 444


RESULT 55
RNU16674
LOCUS       RNU16674                 821 bp    mRNA    linear   ROD 07-NOV-1994
DEFINITION  Rattus norvegicus interleukin-12p40 mRNA, partial cds.
ACCESSION   U16674
VERSION     U16674.1  GI:565093
KEYWORDS    .
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 821)
  AUTHORS   Goodman,R.E. and Toews,G.B.
  TITLE     A partial cDNA of the coding region of rat IL-12p40, cloned by
            RT/PCR from Staphlococcal endotoxin stimulated splenocytes
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 821)
  AUTHORS   Goodman,R.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-OCT-1994) Richard E. Goodman, Internal
            Medicine/Pulmonary, University of Michigan, 1150 W. Medical Center
            Dr., 3311 Med. Sci. I, Ann Arbor, MI 48109-0652, USA
FEATURES             Location/Qualifiers
     source          1. .821
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Fischer"
                     /db_xref="taxon:10116"
                     /tissue_type="cultured splenocytes (SEA plus SEB
                     stimulation)"
     CDS             17. .>821
                     /note="encodes the N-terminal 268 amino acids of the
                     expected 335 amino acids encoded by the mouse gene"
                     /codon_start=1
                     /product="interleukin-12p40"
                     /protein_id="AAA52229.1"
                     /db_xref="GI:565094"
                     /translation="MCHQKLTFSWFAMVLLVSPLMAMWELEKDVYVVEVDWRPDAPGE
                     TVTLTCDSPEEDDITWTSDQRRGVIGSGKTLTITVREFLDAGQYTCHRGGETLSHSHL
                     LLHKKENGIWSTEILKNFKNKTFLKREAPNYSGRFTCSWLVHRNTDLKFNIKSSSSSP
                     ESRAVTCGAASLSAEKVTLNQRDYEKYSVACQEDVTCPTAEETLPIELVVEAQQQNKY
                     ENYSTSFFIRDIIKPDPPKNLQVKPLKNSQVEVSWEYPDSWSTPHSYFSL"
ORIGIN

  Query Match             5.2%;  Score 51;  DB 6;  Length 821;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-16;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCA 728
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 CAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCA 735


RESULT 56
AF133197
LOCUS       AF133197                 1008 bp    mRNA    linear   ROD 08-APR-1999
DEFINITION  Rattus norvegicus interleukin-12 p40 precursor, mRNA, complete cds.
ACCESSION   AF133197
VERSION     AF133197.1  GI:4574731
KEYWORDS    .
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 1008)
  AUTHORS   Khalife,J., Pierrot,C., Cocude,C., Cetre,C., Godin,C. and Capron,A.
  TITLE     Molecular cloning and sequencing of the rat interleukin-12 p40 gene
  JOURNAL   Eur. Cytokine Netw. 9 (1), 69-73 (1998)
   PUBMED   9613680
REFERENCE   2  (bases 1 to 1008)
  AUTHORS   Khalife,J., Pierrot,C., Cocude,C., Cetre,C., Godin,C. and Capron,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAR-1999) InSERM U167, 1, rue du professeur Calmette,
            Lille 59019, France
FEATURES             Location/Qualifiers
     source          1. .1008
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Fischer"
                     /db_xref="taxon:10116"
     CDS             1. .1008
                     /note="IL-12P40"
                     /codon_start=1
                     /product="interleukin-12 p40 precursor"
                     /protein_id="AAD24190.1"
                     /db_xref="GI:4574732"
                     /translation="MCHQKLTFSWFAMVLLVSPLMAMWELEKDVYVVEVDWRPDAPGE
                     TVTLTCDSPEEDDITWTSDQRRGVIGSGKTLTITVREFLDAGQYTCHRGGETLSHSHL
                     LLHKKENGIWSTEILKNFKNKTFLKCEAPNYSGRFTCSWLVHRNTDLKFNIKSSSSSP
                     ESRAVTCGRASLSAEKVTLNQRDYEKYSVACQEDVTCPTAEETLPIELVVEAQQQNKY
                     ENYSTSFFIRDIIKPDPPKNLQVKPLKNSQVEVSWEYPDSWSTPHSYFSLKFFVRIQR
```

```
                    KKEKTKETEEECNQKGAFLVEKTSAEVQCKGANICVQAQDRYYNSSCSKWTCVPCRGR
                    S"
ORIGIN

  Query Match             5.2%;  Score 51;  DB 6;  Length 1008;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-16;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCA 728
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 CAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCA 719


RESULT 57
AF421395
LOCUS       AF421395                1425 bp    mRNA    linear   ROD 07-JUL-2004
DEFINITION  Sigmodon hispidus interleukin 12 p40 subunit precursor, mRNA,
            complete cds.
ACCESSION   AF421395
VERSION     AF421395.1  GI:16304138
KEYWORDS    .
SOURCE      Sigmodon hispidus (hispid cotton rat)
  ORGANISM  Sigmodon hispidus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Cricetidae; Sigmodontinae; Sigmodon.
REFERENCE   1  (bases 1 to 1425)
  AUTHORS   Blanco,J.C., Pletneva,L., Boukhvalova,M., Richardson,J.Y.,
            Harris,K.A. and Prince,G.A.
  TITLE     The cotton rat: an underutilized animal model for human infectious
            diseases can now be exploited using specific reagents to cytokines,
            chemokines, and interferons
  JOURNAL   J. Interferon Cytokine Res. 24 (1), 21-28 (2004)
   PUBMED   14980081
REFERENCE   2  (bases 1 to 1425)
  AUTHORS   Pletneva,L.M., Bacot,S., Blanco,J.C., Langley,R.J. and Prince,G.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-SEP-2001) Molecular Biology, Virion Systems Inc.,
            9610 Medical Center Drive, Suite 100, Rockville, MD 20850, USA
FEATURES             Location/Qualifiers
     source          1. .1425
                     /organism="Sigmodon hispidus"
                     /mol_type="mRNA"
                     /db_xref="taxon:42415"
     CDS             25. .1008
                     /codon_start=1
                     /product="interleukin 12 p40 subunit precursor"
                     /protein_id="AAL16936.1"
                     /db_xref="GI:16304139"
                     /translation="MCHQKLTISWFAMVLLVSPLMAIWELEKDVYVVEVDWSPGAPGE
                     RVVLTCDTSEEDDIIWTSDQSSEVVGSGKTLIVQVKEFSDAGQYTCHKGGETLSHSRL
                     LLHKKEDGIWSTDILKDQKDPKNKTFLKCEAANYSGRFTCWWLTAVSTDLKFSLKSSS
                     SSSDSRSVTCGAASLSTEKVTVDQRDYNKYSVACQEDITCPTAEETLPIELVMEAQHK
                     YKYENYSTGFFIRDIIKPDPPKNLQLKPLKSSQVEVSWEYPDSWSTPHSYFSLKFFVQ
                     VYRKKEKKGESLLVDKPSAKIRCSKGGEVRVRAQDHYYNSSWSEWASVSCN"
ORIGIN

  Query Match             5.0%;  Score 49;  DB 6;  Length 1425;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-15;
  Matches   49;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        680 GCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCA 728
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        704 GCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCA 752


RESULT 58
DQ152965
LOCUS       DQ152965                 224 bp    mRNA    linear   MAM 07-NOV-2005
DEFINITION  Ovis aries interleukin-12 p40 subunit precursor (IL-12) mRNA,
            partial cds.
ACCESSION   DQ152965
VERSION     DQ152965.1  GI:77744673
KEYWORDS    .
SOURCE      Ovis aries (sheep)
  ORGANISM  Ovis aries
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Caprinae; Ovis.
REFERENCE   1  (bases 1 to 224)
  AUTHORS   Ingham,A.B., Menzies,M.L. and Kijas,J.W.
  TITLE     Sequence diversity and rates of molecular evolution between sheep
            and cattle genes
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 224)
  AUTHORS   Ingham,A.B., Menzies,M.L. and Kijas,J.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-2005) Livestock Industries, CSIRO, QBP 306
            Carmody Rd, St Lucia, Queensland 4067, Australia
FEATURES             Location/Qualifiers
     source          1. .224
                     /organism="Ovis aries"
                     /mol_type="mRNA"
                     /db_xref="taxon:9940"
     gene            <1. .>224
                     /gene="IL-12"
     CDS             <1. .>224
                     /gene="IL-12"
                     /codon_start=2
                     /product="interleukin-12 p40 subunit precursor"
                     /protein_id="ABB02298.1"
                     /db_xref="GI:77744674"
                     /translation="IEVVMEAVHKLKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQ
                     VEVSWEYPDTWSTPHSYFSLTFCVQVQGKN"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 14;  Length 224;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db         41 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 84


RESULT 59
CEU10160
LOCUS       CEU10160                 525 bp    mRNA    linear   MAM 09-JUL-1994
DEFINITION  Cervus elaphus interleukin 12 mRNA, partial cds.
ACCESSION   U10160
VERSION     U10160.1  GI:508867
KEYWORDS    .
SOURCE      Cervus elaphus (red deer)
  ORGANISM  Cervus elaphus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Cervidae; Cervinae; Cervus.
REFERENCE   1  (bases 1 to 525)
  AUTHORS   Lockhart,E.A.
  TITLE     Cloning and sequencing of cervine IL-12
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 525)
  AUTHORS   Lockhart,E.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-MAY-1994) Euan A. Lockhart, Microbiology, Deer
            Research Laboratory, University of Otago, Union St., Dunedin, New
            Zealand
FEATURES             Location/Qualifiers
     source          1. .525
                     /organism="Cervus elaphus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9860"
     CDS             <1. .>525
                     /standard_name="IL-12"
                     /codon_start=2
                     /product="interleukin 12"
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                     /protein_id="AAA19658.1"
                     /db_xref="GI:508868"
                     /translation="AGQYTCHKGGEVLSRSLLLLHKKEDGIWSTDILKDQKEPKAKSF
                     LKCEAKDYSGHFTCWWLTAISTDLKFSVKSSRGSSDPRGVTCGAMSLSTEKVIVDHRE
                     YKKYTVECQEGSACPAAEESLPIEVVVEAVHKLKYENYTSSFFIRDIIKPDPPKNLQL
                     RPLKNSRQVEVSWE"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 14;  Length 525;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        413 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 456


RESULT 60
BD021808
LOCUS       BD021808                906 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Natural killer stimulatory factor.
ACCESSION   BD021808
VERSION     BD021808.1  GI:22563031
KEYWORDS    JP 2001245678-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 906)
  AUTHORS   Trinchieri,G., Perussia,B., Kobayashi,M., Clark,S.C., Wong,G.G. and
            Hewick,R.M.
  TITLE     Natural killer stimulatory factor
  JOURNAL   Patent: JP 2001245678-A 1 11-SEP-2001;
            GENETICS INSTITUTE INC,THE WISTAR INSTITUTE
COMMENT     OS   Unidentified
            PN   JP 2001245678-A/1
            PD   11-SEP-2001
            PF   10-JAN-2001 JP 2001002839
            PR   10-NOV-1988 US       269945,07-FEB-1989 US       307817 PI
            GIORGIO TRINCHIERI,BICE PERUSSIA,MICHIKO KOBAYASHI,STEVEN C  PI
            CLARK,
            PI   GORDON G WONG,RODNEY M HEWICK
            PC   C12N15/09,A61K38/00,A61K39/395,A61P35/00,A61P35/02,A61P37/04,
            PC   A61P43/00,
            PC   C07K16/24,G01N33/53//C07K14/52,C12N15/00,A61K37/02 CC
            Natural killer stimulatory factor
            FH   Key             Location/Qualifiers
            FT   source          1. .906
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .906
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 2;  Length 906;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        693 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 736


RESULT 61
BD021809
LOCUS       BD021809                906 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Natural killer stimulatory factor.
ACCESSION   BD021809
VERSION     BD021809.1  GI:22563032
KEYWORDS    JP 2001245678-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 906)
  AUTHORS   Trinchieri,G., Perussia,B., Kobayashi,M., Clark,S.C., Wong,G.G. and
            Hewick,R.M.
  TITLE     Natural killer stimulatory factor
  JOURNAL   Patent: JP 2001245678-A 2 11-SEP-2001;
            GENETICS INSTITUTE INC,THE WISTAR INSTITUTE
COMMENT     OS   Unidentified
            PN   JP 2001245678-A/2
            PD   11-SEP-2001
            PF   10-JAN-2001 JP 2001002839
            PR   10-NOV-1988 US       269945,07-FEB-1989 US       307817 PI
            GIORGIO TRINCHIERI,BICE PERUSSIA,MICHIKO KOBAYASHI,STEVEN C  PI
            CLARK,
            PI   GORDON G WONG,RODNEY M HEWICK
            PC   C12N15/09,A61K38/00,A61K39/395,A61P35/00,A61P35/02,A61P37/04,
            PC   A61P43/00,
            PC   C07K16/24,G01N33/53//C07K14/52,C12N15/00,A61K37/02 CC
            Natural killer stimulatory factor
            FH   Key             Location/Qualifiers
            FT   source          1. .906
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .906
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 2;  Length 906;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        693 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 736


RESULT 62
AX154601
LOCUS       AX154601                969 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 5 from Patent WO0140257.
ACCESSION   AX154601
VERSION     AX154601.1  GI:14536184
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 5 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .969
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 2;  Length 969;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        649 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 692


RESULT 63
AF004024
LOCUS       AF004024                984 bp    mRNA    linear   MAM 14-NOV-2000
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DEFINITION  Ovis aries interleukin-12 p40 subunit precursor, mRNA, complete
            cds.
ACCESSION   AF004024
VERSION     AF004024.2  GI:5870870
KEYWORDS    .
SOURCE      Ovis aries (sheep)
  ORGANISM  Ovis aries
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Caprinae; Ovis.
REFERENCE   1  (bases 1 to 984)
  AUTHORS   Swinburne,S.J., Russ,G.R. and Krishnan,R.
  TITLE     Ovine interleukin 12 has biological activity on ovine and human
            activated peripheral blood mononuclear cells
  JOURNAL   Cytokine 12 (10), 1546-1552 (2000)
   PUBMED   11023671
REFERENCE   2  (bases 1 to 984)
  AUTHORS   Swinburne,S.J., Russ,G.R. and Krishnan,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-MAY-1997) Transplantation Immunology Laboratory,
            Queen Elizabeth Hospital, 28 Woodville Road, Adelaide, South
            Australia 5011, Australia
REFERENCE   3  (bases 1 to 984)
  AUTHORS   Swinburne,S.J., Russ,G.R. and Krishnan,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-SEP-1999) Transplantation Immunology Laboratory, The
            Queen Elizabeth Hospital, 28 Woodville Rd., Adelaide, South
            Australia, Australia
  REMARK    Sequence update by submitter
COMMENT     On Sep 13, 1999 this sequence version replaced gi:2199555.
FEATURES             Location/Qualifiers
     source          1. .984
                     /organism="Ovis aries"
                     /mol_type="mRNA"
                     /db_xref="taxon:9940"
                     /cell_type="peripheral blood mononuclear"
     CDS             1. .984
                     /function="cytokine"
                     /note="IL-12"
                     /codon_start=1
                     /product="interleukin-12 p40 subunit precursor"
                     /protein_id="AAB61368.2"
                     /db_xref="GI:5870871"
                     /translation="MHPQQLVVSWFSLVLLASPIVAIWELEKNVYVVELDWYPNAPGE
                     TVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSRSLL
                     LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCSWLTAISTNLKFSVKSSR
                     GSSDPRGVTCGAASLSAEKVSMDHREYNKYTVECQEGSACPAAEESLPIEVVMEAVHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                     QVQGKNKREKKLFTDQTSAKVTCHKDANIRVQARDRYYSSFWSEWASVSCS"
     sig_peptide     1. .66
     mat_peptide     67. .981
                     /product="interleukin-12 p40 subunit"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 14;  Length 984;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707


RESULT 64
AF209435
LOCUS       AF209435                984 bp    mRNA    linear   MAM 03-FEB-2000
DEFINITION  Ovis aries interleukin 12 p40 subunit precursor (IL-12 p40) mRNA,
            complete cds.
ACCESSION   AF209435
VERSION     AF209435.1  GI:6636341
KEYWORDS    .
SOURCE      Ovis aries (sheep)
  ORGANISM  Ovis aries
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Caprinae; Ovis.
REFERENCE   1  (bases 1 to 984)
  AUTHORS   De Rose,R., Scheerlinck,J.-P.Y., Casey,G., Wood,P.R., Tennent,J.M.
            and Chaplin,P.J.
  TITLE     Ovine Interleukin 12: Analysis of biological function and species
            comparison
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 984)
  AUTHORS   De Rose,R., Scheerlinck,J.-P.Y., Casey,G., Wood,P.R., Tennent,J.M.
            and Chaplin,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-NOV-1999) Animal Health, CSIRO, Park Drive and
            Flemington Road, Parkville, Victoria 3052, Australia
FEATURES             Location/Qualifiers
     source          1. .984
                     /organism="Ovis aries"
                     /mol_type="mRNA"
                     /strain="Merino"
                     /db_xref="taxon:9940"
                     /cell_type="mononuclear"
                     /tissue_type="peripheral blood"
     gene            1. .984
                     /gene="IL-12 p40"
     CDS             1. .984
                     /gene="IL-12 p40"
                     /note="cytokine; contains 10 cysteine residues"
                     /codon_start=1
                     /product="interleukin 12 p40 subunit precursor"
                     /protein_id="AAF20151.1"
                     /db_xref="GI:6636342"
                     /translation="MHPQQLVVSWFSLVLLASPIVAIWELEKNVYVVELDWYPNAPGE
                     TVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSRSLL
                     LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCSWLTAISTNLKFSVKSSR
                     GSSDPRGVTCGAASLSAEKVSMDHREYNKYTVECQEGSACPAAEESLPIEVVMEAVHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                     QVQGKNKREKKLFADQTSAKVTCHKDANIRVQARDRYYSSFWSEWASVSCS"
     sig_peptide     1. .66
                     /gene="IL-12 p40"
     mat_peptide     67. .981
                     /gene="IL-12 p40"
                     /product="interleukin 12 p40 subunit"
     misc_feature    667. .669
                     /gene="IL-12 p40"
                     /note="putative N-linked site; glycosylation site"
     misc_feature    793. .795
                     /gene="IL-12 p40"
                     /note="putative O-linked site; glycosylation site"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 14;  Length 984;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707


RESULT 65
AR008950
LOCUS       AR008950                987 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 1 from patent US 5756085.
ACCESSION   AR008950
VERSION     AR008950.1  GI:3967755
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Sykes,M. and Wolf,S.F.
  TITLE     Use of interleukin-12 to prevent graft versus host disease
```

```
  JOURNAL   Patent: US 5756085-A 1 26-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 66
BD007070
LOCUS       BD007070                 987 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  IL-12 gene expression and delivery systems and uses.
ACCESSION   BD007070
VERSION     BD007070.1  GI:18635441
KEYWORDS    JP 2001503257-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Nodosutoromu,J., Freemark,B. and Dishupande,D.
  TITLE     IL-12 gene expression and delivery systems and uses
  JOURNAL   Patent: JP 2001503257-A 1 13-MAR-2001;
            BARENTISU INC,SYNTEX INC
COMMENT     OS   Unidentified
            PN   JP 2001503257-A/1
            PD   13-MAR-2001
            PF   10-OCT-1997 JP 1998519514
            PR   18-OCT-1996 US    60/028676
            PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
            C12N15/09,A61K31/711,A61K38/00,A61K47/18,A61K47/28,A61K48/00, PC
            A61P11/06,
            PC   C12N15/00,A61K37/02
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .987
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 67
BD007076
LOCUS       BD007076                 987 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Gene expression and delivery systems and uses.
ACCESSION   BD007076
VERSION     BD007076.1  GI:18635447
KEYWORDS    JP 2001503258-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Nodosutoromu,J., Freemark,B. and Dishupande,D.
  TITLE     Gene expression and delivery systems and uses
  JOURNAL   Patent: JP 2001503258-A 1 13-MAR-2001;
            BARENTISU INC
COMMENT     OS   Unidentified
            PN   JP 2001503258-A/1
            PD   13-MAR-2001
            PF   10-OCT-1997 JP 1998519520
            PR   18-OCT-1996 US    60/028687
            PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
            C12N15/09,A61K48/00,A61P11/06,A61P35/00,A61P43/00//C07K14/54, PC
            C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .987
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .987
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 68
BD105974
LOCUS       BD105974                 987 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Animal model for evaluation of vaccines.
ACCESSION   BD105974
VERSION     BD105974.1  GI:23200792
KEYWORDS    JP 2002501375-A/24.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Chang,L.J.
  TITLE     Animal model for evaluation of vaccines
  JOURNAL   Patent: JP 2002501375-A 24 15-JAN-2002;
            LUNG JI CHANG
COMMENT     PN   JP 2002501375-A/24
            PD   15-JAN-2002
            PF   09-APR-1998 JP 1998543062
            PR   09-APR-1997 US    08/838702,01-MAY-1997 US    08/848760 PR
            09-DEC-1997 US    60/069163
            PI   LUNG JI CHANG
            PC   A01K67/027,C12N7/01,C12N1/10,C07K14/16,A61K39/008,C12N1/36, PC
              C12N7/04,
            PC   A61K39/21
            CC   Strandedness: Double;
            CC   Topology: Linear;
            CC   /desc = 'DNA'
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
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```
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 69
BD136034
LOCUS       BD136034                 987 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Interferon alpha plasmid and delivery system and method of
            preparing and using the same.
ACCESSION   BD136034
VERSION     BD136034.1  GI:23230979
KEYWORDS    JP 2002506647-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.
  TITLE     Interferon alpha plasmid and delivery system and method of
            preparing and using the same
  JOURNAL   Patent: JP 2002506647-A 1 05-MAR-2002;
            VALENTIS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002506647-A/1
            PD   05-MAR-2002
            PF   12-MAR-1999 JP 2000536861
            PR   19-MAR-1998 US    60/078654
            PI   JEFF NORDSTROM,FEDERICA PERICLE,ALAIN ROLLAND,ROBERT RALSTON
            PC   C12N15/09,A61K38/21,A61K48/00,A61P35/00,C07K14/54,C07K14/56,
            PC   C12N1/15,
            PC   C12N1/19,C12N1/21,C12N5/10//A61K9/127,C12N15/00,A61K37/66, PC
             C12N5/00
            CC   Interferon alpha plasmid and delivery system and method of  CC
                 preparing and
            CC   using the same
            FH   Key             Location/Qualifiers
            FT   source          1. .987
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 70
CQ803342
LOCUS       CQ803342                 987 bp    DNA     linear   PAT 10-MAY-2004
DEFINITION  Sequence 2 from Patent WO2004035799.
ACCESSION   CQ803342
VERSION     CQ803342.1  GI:47110208
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Waehler,R. and Schnieders,F.
  TITLE     Viral vectors and the use of the same for gene therapy
  JOURNAL   Patent: WO 2004035799-A 2 29-APR-2004;
            Universitaetsklinikum Hamburg-Eppendorf (DE)
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 71
CS131491
LOCUS       CS131491                 987 bp    DNA     linear   PAT 02-AUG-2005
DEFINITION  Sequence 10 from Patent WO2005066348.
ACCESSION   CS131491
VERSION     CS131491.1  GI:71794159
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Gillies,S.
  TITLE     Compounds for targeting
  JOURNAL   Patent: WO 2005066348-A 10 21-JUL-2005;
            Antisoma PLC (GB); EMD Lexigen Research Center Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HuIL12 p40 subunit"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 72
I28591
LOCUS       I28591                   987 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 1 from patent US 5573764.
ACCESSION   I28591
VERSION     I28591.1  GI:1819367
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Sykes,M. and Wolf,S.F.
  TITLE     Use of interleukin-12 to prevent graft versus host disease
  JOURNAL   Patent: US 5573764-A 1 12-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704
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RESULT 73
AR533404
LOCUS       AR533404                 987 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 24 from patent US 6730512.
ACCESSION   AR533404
VERSION     AR533404.1  GI:53923070
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Chang,L.-J.
  TITLE     Combination immunogene therapy
  JOURNAL   Patent: US 6730512-A 24 04-MAY-2004;
            Amdl, Inc.; Tustin, CA
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 74
AX154633
LOCUS       AX154633                 987 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 37 from Patent WO0140257.
ACCESSION   AX154633
VERSION     AX154633.1  GI:14536197
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 37 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 75
AY603406
LOCUS       AY603406                 993 bp    mRNA    linear   MAM 18-JUL-2004
DEFINITION  Capra hircus interleukin 12 p40 subunit precursor, mRNA, complete
            cds.
ACCESSION   AY603406
VERSION     AY603406.1  GI:50261479
KEYWORDS    .
SOURCE      Capra hircus (goat)
  ORGANISM  Capra hircus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Caprinae; Capra.
REFERENCE   1  (bases 1 to 993)
  AUTHORS   Rasool,T.J., Hosamani,M., Shebannavar,S., Sreekumar,E. and
            Singh,R.K.
  TITLE     cloning and sequencing of goat cytokines
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 993)
  AUTHORS   Rasool,T.J., Hosamani,M., Shebannavar,S., Sreekumar,E. and
            Singh,R.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-APR-2004) Division of Virology, Indian Veterinary
            Research Institute, Mukteswar, Nainital, Uttaranchal 263138, India
FEATURES             Location/Qualifiers
     source          1. .993
                     /organism="Capra hircus"
                     /mol_type="mRNA"
                     /isolation_source="peripheral blood mononuclear cells
                     stimulated with Concanavalin A"
                     /db_xref="taxon:9925"
                     /note="breed: Pashmina"
     CDS             1. .984
                     /note="cytokine"
                     /codon_start=1
                     /product="interleukin 12 p40 subunit precursor"
                     /protein_id="AAT72316.1"
                     /db_xref="GI:50261480"
                     /translation="MHPQQLVVSWFSLVLLASPIVAIWELEKNVYVVELDWYPNAPGE
                     TVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSRSLL
                     LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCSWLTAISTNLKFSVKSSR
                     GSSDPRGVTCGAASLSAEKVSMDHREYNKYTVECQEGSACPAAEESLPIEVVMEAVHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                     QVQGKNKREKKLFTDQTSAKVTCHKDANIRVQARDRYYSSFWSEWASVSCS"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 14;  Length 993;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707


RESULT 76
CEU57752
LOCUS       CEU57752                 993 bp    mRNA    linear   MAM 28-OCT-1999
DEFINITION  Cervus elaphus interleukin-12 p40 subunit mRNA, complete cds.
ACCESSION   U57752
VERSION     U57752.1  GI:1373387
KEYWORDS    .
SOURCE      Cervus elaphus (red deer)
  ORGANISM  Cervus elaphus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Cervidae; Cervinae; Cervus.
REFERENCE   1  (bases 1 to 993)
  AUTHORS   Lockhart,E., Slobbe,L. and Buchan,G.
  TITLE     The characterisation of a cervine immunoregulatory cytokine,
            interleukin 12
  JOURNAL   DNA Seq. 10 (2), 139-148 (1999)
   PUBMED   10376218
REFERENCE   2  (bases 1 to 993)
  AUTHORS   Lockhart,E.A. and Buchan,G.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-MAY-1996) Euan A. Lockhart, Microbiology, University
            of Otago, Cumberland St, Dunedin, New Zealand
FEATURES             Location/Qualifiers
     source          1. .993
                     /organism="Cervus elaphus"
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                     /mol_type="mRNA"
                     /db_xref="taxon:9860"
                     /cell_type="peripheral blood mononuclear cells"
     CDS             1. .984
                     /codon_start=1
                     /product="interleukin-12 p40 subunit"
                     /protein_id="AAB02258.1"
                     /db_xref="GI:1373388"
                     /translation="MHPQQLVVSWFSLVLLTSPIVAIWELEKNVYVVELDWYPDAPGE
                     TVVLRCDTPEEDGITWTSDQSSEVLGSGKTLTVQVKEFGDAGQYTCHKGGEVLSRSLL
                     LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCWWLTAISTDLKFSVKSSR
                     GSSDPRGVTCGAASLSTEKVIVDHREYKKYTVECQEGSACPAAEESLPIEVVVEAVHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                     QVQGKNKREKKLFMDQTSAKVTCHKDASIRVQARDRYYNSFWSEWASVSCS"
     primer_bind     1. .33
     primer_bind     complement(961. .993)
ORIGIN

  Query Match             4.5%;  Score 44;  DB 14;  Length 993;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707


RESULT 77
AY234218
LOCUS       AY234218               1005 bp    mRNA    linear   PRI 07-APR-2003
DEFINITION  Papio anubis interleukin-12 alpha p40 subunit precursor (IL12a)
            mRNA, complete cds.
ACCESSION   AY234218
VERSION     AY234218.1  GI:29569754
KEYWORDS    .
SOURCE      Papio anubis (olive baboon)
  ORGANISM  Papio anubis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Papio.
REFERENCE   1  (bases 1 to 1005)
  AUTHORS   Villinger,F.
  TITLE     Nonhuman primate cytokines
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1005)
  AUTHORS   Villinger,F.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-FEB-2003) Pathology & Laboratory Medicine, Emory
            University School of Medicine, Woodruff Memorial Building Rm 2339,
            1639 Pierce Drive, Atlanta, GA 30322, USA
FEATURES             Location/Qualifiers
     source          1. .1005
                     /organism="Papio anubis"
                     /mol_type="mRNA"
                     /db_xref="taxon:9555"
     gene            1. .1005
                     /gene="IL12a"
     CDS             9. .995
                     /gene="IL12a"
                     /codon_start=1
                     /product="interleukin-12 alpha p40 subunit precursor"
                     /protein_id="AAO85331.1"
                     /db_xref="GI:29569755"
                     /translation="MCHQQLVISWFSLVFLASPLMAIWELKKDVYVVELDWYPDAPGE
                     MVVLTCDTPEEDGITWTLDQSGEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSHSLL
                     LLHKKEDGIWSTDVLKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                     GSSNPQGVTCGAVTLSAERVRGDNKEYEYSVECQEDSACPAAEERLPIEVMVDAIHKL
                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQAEVSWEYPDTWSTPHSYFSLTFCIQ
                     VQGKSKREKKDRIFTDKTSATVICRKNASFSVQAQDRYYSSSWSEWASVPCS"
     sig_peptide     9. .74
                     /gene="IL12a"
     mat_peptide     75. .992
                     /gene="IL12a"
                     /product="interleukin-12 alpha p40 subunit"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 5;  Length 1005;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        669 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 712


RESULT 78
CTU19834
LOCUS       CTU19834               1005 bp    mRNA    linear   PRI 03-FEB-1996
DEFINITION  Cercocebus torquatus interleukin-12 alpha p40 subunit (IL-12a)
            mRNA, complete cds.
ACCESSION   U19834
VERSION     U19834.1  GI:644785
KEYWORDS    .
SOURCE      Cercocebus torquatus (red-crowned mangabey)
  ORGANISM  Cercocebus torquatus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Cercocebus.
REFERENCE   1  (bases 1 to 1005)
  AUTHORS   Villinger,F., Brar,S.S., Mayne,A., Chikkala,N. and Ansari,A.A.
  TITLE     Comparative sequence analysis of cytokine genes from human and
            nonhuman primates
  JOURNAL   J. Immunol. 155 (8), 3946-3954 (1995)
   PUBMED   7561102
REFERENCE   2  (bases 1 to 1005)
  AUTHORS   Villinger,F.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JAN-1995) Francois J. Villinger, Emory University,
            Pathology, 1327 Clifton Rd, Atlanta, GA 30322, USA
FEATURES             Location/Qualifiers
     source          1. .1005
                     /organism="Cercocebus torquatus"
                     /mol_type="mRNA"
                     /sub_species="atys"
                     /db_xref="taxon:9530"
                     /clone="FPn IL-12a"
                     /cell_type="peripheral blood mononuclear cells"
                     /tissue_type="blood"
     gene            1. .1005
                     /gene="IL-12a"
     CDS             9. .995
                     /gene="IL-12a"
                     /function="NK cell stimulatory factor"
                     /codon_start=1
                     /product="interleukin-12 alpha p40 subunit"
                     /protein_id="AAA86701.1"
                     /db_xref="GI:644786"
                     /translation="MCHQQLVISWFSLVFLASPLMAIWELKKDVYVVELDWYPDAPGE
                     MVVLTCDTPEEDGITWTLDQSGEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSHSLL
                     LPHKKEDGIWSTDILKDQKEPKNETFLRCEAKNYSGRITCWWLSTISTDLTFSIISSR
                     GSSNPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEERLPIEVMVDAIHKL
                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCIQ
                     VQGKSKREKKDRIFTDKTSATVICRKNASFSVQAQDRYYSSSWNEWTSVPCS"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 5;  Length 1005;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        669 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 712


RESULT 79
AF180563
```

```
LOCUS       AF180563               1007 bp    mRNA    linear   PRI 26-SEP-1999
DEFINITION  Homo sapiens interleukin 12, P40 mRNA, complete cds.
ACCESSION   AF180563
VERSION     AF180563.1  GI:5923854
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1007)
  AUTHORS   Hongyuan,J. and Meiyun,Z.
  TITLE     Cloning and sequence analysis of IL-12 cDNA from Chinese
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1007)
  AUTHORS   Hongyuan,J. and Meiyun,Z.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-AUG-1999) Hepatitis, Institute of Virology, CAPM, 100
            Yingxinjie, Xuanwuqu, Beijing 100052, China
FEATURES             Location/Qualifiers
     source          1. .1007
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_type="peripheral mononuclear"
     CDS             7. .993
                     /note="NKSF/CLMF; IL12p40; 40kD"
                     /codon_start=1
                     /product="interleukin 12, P40"
                     /protein_id="AAD56386.1"
                     /db_xref="GI:5923855"
                     /translation="MCHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGE
                     MVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLL
                     LLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                     GSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKL
                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
                     VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 5;  Length 1007;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db        667 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 710


RESULT 80
AB246273
LOCUS       AB246273               1008 bp    mRNA    linear   MAM 13-JAN-2006
DEFINITION  Bubalus carabanensis IL-12p40 mRNA for interleukin-12p40, complete
            cds.
ACCESSION   AB246273
VERSION     AB246273.1  GI:84871695
KEYWORDS    .
SOURCE      Bubalus carabanensis
  ORGANISM  Bubalus carabanensis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bubalus.
REFERENCE   1
  AUTHORS   Mingala,C.N., Raadan,O., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Comparative assessment of Th1 and Th2 cytokines of swamp type
            buffalo and other bubaline breeds by molecular cloning, sequencing
            and phylogenetics
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1008)
  AUTHORS   Mingala,C.N., Odbileg,R., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JAN-2006) Claro N Mingala, Graduate School of
            Veterinary Medicine, Hokkaido University, Department of Disease
            Control, Laboratory of Infectious Diseases; Kita-ku Kita 18 Nishi
            9, Sapporo, Hokkaido 060-0818, Japan (E-mail:cnmingala@hotmail.com,
            Tel:81-11-706-5216, Fax:81-11-706-5217)
FEATURES             Location/Qualifiers
     source          1. .1008
                     /organism="Bubalus carabanensis"
                     /mol_type="mRNA"
                     /db_xref="taxon:346063"
                     /sex="female"
                     /cell_type="PBMC"
     gene            1. .1008
                     /gene="IL-12p40"
     CDS             1. .984
                     /gene="IL-12p40"
                     /codon_start=1
                     /product="interleukin-12p40"
                     /protein_id="BAE75850.1"
                     /db_xref="GI:84871696"
                     /translation="MHPQQLVVSWFSLVLLASPIVAIWELEKNVYIVELDWYPDAPGE
                     TVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSRSLL
                     LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCWWLTAISTDLKFSVKSSR
                     GSSDPRGVTCGAASLSAEKVSVDHREYNKYTVECQEGSTCPAAEESLLIEVVVEAVHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                     QVQGKNKREKKLFMDQTSAKVTCHKDANVRVQARDRYYSSFWSEWASVSCS"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 14;  Length 1008;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707


RESULT 81
AB246353
LOCUS       AB246353               1008 bp    mRNA    linear   MAM 13-JAN-2006
DEFINITION  Bubalus bubalis IL-12p40 mRNA for interleukin-12p40, complete cds.
ACCESSION   AB246353
VERSION     AB246353.1  GI:84871717
KEYWORDS    .
SOURCE      Bubalus bubalis (water buffalo)
  ORGANISM  Bubalus bubalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bubalus.
REFERENCE   1
  AUTHORS   Mingala,C.N., Raadan,O., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Comparative assessment of Th1 and Th2 cytokines of swamp type
            buffalo and other bubaline breeds by molecular cloning, sequencing
            and phylogenetics
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1008)
  AUTHORS   Mingala,C.N., Odbileg,R., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2006) Claro N Mingala, Graduate School of
            Veterinary Medicine, Hokkaido University, Department of Disease
            Control, Laboratory of Infectious Diseases; Kita-ku Kita 18 Nishi
            9, Sapporo, Hokkaido 060-0818, Japan (E-mail:cnmingala@hotmail.com,
            Tel:81-11-706-5216, Fax:81-11-706-5217)
FEATURES             Location/Qualifiers
     source          1. .1008
                     /organism="Bubalus bubalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:89462"
                     /sex="female"
                     /cell_type="PBMC"
                     /note="Bulgarian Murrah buffalo - crossbreed between
                     Mediterranean and Indian buffalo both are Riverine type
                     water buffalo"
     gene            1. .1008
                     /gene="IL-12p40"
     CDS             1. .984
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                     /gene="IL-12p40"
                     /codon_start=1
                     /product="interleukin-12p40"
                     /protein_id="BAE75858.1"
                     /db_xref="GI:84871718"
                     /translation="MHPQQLVVSWFSLVLLASPIVAIWELEKNVYVVELDWYPDAPGE
                     TVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSRSLL
                     LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCWWLTAISTDLKFSVKSSR
                     GSSDPRGVTCEAASLSAEKVSVDHREYNKYTVECQEGSTCPAAEESLLIEVVVEAVHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                     QVQGKNKREKKLFMDQTSAKVTCHKDANVRVQARDRYYSSFWSEWASVSCS"
ORIGIN

  Query Match              4.5%;  Score 44;  DB 14;  Length 1008;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707


RESULT 82
AB246358
LOCUS       AB246358               1008 bp    mRNA    linear   MAM 14-JAN-2006
DEFINITION  Bubalus bubalis x Bubalus carabanensis IL-12p40 mRNA for
            interleukin-12p40, complete cds.
ACCESSION   AB246358
VERSION     AB246358.1  GI:84875356
KEYWORDS    .
SOURCE      Bubalus bubalis x Bubalus carabanensis
  ORGANISM  Bubalus bubalis x Bubalus carabanensis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bubalus.
REFERENCE   1
  AUTHORS   Mingala,C.N., Raadan,O., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Comparative assessment of Th1 and Th2 cytokines of swamp type
            buffalo and other bubaline breeds by molecular cloning, sequencing
            and phylogenetics
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1008)
  AUTHORS   Mingala,C.N., Odbileg,R., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2006) Claro N Mingala, Graduate School of
            Veterinary Medicine, Hokkaido University, Department of Disease
            Control, Laboratory of Infectious Diseases; Kita-ku Kita 18 Nishi
            9, Sapporo, Hokkaido 060-0818, Japan (E-mail:cnmingala@hotmail.com,
            Tel:81-11-706-5216, Fax:81-11-706-5217)
FEATURES             Location/Qualifiers
     source          1. .1008
                     /organism="Bubalus bubalis x Bubalus carabanensis"
                     /mol_type="mRNA"
                     /db_xref="taxon:365610"
                     /sex="female"
                     /cell_type="PBMC"
                     /note="Philippine carabao crossbreed (CB) - crossbreed
                     between Philippine carabao (Swamp type water buffalo) and
                     Indian Murrah buffalo (Riverine type water buffalo)"
     gene            1. .1008
                     /gene="IL-12p40"
     CDS             1. .984
                     /gene="IL-12p40"
                     /codon_start=1
                     /product="interleukin-12p40"
                     /protein_id="BAE75892.1"
                     /db_xref="GI:84875357"
                     /translation="MHPQQLVVSWFSLVLLASPIVAIWELEKNVYVVELDWYPDAPGE
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                     LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSEHFTGWWLTAISTNLKFSVKSSR
                     GSSDPRGVTCGAASLSAEKVSVDHREYNKYTVECQEGSTCPAAEESLLIEVVVEAVHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                     QVQGKNKREKKLFMDQTSAKVTCHKDANVRVQARDRYYSSFWSEWASVSCS"
ORIGIN

  Query Match              4.5%;  Score 44;  DB 14;  Length 1008;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707


RESULT 83
AF007576
LOCUS       AF007576               1012 bp    mRNA    linear   MAM 14-JUL-1997
DEFINITION  Capra hircus interleukin 12 p40 subunit (IL-12) mRNA, complete cds.
ACCESSION   AF007576
VERSION     AF007576.1  GI:2253433
KEYWORDS    .
SOURCE      Capra hircus (goat)
  ORGANISM  Capra hircus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Caprinae; Capra.
REFERENCE   1  (bases 1 to 1012)
  AUTHORS   Beyer,J.C., Cheevers,W.P. and Kumpula-McWhirter,N.M.
  TITLE     CLoning of caprine IL-12 40 kDa subunit
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1012)
  AUTHORS   Beyer,J.C., Cheevers,W.P. and Kumpula-McWhirter,N.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JUN-1997) Veterinary Microbiology and Pathology,
            Washington State University, P.O. Box 647040, Pullman, WA
            99164-7040, USA
FEATURES             Location/Qualifiers
     source          1. .1012
                     /organism="Capra hircus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9925"
                     /cell_type="LPS-stimulated microglial cell"
     gene            1. .1012
                     /gene="IL-12"
     CDS             1. .984
                     /gene="IL-12"
                     /codon_start=1
                     /product="interleukin 12 p40 subunit"
                     /protein_id="AAB62945.1"
                     /db_xref="GI:2253434"
                     /translation="MHPQQLVVSWFSLVLLASPIVAIWELEKNVYVVELDWYPNAPGE
                     TVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSRSLL
                     LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCSWLTAISTNLKFSVKSSR
                     GSSDPRGVTCGAASLSAEKVSMDHREYNKYTVECQEGSACPAAEESLPIEVVMEAVHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                     QVQGKNKREKKLFTDQTSAKVTCHKDANIRVQARDRYYSSFWSEWASVSCS"
ORIGIN

  Query Match              4.5%;  Score 44;  DB 14;  Length 1012;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707


RESULT 84
AY198121
LOCUS       AY198121               1012 bp    mRNA    linear   MAM 09-JUN-2005
DEFINITION  Bubalus bubalis interleukin 12 p40 subunit precursor, mRNA,
            complete cds.
ACCESSION   AY198121
VERSION     AY198121.1  GI:28192687
KEYWORDS    .
SOURCE      Bubalus bubalis (water buffalo)
```

```
  ORGANISM  Bubalus bubalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bubalus.
REFERENCE   1  (bases 1 to 1012)
  AUTHORS   Premraj,A., Sreekumar,E., Nautiyal,B. and Rasool,T.J.
  TITLE     Interleukin-12 subunits p35 and p40 of Indian water buffalo
            (Bubalus bubalis) maintain high sequence homology with those of
            other ruminants
  JOURNAL   Eur. J. Immunogenet. 32 (3), 179-186 (2005)
REFERENCE   2  (bases 1 to 1012)
  AUTHORS   Premraj,A., Sreekumar,E. and Rasool,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-DEC-2002) Animal Biotechnology, Rajiv Gandhi Center
            for Biotechnology, Jagathy, Thycaud PO, Trivandrum, Kerala 695014,
            India
FEATURES             Location/Qualifiers
     source          1. .1012
                     /organism="Bubalus bubalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:89462"
     CDS             1. .984
                     /note="cytokine; 40 kDa subunit"
                     /codon_start=1
                     /product="interleukin 12 p40 subunit precursor"
                     /protein_id="AAO25629.1"
                     /db_xref="GI:28192688"
                     /translation="MHPQQLVVSWFSLVLLASPIVAIWELEKNVYIVELDWYPDAPGE
                     TVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSRSLL
                     LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCWWLTAISTDLKFSVKSSR
                     GSADPRGVTCGAASLSAEKVSVDHREYNKYTVECQEGSTCPAAEESLLIEVVVEAVHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                     QVQGKNKREKKLFMDQTSAKVTCHKDANVRVQARDRYYSSFWSEWASVSCS"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 14;  Length 1012;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707


RESULT 85
BTU11815
LOCUS       BTU11815                1012 bp    mRNA    linear   MAM 27-JAN-1996
DEFINITION  Bos taurus interleukin 12 40 kDa subunit mRNA, complete cds.
ACCESSION   U11815
VERSION     U11815.1  GI:555795
KEYWORDS    .
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 1012)
  AUTHORS   Zarlenga,D.S., Canals,A., Aschenbrenner,R.A. and Gasbarre,L.C.
  TITLE     Enzymatic amplification and molecular cloning of cDNA encoding the
            small and large subunits of bovine interleukin 12
  JOURNAL   Biochim. Biophys. Acta 1270 (2-3), 215-217 (1995)
   PUBMED   7727547
REFERENCE   2  (bases 1 to 1012)
  AUTHORS   Zarlenga,D.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JUL-1994) Dante S. Zarlenga, U.S. Department of
            Agriculture, ARS, LPSI, PIL, Beltsville, MD 20705, USA
FEATURES             Location/Qualifiers
     source          1. .1012
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /strain="Holstein"
                     /db_xref="taxon:9913"
                     /clone="BIL12 40"
                     /sex="male"
                     /cell_type="lymphocytes and macrophages"
                     /tissue_type="lymphoid"
     CDS             1. .984
                     /codon_start=1
                     /product="interleukin 12 40 kDa subunit"
                     /protein_id="AAA85792.1"
                     /db_xref="GI:555796"
                     /translation="MHPQQLVVSWFSLVLLASPIVAMWELEKNVYVVELDWYPDAPGE
                     TVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSRSLL
                     LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCWWLTAISTDLKFSVKSSR
                     GSSDPRGVTCGAALLSAEKVSLEHREYNKYTVECQEGSACPAAEESLLIEVVVEAVHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                     QVQGKNKREKKLFMDQTSAKVTCHKDANVRVQARDRYYSSFWSEWASVSCS"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 14;  Length 1012;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707


RESULT 86
AR052857
LOCUS       AR052857                1018 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 194 from patent US 5833975.
ACCESSION   AR052857
VERSION     AR052857.1  GI:5977719
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1018)
  AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
  TITLE     Canarypox virus expressing cytokine and/or tumor-associated antigen
            DNA sequence
  JOURNAL   Patent: US 5833975-A 194 10-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .1018
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 2;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 87
AR288169
LOCUS       AR288169                1018 bp    mRNA    linear   PAT 12-JUN-2003
DEFINITION  Sequence 194 from patent US 6537594.
ACCESSION   AR288169
VERSION     AR288169.1  GI:31675448
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1018)
  AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
  TITLE     Vaccina virus comprising cytokine and/or tumor associated antigen
            genes
  JOURNAL   Patent: US 6537594-A 194 25-MAR-2003;
            Virogenetics Corporation; Troy, NY
FEATURES             Location/Qualifiers
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     source          1. .1018
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match              4.5%;  Score 44;  DB 2;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 88
AR567156
LOCUS       AR567156               1018 bp    mRNA    linear   PAT 08-OCT-2004
DEFINITION  Sequence 194 from patent US 6780407.
ACCESSION   AR567156
VERSION     AR567156.1  GI:53984798
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1018)
  AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
  TITLE     Pox virus comprising DNA sequences encoding CEA and B7 antigen
  JOURNAL   Patent: US 6780407-A 194 24-AUG-2004;
            Aventis Pasteur; Swiftwater, PA
FEATURES             Location/Qualifiers
     source          1. .1018
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match              4.5%;  Score 44;  DB 2;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 89
E35794
LOCUS       E35794                 1019 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Process for producing interleukin 12.
ACCESSION   E35794
VERSION     E35794.1  GI:18624618
KEYWORDS    JP 2000157274-A/6.
SOURCE      Bos sp.
  ORGANISM  Bos sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 1019)
  AUTHORS   Nakamura,M., Takehara,K. and Ohara,E.
  TITLE     Process for producing interleukin 12
  JOURNAL   Patent: JP 2000157274-A 6 13-JUN-2000;
            DAI ICHI SEIYAKU CO LTD
COMMENT     OS   Bos sp. (bovine)
            PN   JP 2000157274-A/6
            PD   13-JUN-2000
            PF   20-NOV-1998 JP 1998331052
            PR
            PI   MASAYUKI NAKAMURA,KAZUAKI TAKEHARA,EIJI OHARA PC
            C12N15/09,C07K14/54,C12N5/10,C12P21/02//(C12N15/09,C12R1:91), PC
            (C12N5/10,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00, PC
            (C12N15/00,C12R1:91),(C12N5/00,C12R1:91)
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            FH   Key             Location/Qualifiers
            FT   source          1. .1019
            FT                   /organism='Bos sp. (bovine)'.
FEATURES             Location/Qualifiers
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                     /organism="Bos sp."
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ORIGIN

  Query Match              4.5%;  Score 44;  DB 2;  Length 1019;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        675 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 718


RESULT 90
CQ829448
LOCUS       CQ829448               1029 bp    DNA     linear   PAT 05-JUL-2004
DEFINITION  Sequence 7 from Patent WO2004052929.
ACCESSION   CQ829448
VERSION     CQ829448.1  GI:49732784
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Vandenbroeck,K. and Alloza,I.
  TITLE     Recombinant cell line
  JOURNAL   Patent: WO 2004052929-A 7 24-JUN-2004;
            The Queen's University of Belfast (GB)
FEATURES             Location/Qualifiers
     source          1. .1029
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="cDNA for beta chain of IL-12"
ORIGIN

  Query Match              4.5%;  Score 44;  DB 2;  Length 1029;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db        676 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 719


RESULT 91
BC074723
LOCUS       BC074723               1046 bp    mRNA    linear   PRI 28-JUL-2005
DEFINITION  Homo sapiens interleukin 12B (natural killer cell stimulatory
            factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA
            (cDNA clone MGC:103792 IMAGE:30915173), complete cds.
ACCESSION   BC074723
VERSION     BC074723.2  GI:50960609
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1046)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
```

McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

CONSRTM Mammalian Gene Collection Program Team

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

PUBMED 12477932

REFERENCE 2 (bases 1 to 1046)

AUTHORS .

CONSRTM NIH MGC Project

TITLE Direct Submission

JOURNAL Submitted (25-JUN-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov

COMMENT On Aug 4, 2004 this sequence version replaced gi:49901500.
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Genome Sequence Centre, British Columbia Cancer Center
cDNA Library Preparation: British Columbia Cancer Research Center
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Martin Hirst, Thomas Zeng, Ryan Morin, Michelle Moksa, Johnson Pang, Diana Mah, Jing Wang, Kieth Fichter, Eric Chuah, Allen Delaney, Rob Kirkpatrick, Agnes Baross, Sarah Barber, Mabel Brown-John, Steve S. Chand, William Chow, Ryan Babakaiff, Dave Wong, Corey Matsuo, Jaclyn Beland, Susan Gibson, Luis delRio, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Mike R. Mayo, Josh Moran, Diana Palmquist, JR Santos, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui,Steven Jones, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRBU Plate: 1 Row: A Column: 6.

FEATURES Location/Qualifiers

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/db_xref="taxon:9606"
/clone="MGC:103792 IMAGE:30915173"
/tissue_type="Brain, PCR rescued clones"
/clone_lib="NIH_MGC_272"
/lab_host="DH10B"
/note="Vector: pCR4 Topo TA with reversed insert"

gene 1. .1046
/gene="IL12B"
/note="synonyms: CLMF2, IL-12B, NKSF, CLMF"
/db_xref="GeneID:3593"
/db_xref="MIM:161561"

CDS 32. .1018
/gene="IL12B"
/codon_start=1
/product="interleukin 12B, precursor"
/protein_id="AAH74723.1"
/db_xref="GI:50960610"
/db_xref="GeneID:3593"
/db_xref="MIM:161561"
/translation="MCHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGE
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LLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
GSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKL
KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"

ORIGIN

Query Match 4.5%; Score 44; DB 5; Length 1046;
Best Local Similarity 100.0%; Pred. No. 2.6e-12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db 692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735

RESULT 92
BC067498
LOCUS BC067498 1073 bp mRNA linear PRI 28-JUL-2005
DEFINITION Homo sapiens interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA (cDNA clone MGC:79355 IMAGE:6971868), complete cds.
ACCESSION BC067498
VERSION BC067498.1 GI:45768642
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1073)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
CONSRTM Mammalian Gene Collection Program Team
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REFERENCE 2 (bases 1 to 1073)
AUTHORS .
CONSRTM NIH MGC Project
TITLE Direct Submission
JOURNAL Submitted (19-MAR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 172 Row: d Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 24497437.

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FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_195"
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                     /note="Vector: pDNR-Dual"
     gene            1. .1073
                     /gene="IL12B"
                     /note="synonyms: CLMF2, IL-12B, NKSF, CLMF"
                     /db_xref="GeneID:3593"
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     CDS             5. .991
                     /gene="IL12B"
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                     /translation="MCHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGE
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                     GSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKL
                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
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ORIGIN

  Query Match             4.5%;  Score 44;  DB 5;  Length 1073;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
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RESULT 93
BC067499
LOCUS       BC067499               1073 bp    mRNA    linear   PRI 28-JUL-2005
DEFINITION  Homo sapiens interleukin 12B (natural killer cell stimulatory
            factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA
            (cDNA clone MGC:79356 IMAGE:6971869), complete cds.
ACCESSION   BC067499
VERSION     BC067499.1  GI:45768645
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1073)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
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            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1073)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 172 Row: d Column: 12
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 24497437.
FEATURES             Location/Qualifiers
     source          1. .1073
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:79356 IMAGE:6971869"
                     /tissue_type="PCR rescued clones"
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                     /lab_host="DH10B"
                     /note="Vector: pDNR-Dual"
     gene            1. .1073
                     /gene="IL12B"
                     /note="synonyms: CLMF2, IL-12B, NKSF, CLMF"
                     /db_xref="GeneID:3593"
                     /db_xref="MIM:161561"
     CDS             5. .991
                     /gene="IL12B"
                     /codon_start=1
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                     /translation="MCHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGE
                     MVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLL
                     LLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                     GSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKL
                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
                     VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 5;  Length 1073;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        665 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 708


RESULT 94
BC067500
LOCUS       BC067500               1073 bp    mRNA    linear   PRI 28-JUL-2005
DEFINITION  Homo sapiens interleukin 12B (natural killer cell stimulatory
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            factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA
            (cDNA clone MGC:79358 IMAGE:6971872), complete cds.
ACCESSION   BC067500
VERSION     BC067500.1  GI:45768649
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1073)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1073)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 172 Row: d Column: 21
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 24497437.
FEATURES             Location/Qualifiers
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                     /lab_host="DH10B"
                     /note="Vector: pDNR-Dual"
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                     /note="synonyms: CLMF2, IL-12B, NKSF, CLMF"
                     /db_xref="GeneID:3593"
                     /db_xref="MIM:161561"
     CDS             5. .991
                     /gene="IL12B"
                     /codon_start=1
                     /product="interleukin 12B, precursor"
                     /protein_id="AAH67500.1"
                     /db_xref="GI:45768650"
                     /db_xref="GeneID:3593"
                     /db_xref="MIM:161561"
                     /translation="MCHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGE
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                     LLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                     GSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKL
                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
                     VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 5;  Length 1073;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||
Db        665 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 708


RESULT 95
BC067501
LOCUS       BC067501                1073 bp    mRNA    linear   PRI 28-JUL-2005
DEFINITION  Homo sapiens interleukin 12B (natural killer cell stimulatory
            factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA
            (cDNA clone MGC:79359 IMAGE:6971873), complete cds.
ACCESSION   BC067501
VERSION     BC067501.1  GI:45767736
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1073)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1073)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
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            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 172 Row: d Column: 22
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 24497437.
FEATURES              Location/Qualifiers
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                      /tissue_type="PCR rescued clones"
                      /clone_lib="NIH_MGC_195"
                      /lab_host="DH10B"
                      /note="Vector: pDNR-Dual"
     gene             1. .1073
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                      /note="synonyms: CLMF2, IL-12B, NKSF, CLMF"
                      /db_xref="GeneID:3593"
                      /db_xref="MIM:161561"
     CDS              5. .991
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                      GSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKL
                      KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
                      VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 5;  Length 1073;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db        665 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 708


RESULT 96
BC067502
LOCUS       BC067502                1073 bp    mRNA    linear   PRI 28-JUL-2005
DEFINITION  Homo sapiens interleukin 12B (natural killer cell stimulatory
            factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA
            (cDNA clone MGC:79360 IMAGE:6971874), complete cds.
ACCESSION   BC067502
VERSION     BC067502.1  GI:45768652
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1073)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
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            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1073)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 172 Row: d Column: 23
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 24497437.
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                      /lab_host="DH10B"
                      /note="Vector: pDNR-Dual"
     gene             1. .1073
                      /gene="IL12B"
                      /note="synonyms: CLMF2, IL-12B, NKSF, CLMF"
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                      /db_xref="MIM:161561"
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  Query Match             4.5%;  Score 44;  DB 5;  Length 1073;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db        665 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 708


RESULT 97
MMU19841
LOCUS       MMU19841               1080 bp    mRNA    linear   PRI 03-FEB-1996
DEFINITION  Macaca mulatta interleukin-12 alpha (IL-12a) mRNA, complete cds.
ACCESSION   U19841
VERSION     U19841.1  GI:644799
KEYWORDS    .
SOURCE      Macaca mulatta (rhesus monkey)
  ORGANISM  Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 1080)
  AUTHORS   Villinger,F., Brar,S.S., Mayne,A., Chikkala,N. and Ansari,A.A.
  TITLE     Comparative sequence analysis of cytokine genes from human and
            nonhuman primates
  JOURNAL   J. Immunol. 155 (8), 3946-3954 (1995)
   PUBMED   7561102
REFERENCE   2  (bases 1 to 1080)
  AUTHORS   Villinger,F.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JAN-1995) Francois J. Villinger, Emory University,
            Pathology, 1327 Clifton Rd, Atlanta, GA 30322, USA
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ORIGIN

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Db        673 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 716


RESULT 98
AR393788
LOCUS       AR393788               1389 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 4 from patent US 6617135.
ACCESSION   AR393788
VERSION     AR393788.1  GI:40120790
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1389)
  AUTHORS   Gillies,S.D. and Lo,K.-M.
  TITLE     Multiple cytokine protein complexes
  JOURNAL   Patent: US 6617135-A 4 09-SEP-2003;
            EMD Lexigen Research Center Corp.; Billerica, MA
FEATURES             Location/Qualifiers
     source          1. .1389
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                     /mol_type="genomic DNA"
ORIGIN

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  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 99
AX084106
LOCUS       AX084106               1389 bp    DNA     linear   PAT 28-FEB-2001
DEFINITION  Sequence 4 from Patent WO0110912.
ACCESSION   AX084106
VERSION     AX084106.1  GI:13185656
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Gillies,S.D. and Lo,K.M.
  TITLE     Multiple cytokine-antibody complexes
  JOURNAL   Patent: WO 0110912-A 4 15-FEB-2001;
            Lexigen Pharmaceuticals Corp. (US)
FEATURES             Location/Qualifiers
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                     /note="human p40-IL-2 fusion protein coding sequence"
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ORIGIN

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  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 100
BD165800
LOCUS       BD165800               1397 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Antibody against cytotoxic lymphocyte maturing factors.
ACCESSION   BD165800
VERSION     BD165800.1  GI:27871612
KEYWORDS    JP 2002167400-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 1397)
  AUTHORS   Chizzonite,R.A., Gately,M.K., Gubler,U.A., Hulmes,J.D., Pan,Y.C.E.,
            Podlanski,F.J. and Stern,A.S.
  TITLE     Antibody against cytotoxic lymphocyte maturing factors
  JOURNAL   Patent: JP 2002167400-A 1 11-JUN-2002;
            PROTEIN DESIGN LABS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002167400-A/1
            PD   11-JUN-2002
            PF   14-AUG-2001 JP 2001246031
            PR   22-DEC-1989 US       455708,09-MAY-1990 US       520935 PR
            27-AUG-1990 US       572284
            PI   RICHARD ANTHONY CHIZZONITE,MAURICE KENT GATELY,ULRICH ANDREAS
            PI   GUBLER,
            PI   JEFFREY DAVID HULMES,YU CHING EUGENE PAN,FRANK JOHN PODLANSKI,
            PI   ALVIN SETH STERN
            PC   C07K16/24,C12N15/02,C12N15/02,C12P21/08,C12N15/00,C12N15/00 CC
              Antibody against cytotoxic lymphocyte maturing factors FH   Key
                    Location/Qualifiers
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ORIGIN

  Query Match             4.5%;  Score 44;  DB 2;  Length 1397;
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  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        701 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 744


Search completed: June 10, 2006, 06:52:38
Job time : 6245.73 secs
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2006, 22:28:48 ; Search time 762.533 Seconds
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Title: US-10-821-670A-55
Perfect score: 985
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 5244920 seqs, 3486124231 residues

Word size : 1

Total number of hits satisfying chosen parameters: 10489196

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 200 summaries

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15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	2	985	100.0	985	6	ABK98961	Abk98961 Feline in
	3	985	100.0	985	14	ADV34707	Adv34707 Feline N-
c	4	985	100.0	985	14	ADV34709	Adv34709 Feline N-
	5	985	100.0	987	6	ABK98944	Abk98944 Feline in
c	6	985	100.0	987	6	ABK98945	Abk98945 Feline in
	7	985	100.0	987	14	ADV34682	Adv34682 Feline si
c	8	985	100.0	987	14	ADV34684	Adv34684 Feline si
	9	928	94.2	2193	2	AAV56625	Aav56625 Feline FL
	10	919	93.3	921	2	AAV56626	Aav56626 Feline FL
	11	903	91.7	1599	6	ABK98950	Abk98950 Feline in
c	12	903	91.7	1599	6	ABK98951	Abk98951 Feline in
	13	903	91.7	1599	14	ADV34691	Adv34691 Feline si
c	14	903	91.7	1599	14	ADV34693	Adv34693 Feline si
	15	884	89.7	990	4	AAF26082	Aaf26082 Feline IL
	16	884	89.7	990	4	AAF26085	Aaf26085 Feline IL
	17	884	89.7	4522	4	AAF26076	Aaf26076 Feline IL
	18	884	89.7	4522	4	AAF26094	Aaf26094 Plasmid p
	19	868	88.1	921	2	AAV56627	Aav56627 Feline FL
	20	868	88.1	921	6	ABK98942	Abk98942 Feline in
c	21	868	88.1	921	6	ABK98943	Abk98943 Feline in
c	22	868	88.1	921	14	ADV34681	Adv34681 Feline si
	23	868	88.1	921	14	ADV34679	Adv34679 Feline si
c	24	868	88.1	1533	6	ABK98954	Abk98954 Feline in
	25	868	88.1	1533	6	ABK98953	Abk98953 Feline in
c	26	868	88.1	1533	14	ADV34697	Adv34697 Feline si
	27	868	88.1	1533	14	ADV34695	Adv34695 Feline si
	28	83	8.4	990	5	AAD15209	Aad15209 Modified
	29	66	6.7	921	6	ABK98959	Abk98959 Canine in
c	30	66	6.7	921	6	ABK98960	Abk98960 Canine in
c	31	66	6.7	921	14	ADV34706	Adv34706 Canine si
	32	66	6.7	921	14	ADV34704	Adv34704 Canine si
	33	66	6.7	924	2	AAX18177	Aax18177 Canine ma
	34	66	6.7	987	6	ABK98963	Abk98963 Canine in
c	35	66	6.7	987	6	ABK98964	Abk98964 Canine in
c	36	66	6.7	987	14	ADV34712	Adv34712 Canine si
	37	66	6.7	987	14	ADV34710	Adv34710 Canine si
	38	66	6.7	990	2	AAV13816	Aav13816 Canine IL
	39	66	6.7	990	2	AAV13817	Aav13817 Canine IL
	40	66	6.7	990	2	AAX03162	Aax03162 Nucleic a
	41	66	6.7	990	2	AAX03152	Aax03152 Nucleic a
	42	66	6.7	990	2	AAX35625	Aax35625 Nucleic a
	43	66	6.7	990	2	AAX35615	Aax35615 Nucleic a
	44	66	6.7	990	4	AAI64378	Aai64378 Canine co
	45	66	6.7	990	4	AAI64388	Aai64388 Canine co
	46	66	6.7	990	11	ADZ25698	Adz25698 Canine in
	47	66	6.7	1533	6	ABK98967	Abk98967 Canine in
c	48	66	6.7	1533	6	ABK98968	Abk98968 Canine in
c	49	66	6.7	1533	14	ADV34718	Adv34718 Canine si
	50	66	6.7	1533	14	ADV34716	Adv34716 Canine si
	51	66	6.7	1599	6	ABK98965	Abk98965 Canine in
c	52	66	6.7	1599	6	ABK98966	Abk98966 Canine in
c	53	66	6.7	1599	14	ADV34715	Adv34715 Canine si
	54	66	6.7	1599	14	ADV34713	Adv34713 Canine si
	55	66	6.7	2154	2	AAX18176	Aax18176 Canine fu
c	56	66	6.7	2267	6	ABK99006	Abk99006 Canine in
	57	66	6.7	2267	6	ABK99005	Abk99005 Canine in
	58	66	6.7	2267	14	ADV34757	Adv34757 Canine si
c	59	66	6.7	2267	14	ADV34759	Adv34759 Canine si
	60	65	6.6	984	5	AAD15206	Aad15206 Modified
	61	63	6.4	1015	13	ADT04849	Adt04849 Canine in
	62	61	6.2	984	5	AAD15204	Aad15204 Modified
	63	60	6.1	984	5	AAD15205	Aad15205 Modified
	64	53	5.4	975	5	AAD15208	Aad15208 Modified
	65	44	4.5	906	2	AAQ04701	Aaq04701 Sequence
	66	44	4.5	969	5	AAD15207	Aad15207 Modified
	67	44	4.5	979	2	AAQ12149	Aaq12149 Cytotoxic
	68	44	4.5	984	2	AAT50759	Aat50759 Sequence
	69	44	4.5	984	12	ADG39430	Adg39430 Human CLM
	70	44	4.5	985	10	ADK98707	Adk98707 Human int
	71	44	4.5	987	2	AAQ97484	Aaq97484 Human int
	72	44	4.5	987	2	AAV07273	Aav07273 Human Int
	73	44	4.5	987	2	AAV07217	Aav07217 DNA encod
	74	44	4.5	987	2	AAZ40404	Aaz40404 Human int
	75	44	4.5	987	2	AAV83199	Aav83199 Interleuk
	76	44	4.5	987	5	AAD15210	Aad15210 Human cyt
	77	44	4.5	987	6	ACC47592	Acc47592 Human int
	78	44	4.5	987	12	ADF77276	Adf77276 Human IL-
	79	44	4.5	987	12	ADO07653	Ado07653 Human int
	80	44	4.5	987	13	ADS00006	Ads00006 Human int
	81	44	4.5	987	14	ADV42753	Adv42753 Human psy
	82	44	4.5	987	14	ADW97242	Adw97242 Human p40
	83	44	4.5	987	14	AEB48822	Aeb48822 Human int
	84	44	4.5	1007	5	AAD18585	Aad18585 Human int
	85	44	4.5	1018	2	AAQ67879	Aaq67879 EPV 42 kD
	86	44	4.5	1018	2	AAZ08510	Aaz08510 EPV 42 kD
	87	44	4.5	1018	13	ADR21886	Adr21886 EPV 42kDa
	88	44	4.5	1019	3	AAA70709	Aaa70709 Bovine in
	89	44	4.5	1029	12	ADP88402	Adp88402 Human int
	90	44	4.5	1389	4	AAF76880	Aaf76880 Human p40
	91	44	4.5	1397	2	AAT77849	Aat77849 40 kDa su

	92	44	4.5	1397	2	AAT97969 Aat97969 40 kDa su
	93	44	4.5	1397	2	AAV00401 Aav00401 40 kDa su
	94	44	4.5	1397	2	AAV37767 Aav37767 Cytotoxic
	95	44	4.5	1397	12	ADG39387 Adg39387 Human cyt
	96	44	4.5	1397	12	ADO03758 Ado03758 Human CLM
	97	44	4.5	1399	3	AAZ40021 Aaz40021 Human p40
	98	44	4.5	1399	14	ADY86632 Ady86632 Human int
	99	44	4.5	1580	12	ADQ14472 Adq14472 DNA encod
	100	44	4.5	2300	3	AAA92406 Aaa92406 Human int
	101	44	4.5	2318	8	ACA61267 Aca61267 DNA encod
	102	44	4.5	2318	10	ABX33940 Abx33940 Human cDN
	103	44	4.5	2336	14	AEE03207 Aee03207 Human int
	104	44	4.5	2347	12	ACF57534 Acf57534 Human IL1
	105	44	4.5	2347	12	ADJ62892 Adj62892 Human int
	106	44	4.5	2347	14	ADZ26728 Adz26728 Human IL1
	107	44	4.5	2362	2	AAQ23586 Aaq23586 Natural k
	108	44	4.5	2362	2	AAT48098 Aat48098 Human int
	109	44	4.5	2362	2	AAV42535 Aav42535 Human int
	110	44	4.5	2362	2	AAV15227 Aav15227 Heterodim
	111	44	4.5	2362	3	AAZ28862 Aaz28862 Human int
	112	44	4.5	2362	4	AAF56280 Aaf56280 IL-12 vac
	113	44	4.5	4727	14	AEA40942 Aea40942 T-DNA reg
	114	44	4.5	5686	2	AAZ40415 Aaz40415 Plasmid p
	115	44	4.5	5686	12	ADF77239 Adf77239 Human IL-
	116	44	4.5	6139	3	AAZ40023 Aaz40023 Interleuk
	117	44	4.5	8578	6	AAD31546 Aad31546 pIRES-hB7
	118	44	4.5	8578	6	AAD31545 Aad31545 pIRES-hB7
	119	44	4.5	8608	6	AAD31548 Aad31548 pIRES-hB7
	120	44	4.5	8623	6	AAD31547 Aad31547 pIRES-hB7
	121	44	4.5	8629	6	AAD31552 Aad31552 pIRES-IL1
	122	44	4.5	8638	6	AAD31549 Aad31549 pIRES-hB7
	123	44	4.5	8644	6	AAD31551 Aad31551 pIRES-IL1
	124	44	4.5	8659	6	AAD31550 Aad31550 pIRES-IL1
	125	44	4.5	11453	10	ADG25152 Adg25152 Vector pS
	126	44	4.5	11569	10	ADG25150 Adg25150 Vector pA
	127	39	4.0	1007	10	ACD26421 Acd26421 cDNA enco
	128	39	4.0	2390	12	ADM29103 Adm29103 Human int
	129	39	4.0	18110	6	ABK15357 Abk15357 Human int
	130	39	4.0	18340	5	AAD19368 Aad19368 Mammalian
c	131	35	3.6	270	12	ACH83638 Ach83638 Human gen
c	132	35	3.6	556	12	ACH69938 Ach69938 Human gen
	133	35	3.6	975	5	AAD15203 Aad15203 Modified
c	134	30	3.0	30	3	AAA48905 Aaa48905 Probe 12.
	135	30	3.0	73	4	AAS15322 Aas15322 Mouse IL-
	136	30	3.0	600	2	AAX78397 Aax78397 IL-12p40
	137	30	3.0	600	2	AAX25947 Aax25947 Interleuk
	138	30	3.0	1008	13	ADS00008 Ads00008 Murine in
	139	30	3.0	1008	14	ADW97243 Adw97243 Murine p4
	140	30	3.0	1056	2	AAV28472 Aav28472 Murine in
	141	30	3.0	1061	2	AAT35200 Aat35200 Mouse int
	142	30	3.0	1409	4	AAF76879 Aaf76879 Murine p4
	143	30	3.0	1472	4	AAF76878 Aaf76878 Murine p4
	144	30	3.0	1569	4	AAF76888 Aaf76888 Single-ch
	145	30	3.0	1610	12	ADQ14470 Adq14470 DNA encod
	146	30	3.0	1840	8	ACA61265 Aca61265 DNA encod
	147	30	3.0	2013	4	AAF76887 Aaf76887 Murine p3
	148	30	3.0	2334	14	AEE03206 Aee03206 Murine in
	149	30	3.0	2438	12	ADO43004 Ado43004 DNA encod
	150	30	3.0	2709	4	AAF76889 Aaf76889 Coding se
	151	30	3.0	5252	12	ADO07652 Ado07652 Tricistro
	152	30	3.0	5966	2	AAZ40417 Aaz40417 Plasmid p
	153	30	3.0	5966	12	ADF77241 Adf77241 Mouse IL-
	154	30	3.0	5985	12	ADQ82718 Adq82718 Anticance
	155	30	3.0	6295	2	AAV02043 Aav02043 Plasmid p
	156	30	3.0	7287	2	AAV02042 Aav02042 Plasmid p
	157	30	3.0	9049	12	ADO07661 Ado07661 Viral vec
	158	30	3.0	10633	12	ADO07660 Ado07660 Viral vec
	159	30	3.0	11458	10	ADG25151 Adg25151 Vector pA
	160	30	3.0	11746	12	ADO07659 Ado07659 Viral vec
	161	30	3.0	28191	14	AEE03204 Aee03204 Adenovira
	162	30	3.0	28892	14	AEE03202 Aee03202 Adenovira
	163	30	3.0	38246	12	ADO07662 Ado07662 Viral vec
	164	28	2.8	28	6	ABK98985 Abk98985 Feline PC
	165	28	2.8	28	14	ADV34735 Adv34735 Feline IL
	166	28	2.8	37	6	ABK98987 Abk98987 Feline PC
	167	28	2.8	37	14	ADV34737 Adv34737 Feline IL
c	168	25	2.5	25	6	ABK98986 Abk98986 Feline PC
c	169	25	2.5	25	14	ADV34736 Adv34736 Feline IL
c	170	25	2.5	25	14	AEC56176 Aec56176 Antisense
c	171	24	2.4	26	2	AAX78412 Aax78412 Rat GADPH
c	172	24	2.4	26	2	AAX25927 Aax25927 IL12 p40
	173	24	2.4	30	4	AAI65149 Aai65149 Canine IL
	174	24	2.4	30	8	ACD27994 Acd27994 Interleuk
	175	24	2.4	39	2	AAV13826 Aav13826 Primer fo
	176	24	2.4	39	2	AAX03164 Aax03164 PCR prime
	177	24	2.4	39	2	AAX35627 Aax35627 PCR prime
	178	24	2.4	39	4	AAI64390 Aai64390 PCR prime
	179	24	2.4	540	2	AAX27732 Aax27732 Recombina
	180	24	2.4	540	3	AAA13801 Aaa13801 Canine in
	181	24	2.4	987	2	AAZ40406 Aaz40406 Human int
	182	24	2.4	987	2	AAZ40405 Aaz40405 Human int
	183	24	2.4	987	12	ADF77278 Adf77278 Human IL-
	184	24	2.4	987	12	ADF77277 Adf77277 Human IL-
	185	23	2.3	200	2	AAV03357 Aav03357 Homo sapi
	186	22	2.2	399	14	AEE14792 Aee14792 Hamster S
	187	22	2.2	399	14	AEE11150 Aee11150 Hamster c
c	188	22	2.2	87350	2	AAX83003 Aax83003 Human WRN
c	189	22	2.2	87543	7	ADJ84092 Adj84092 Human WRN
	190	21	2.1	21	3	AAA48904 Aaa48904 Reverse p
c	191	21	2.1	21	3	AAA48903 Aaa48903 Forward p
	192	21	2.1	21	12	ADG14584 Adg14584 IL-12p40
	193	21	2.1	23	2	AAX78422 Aax78422 Rat GADPH
	194	21	2.1	23	2	AAX25940 Aax25940 IL12 p40
	195	21	2.1	44	2	AAV56632 Aav56632 Feline FL
	196	20	2.0	20	5	AAD19313 Aad19313 Mammalian
c	197	20	2.0	20	10	ABX33973 Abx33973 Human int
c	198	20	2.0	20	10	ABX33972 Abx33972 Human int
c	199	20	2.0	20	10	ABX33959 Abx33959 Human int
c	200	20	2.0	20	10	ABX33954 Abx33954 Human int

ALIGNMENTS

RESULT 1
ABK98962/c
ID ABK98962 standard; cDNA; 985 BP.
XX
AC ABK98962;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p40-N985 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single

```
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 3; Page 75-76; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 985 BP; 207 A; 245 C; 250 G; 283 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 985;  DB 6;  Length 985;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGCA 1


RESULT 2
ABK98961
ID   ABK98961 standard; cDNA; 985 BP.
XX
AC   ABK98961;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p40-N985 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69311.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 3; Page 73-74; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
```

```
SQ   Sequence 985 BP; 283 A; 250 C; 245 G; 207 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 985;  DB 6;  Length 985;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985
```

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RESULT 3
ADV34707
ID   ADV34707 standard; cDNA; 985 BP.
XX
AC   ADV34707;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline N-terminal IL-12p40 protein encoding cDNA, nFeIL-12p40-N985.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .984
FT                   /*tag=  a
FT                   /product= "PCaIL-12P40-N328 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34708.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 55; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline N-terminal single chain IL-12p40 protein
CC   encoding cDNA.
XX
SQ   Sequence 985 BP; 283 A; 250 C; 245 G; 207 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 985;  DB 14;  Length 985;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
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Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985
```

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RESULT 4
ADV34709/c
ID   ADV34709 standard; DNA; 985 BP.
XX
AC   ADV34709;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline N-terminal IL-12p40 protein complementary DNA, nFeIL-12p40-N985.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 57; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline N-terminal single chain IL-12p40
CC   complementary DNA.
XX
SQ   Sequence 985 BP; 207 A; 245 C; 250 G; 283 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 985;  DB 14;  Length 985;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446
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Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGCA 1
```

RESULT 5
ABK98944
ID ABK98944 standard; cDNA; 987 BP.
XX
AC ABK98944;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p40-987 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69303.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 1; Page 51-53; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 987 BP; 283 A; 250 C; 246 G; 208 T; 0 U; 0 Other;

  Query Match   100.0%; Score 985; DB 6; Length 987;
  Best Local Similarity 100.0%; Pred. No. 0;
  Matches 985; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
```

```
Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 6
ABK98945/c
ID   ABK98945 standard; cDNA; 987 BP.
XX
AC   ABK98945;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p40-987 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 3; Page 54; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 987 BP; 208 A; 246 C; 250 G; 283 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 985;  DB 6;  Length 987;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGCA 3


RESULT 7
ADV34682
ID   ADV34682 standard; cDNA; 987 BP.
XX
AC   ADV34682;
XX
```

```
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12p40 full-length cDNA, nFeIL-12p40 987.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .987
FT                   /*tag=  a
FT                   /product= "PFeIL-12p40 329 protein "
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34683.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 23; SEQ ID NO 29; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12p40 subunit protein
CC   encoding full-length cDNA.
XX
SQ   Sequence 987 BP; 283 A; 250 C; 246 G; 208 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 985;  DB 14;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 8
ADV34684/c
ID   ADV34684 standard; DNA; 987 BP.
XX
AC   ADV34684;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12p40 complementary DNA, nFeIL-12p40 987.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
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XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 31; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12p40 subunit full-length
CC   complementary DNA.
XX
SQ   Sequence 987 BP; 208 A; 246 C; 250 G; 283 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 985;  DB 14;  Length 987;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGCA 3


RESULT 9
AAV56625
ID   AAV56625 standard; cDNA; 2193 BP.
XX
AC   AAV56625;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp40 cDNA.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             64. .1053
FT                   /*tag=  a
FT   sig_peptide     64. .129
FT                   /*tag=  b
FT   mat_peptide     130. .1050
FT                   /*tag=  c
FT                   /product= "FLAFp40"
FT                   /note= "feline cytokine"
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP001824.
XX
PR   04-JUN-1996;   96JP-00165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76173.
XX
PT   Novel feline cytokine protein - useful for treating feline auto:immune
PT   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS   Claim 19; Page 52-54; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine protein, FLAFp40. This
CC   protein can be used in the production of a FLAFp35/FLAFp40 heterodimer
CC   which can potentiate the cytotoxic activity of feline cytotoxic T
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CC   lymphocyte cells. Such proteins are used for treatment of feline
CC   autoimmune diseases e.g. as caused by feline herpes virus or feline
CC   calcivirus
XX
SQ   Sequence 2193 BP; 680 A; 451 C; 493 G; 569 T; 0 U; 0 Other;

  Query Match             94.2%;  Score 928;  DB 2;  Length 2193;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  928;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         58 CTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCT 117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCT 180

Qy        118 GATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACC 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACC 240

Qy        178 TGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTC 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTC 300

Qy        238 AAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCAT 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCAT 360

Qy        298 TCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAA 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAA 420

Qy        358 CAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGT 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGT 480

Qy        418 TTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGC 477
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGC 540

Qy        478 AGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAG 537
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAG 600

Qy        538 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 597
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 660

Qy        598 TGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTC 657
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTC 720

Qy        658 AAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCC 717
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCC 780

Qy        718 AAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATAC 777
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATAC 840

Qy        778 CCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAG 837
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAG 900

Qy        838 GGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTC 897
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTC 960

Qy        898 GTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCC 957
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCC 1020

Qy        958 TGGAGCAACTGGGCATCCGTGTCCTGCA 985
              ||||||||||||||||||||||||||||
Db       1021 TGGAGCAACTGGGCATCCGTGTCCTGCA 1048
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RESULT 10
AAV56626
ID   AAV56626 standard; cDNA; 921 BP.
XX
AC   AAV56626;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp40 cDNA mature transcript #1.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP001824.
XX
PR   04-JUN-1996;   96JP-00165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76174.
XX
PT   Novel feline cytokine protein - useful for treating feline auto:immune
PT   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS   Claim 20; Page 55; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine mature protein, FLAFp40.
CC   This protein can be used in the production of a FLAFp35/FLAFp40
CC   heterodimer which can potentiate the cytotoxic activity of feline
CC   cytotoxic T lymphocyte cells. Such proteins are used for treatment of
CC   feline autoimmune diseases e.g. as caused by feline herpes virus or
CC   feline calcivirus
XX
SQ   Sequence 921 BP; 276 A; 227 C; 231 G; 187 T; 0 U; 0 Other;

  Query Match             93.3%;  Score 919;  DB 2;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  919;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
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Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCA 985
              ||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCA 919
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RESULT 11
ABK98950
ID   ABK98950 standard; cDNA; 1599 BP.
XX
AC   ABK98950;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1599 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69306.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 58-60; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

  Query Match             91.7%;  Score 903;  DB 6;  Length 1599;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  953;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91

Qy         92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151

Qy        152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211

Qy        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271

Qy        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331

Qy        332 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 391

Qy        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451

Qy        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTG 511
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTG 511

Qy        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571

Qy        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631

Qy        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691

Qy        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751

Qy        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811

Qy        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 871
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 871

Qy        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931

Qy        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 12
ABK98951/c
ID   ABK98951 standard; cDNA; 1599 BP.
XX
AC   ABK98951;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1599 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 61-62; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

  Query Match             91.7%;  Score 903;  DB 6;  Length 1599;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  953;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1568 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 1509

Qy         92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1508 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 1449

Qy        152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1448 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 1389

Qy        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1388 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 1329

Qy        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1328 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 1269

Qy        332 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1268 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 1209

Qy        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1208 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 1149

Qy        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTG 511
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       1148 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTG 1089

Qy        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1088 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 1029

Qy        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1028 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 969

Qy        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        968 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 909

Qy        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        908 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 849

Qy        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 789

Qy        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 871
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        788 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 729

Qy        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 669

Qy        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCA 615


RESULT 13
ADV34691
ID   ADV34691 standard; cDNA; 1599 BP.
XX
AC   ADV34691;
```

```
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1599
FT                   /*tag=  a
FT                   /product= "PFeIL-12p533 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34692.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 38; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

  Query Match             91.7%;  Score 903;  DB 14;  Length 1599;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  953;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91

Qy         92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151

Qy        152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211

Qy        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271

Qy        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331

Qy        332 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 391

Qy        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451

Qy        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTG 511
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTG 511

Qy        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571

Qy        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631

Qy        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691

Qy        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751

Qy        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811

Qy        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 871
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 871

Qy        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931

Qy        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCA 985
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 14
ADV34693/c
ID   ADV34693 standard; DNA; 1599 BP.
XX
AC   ADV34693;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 complementary DNA, nFeIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
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```
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 40; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 complementary DNA.
XX
SQ   Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

  Query Match             91.7%;  Score 903;  DB 14;  Length 1599;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  953;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1568 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 1509

Qy         92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1508 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 1449

Qy        152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1448 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 1389

Qy        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1388 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 1329

Qy        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1328 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 1269

Qy        332 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1268 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 1209

Qy        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1208 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 1149

Qy        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTG 511
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       1148 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTG 1089

Qy        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1088 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 1029

Qy        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1028 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 969

Qy        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        968 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 909

Qy        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        908 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 849

Qy        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 789

Qy        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 871
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        788 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 729

Qy        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 669

Qy        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCA 985
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCA 615


RESULT 15
AAF26082
ID   AAF26082 standard; DNA; 990 BP.
XX
AC   AAF26082;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p40 encoding DNA SEQ ID 8.
XX
KW   Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW   interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS   Felis sp.
XX
PN   WO200104280-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002262.
XX
PR   08-JUL-1999;   99CH-00001258.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
XX
PI   Leutenegger C,  Schroff M,  Wittig B,  Lutz H;
XX
DR   WPI; 2001-147190/15.
XX
PT   Vaccine for treating or preventing lentivirus infection in cats, contains
PT   nucleic acid sequence encoding viral protein under control of eukaryotic
PT   promoter.
XX
PS   Claim 14; Page 36; 37pp; German.
XX
CC   This invention describes a novel vaccine (A) for prevention or treatment
CC   of lentivirus infection in felines which comprises an immunizing nucleic
CC   acid sequence (I) that contains, or comprises, at least part of a gene
CC   encoding a protein (II) of the virus, under control of a eukaryotic
CC   promoter functional in the relevant animal. (II) is especially the
CC   envelope (env) protein. The invention also describes (1) vaccine (A)
CC   containing an immunizing protein, or fragment, from a lentivirus plus at
CC   least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC   lentivirus protein, or fragment, especially derived from feline immune
CC   deficiency virus (FIV), by expressing the corresponding nucleic acid
CC   sequence in a host cell. The products of the invention have antiviral
CC   activity. The vaccine (A) and related protein-based vaccines, are
CC   particularly used to treat or prevent lentivirus infections in domestic
CC   cats, especially feline immune deficiency virus (FIV). Vaccination with
CC   (A) allows differentiation between vaccinated and infected animals, from
CC   the antibody status. The vaccines may be formulated with an adjuvant
CC   (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC   immune response, particularly a Th1 response
XX
SQ   Sequence 990 BP; 283 A; 249 C; 248 G; 210 T; 0 U; 0 Other;
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  Query Match             89.7%;  Score 884;  DB 4;  Length 990;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  934;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAG 935
              |||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAG 935


RESULT 16
AAF26085
ID   AAF26085 standard; DNA; 990 BP.
XX
AC   AAF26085;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p40 encoding DNA.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS   Felis sp.
XX
PN   WO200104155-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002263.
XX
PR   08-JUL-1999;   99CH-00001259.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Lutz H,  Leutenegger C,  Pedersen N,  Schroff M,  Wittig B;
XX
DR   WPI; 2001-147178/15.
XX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs.
XX
PS   Claim 3; Page 30; 35pp; German.
XX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
CC   following: (i) as immunostimulant, for preventative or therapeutic use;
CC   and (ii) treating tumors and autoimmune diseases, or diseases associated
CC   with a Th1 defect, especially pre-existing infections by feline immune
CC   deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ   Sequence 990 BP; 283 A; 249 C; 248 G; 210 T; 0 U; 0 Other;

  Query Match             89.7%;  Score 884;  DB 4;  Length 990;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  934;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
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Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAG 935
              |||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAG 935


RESULT 17
AAF26076
ID   AAF26076 standard; DNA; 4522 BP.
XX
AC   AAF26076;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p40 encoding DNA SEQ ID 2.
XX
KW   Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW   interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS   Felis sp.
XX
PN   WO200104280-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002262.
XX
PR   08-JUL-1999;   99CH-00001258.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
XX
PI   Leutenegger C,  Schroff M,  Wittig B,  Lutz H;
XX
DR   WPI; 2001-147190/15.
XX
PT   Vaccine for treating or preventing lentivirus infection in cats, contains
PT   nucleic acid sequence encoding viral protein under control of eukaryotic
PT   promoter.
XX
PS   Disclosure; Page 29-31; 37pp; German.
XX
CC   This invention describes a novel vaccine (A) for prevention or treatment
CC   of lentivirus infection in felines which comprises an immunizing nucleic
CC   acid sequence (I) that contains, or comprises, at least part of a gene
CC   encoding a protein (II) of the virus, under control of a eukaryotic
CC   promoter functional in the relevant animal. (II) is especially the
CC   envelope (env) protein. The invention also describes (1) vaccine (A)
CC   containing an immunizing protein, or fragment, from a lentivirus plus at
CC   least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC   lentivirus protein, or fragment, especially derived from feline immune
CC   deficiency virus (FIV), by expressing the corresponding nucleic acid
CC   sequence in a host cell. The products of the invention have antiviral
CC   activity. The vaccine (A) and related protein-based vaccines, are
CC   particularly used to treat or prevent lentivirus infections in domestic
CC   cats, especially feline immune deficiency virus (FIV). Vaccination with
CC   (A) allows differentiation between vaccinated and infected animals, from
CC   the antibody status. The vaccines may be formulated with an adjuvant
CC   (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC   immune response, particularly a Th1 response
XX
SQ   Sequence 4522 BP; 1180 A; 1126 C; 1106 G; 1110 T; 0 U; 0 Other;

  Query Match             89.7%;  Score 884;  DB 4;  Length 4522;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  934;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526
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Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAG 935
              |||||||||||||||||||||||||||||||||||
Db       3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAG 3981
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RESULT 18
AAF26094
ID AAF26094 standard; DNA; 4522 BP.
XX
AC AAF26094;
XX
DT 24-APR-2001 (first entry)
XX
DE Plasmid pMol-fil12p40 DNA SEQ ID 10.
XX
KW Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS Synthetic.
XX
PN WO200104155-A2.
XX
PD 18-JAN-2001.
XX
PF 08-JUL-2000; 2000WO-DE002263.
XX
PR 08-JUL-1999; 99CH-00001259.
XX
PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA (UYZU-) UNIV ZUERICH.
PA (REGC) UNIV CALIFORNIA.
XX
PI Lutz H, Leutenegger C, Pedersen N, Schroff M, Wittig B;
XX
DR WPI; 2001-147178/15.
XX
PT Recombinant feline interleukin-12, useful as immunostimulant and for
PT treating e.g. viral infections in cats, and related nucleic acid
PT constructs.
XX
PS Example 1c; Page 33-35; 35pp; German.
XX
CC This invention describes a novel feline interleukin-12 (fIL-12)
CC polypeptide (I) that is expressed, by recombinant gene expression in
CC eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC of subunits p35 and p40. These proteins are formed so that, in equimolar
CC concentrations and in presence of an immunizing antigen, they can be
CC administered to carnivores, particularly domestic cats. The invention
CC also describes a nucleic acid construct (II) encoding fIL-12 containing
CC sequences at least 95% identical with the p40- and p35-encoding sequences
CC (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC as immunostimulants for immunization against infectious diseases and/or
CC for treating infections or tumors in felines, especially domestic cats.
CC The products of the invention have immunostimulatory, antiviral and
CC antitumor activity. Nucleic acid constructs that encode (II) are useful
CC as adjuvants for prophylactic immunization against viral diseases and for
CC treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC is useful for carnivores, and particularly domestic cats in the
CC following: (i) as immunostimulant, for preventative or therapeutic use;
CC and (ii) treating tumors and autoimmune diseases, or diseases associated
CC with a Th1 defect, especially pre-existing infections by feline immune
CC deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ Sequence 4522 BP; 1180 A; 1126 C; 1106 G; 1110 T; 0 U; 0 Other;

Query Match 89.7%; Score 884; DB 4; Length 4522;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 934; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db       3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAG 935
              |||||||||||||||||||||||||||||||||||
Db       3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAG 3981


RESULT 19
AAV56627
ID   AAV56627 standard; cDNA; 921 BP.
XX
AC   AAV56627;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp40 cDNA mature transcript #2.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP001824.
XX
PR   04-JUN-1996;   96JP-00165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76174.
XX
PT   Novel feline cytokine protein - useful for treating feline auto:immune
PT   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS   Claim 21; Page 56-57; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine mature protein, FLAFp40.
CC   This protein can be used in the production of a FLAFp35/FLAFp40
CC   heterodimer which can potentiate the cytotoxic activity of feline
CC   cytotoxic T lymphocyte cells. Such proteins are used for treatment of
CC   feline autoimmune diseases e.g. as caused by feline herpes virus or
CC   feline calcivirus
XX
SQ   Sequence 921 BP; 276 A; 228 C; 230 G; 187 T; 0 U; 0 Other;

  Query Match             88.1%;  Score 868;  DB 2;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy         367 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy         427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy         487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy         547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy         607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy         667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy         727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy         787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy         847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy         907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy         967 TGGGCATCCGTGTCCTGCA 985
               ||||||||||||||||||
Db         901 TGGGCATCCGTGTCCTGCA 919


RESULT 20
ABK98942
ID   ABK98942 standard; cDNA; 921 BP.
XX
AC   ABK98942;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p40-921 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
```

```
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69302.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 49-50; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 921 BP; 277 A; 227 C; 230 G; 187 T; 0 U; 0 Other;

  Query Match             88.1%;  Score 868;  DB 6;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy         367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy         427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy         487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
               ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db         421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy         547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy         607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy         667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy         727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy         787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy         847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy         907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy         967 TGGGCATCCGTGTCCTGCA 985
               ||||||||||||||||||
Db         901 TGGGCATCCGTGTCCTGCA 919


RESULT 21
ABK98943/c
ID   ABK98943 standard; cDNA; 921 BP.
XX
AC   ABK98943;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p40-921 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Disclosure; Page 51; 106pp; English.
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XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 921 BP; 187 A; 230 C; 227 G; 277 T; 0 U; 0 Other;

  Query Match             88.1%;  Score 868;  DB 6;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        967 TGGGCATCCGTGTCCTGCA 985
              ||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCA 3


RESULT 22
ADV34681/c
ID   ADV34681 standard; DNA; 921 BP.
XX
AC   ADV34681;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain mature IL-12p40 complementary DNA, nFeIL-12p40 921.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 28; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain mature IL-12p40 subunit
CC   complementary DNA.
XX
SQ   Sequence 921 BP; 187 A; 230 C; 227 G; 277 T; 0 U; 0 Other;

  Query Match             88.1%;  Score 868;  DB 14;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
                    |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        967 TGGGCATCCGTGTCCTGCA 985
                    ||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCA 3
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RESULT 23
ADV34679
ID   ADV34679 standard; cDNA; 921 BP.
XX
AC   ADV34679;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain mature IL-12p40 protein cDNA, nFeIL-12p40 921.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .921
FT                   /*tag=  a
FT                   /product= "PFeIL-12p40 307 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34680.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 23; SEQ ID NO 26; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain mature IL-12p40 subunit
CC   protein encoding cDNA.
XX
SQ   Sequence 921 BP; 277 A; 227 C; 230 G; 187 T; 0 U; 0 Other;

  Query Match           88.1%;  Score 868;  DB 14;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCA 985
              ||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCA 919
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RESULT 24
ABK98954/c
ID   ABK98954 standard; cDNA; 1533 BP.
XX
AC   ABK98954;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1533 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 66-67; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

  Query Match           88.1%;  Score 868;  DB 6;  Length 1533;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        967 TGGGCATCCGTGTCCTGCA 985
              ||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCA 615


RESULT 25
ABK98953
ID   ABK98953 standard; cDNA; 1533 BP.
XX
AC   ABK98953;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1533 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69307.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 63-64; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

  Query Match             88.1%;  Score 868;  DB 6;  Length 1533;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCA 985
              ||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCA 919


RESULT 26
ADV34697/c
ID   ADV34697 standard; DNA; 1533 BP.
XX
AC   ADV34697;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 complementary DNA, nFeIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
```

```
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 45; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 complementary DNA.
XX
SQ   Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

  Query Match             88.1%;  Score 868;  DB 14;  Length 1533;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        967 TGGGCATCCGTGTCCTGCA 985
              ||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCA 615


RESULT 27
ADV34695
ID   ADV34695 standard; cDNA; 1533 BP.
XX
AC   ADV34695;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1533
FT                   /*tag=  a
FT                   /product= "PFeIL-12 511 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34696.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
```

```
XX
PS   Claim 24; SEQ ID NO 43; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

  Query Match             88.1%;  Score 868;  DB 14;  Length 1533;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCA 985
              ||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCA 919


RESULT 28
AAD15209
ID   AAD15209 standard; DNA; 990 BP.
XX
AC   AAD15209;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p40 encoding DNA from clone R16-51.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p40; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
FT                   /product= "Modified p40 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .987
FT                   /*tag=  c
FT                   /product= "Mature modified p40 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08602.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 1; Page 137-138; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p40 protein encoding
CC   DNA
XX
SQ   Sequence 990 BP; 270 A; 250 C; 254 G; 216 T; 0 U; 0 Other;

  Query Match              8.4%;  Score 83;  DB 5;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-31;
```

```
  Matches   83;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        865 AGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGC 924
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 AGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGC 924

Qy        925 GTGCAAGCCAGAGACCGCTACTA 947
              |||||||||||||||||||||||
Db        925 GTGCAAGCCAGAGACCGCTACTA 947


RESULT 29
ABK98959
ID   ABK98959 standard; cDNA; 921 BP.
XX
AC   ABK98959;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p40-921 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69310.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 71; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 921 BP; 272 A; 221 C; 234 G; 194 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 6;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy        597 CTGCCC 602
              ||||||
Db        531 CTGCCC 536


RESULT 30
ABK98960/c
ID   ABK98960 standard; cDNA; 921 BP.
XX
AC   ABK98960;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p40-921 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Disclosure; Page 73; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 921 BP; 194 A; 234 C; 221 G; 272 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 6;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy        597 CTGCCC 602
              ||||||
Db        391 CTGCCC 386


RESULT 31
ADV34706/c
```

```
ID   ADV34706 standard; DNA; 921 BP.
XX
AC   ADV34706;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain mature IL-12p40 complementary DNA, nCaIL-12p40 921.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Disclosure; SEQ ID NO 54; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p40 subunit reverse
CC   complementary DNA.
XX
SQ   Sequence 921 BP; 194 A; 234 C; 221 G; 272 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 14;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy        597 CTGCCC 602
              ||||||
Db        391 CTGCCC 386


RESULT 32
ADV34704
ID   ADV34704 standard; cDNA; 921 BP.
XX
AC   ADV34704;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain mature IL-12p40 protein cDNA, nCaIL-12p40 921.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .921
FT                   /*tag=  a
FT                   /product= "PCaIL-12P40 307 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34705.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 52; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p40 subunit protein
CC   encoding cDNA.
XX
SQ   Sequence 921 BP; 272 A; 221 C; 234 G; 194 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 14;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy        597 CTGCCC 602
              ||||||
Db        531 CTGCCC 536


RESULT 33
AAX18177
ID   AAX18177 standard; cDNA; 924 BP.
XX
AC   AAX18177;
XX
DT   07-MAY-1999  (first entry)
XX
DE   Canine mature CLAF p40 subunit coding sequence.
XX
KW   CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW   viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW   canine infectious hepatitis; ds.
XX
OS   Canis sp.
XX
PN   WO9855511-A1.
XX
```

PD 10-DEC-1998.
XX
PF 26-MAY-1998; 98WO-JP002295.
XX
PR 03-JUN-1997; 97JP-00161936.
XX
PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI Imamura T, Maeda H, Tokiyoshi S, Eda Y;
XX
DR WPI; 1999-070260/06.
DR P-PSDB; AAW74323.
XX
PT Canine cytokine protein which activates canine cytotoxic T lymphocytes -
PT is useful for treatment of viral and autoimmune diseases in dogs.
XX
PS Claim 8; Page 32; 51pp; Japanese.
XX
CC This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC the invention. CLAF activates lymphocytes, especially canine cytotoxic T
CC cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC recognising it may be used in the treatment of viral diseases in dogs
CC (such as canine distemper, canine parvovirus and canine infectious
CC hepatitis). The antibodies may also be used in isolation of CLAF from
CC culture of the transformant host cells by affinity chromatography. The
CC p40 homodimer can be used for the treatment of autoimmune diseases in
CC dogs
XX
SQ Sequence 924 BP; 273 A; 222 C; 234 G; 195 T; 0 U; 0 Other;

Query Match 6.7%; Score 66; DB 2; Length 924;
Best Local Similarity 100.0%; Pred. No. 2.4e-22;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
||||||

PS Example 4; Page 78; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 987 BP; 216 A; 248 C; 244 G; 279 T; 0 U; 0 Other;

Query Match 6.7%; Score 66; DB 6; Length 987;
Best Local Similarity 100.0%; Pred. No. 2.4e-22;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy 597 CTGCCC 602
||||||
Db 391 CTGCCC 386

RESULT 36
ADV34712/c
ID ADV34712 standard; DNA; 987 BP.
XX
AC ADV34712;
XX
DT 24-FEB-2005 (first entry)
XX
DE Canine single chain IL-12p40 complementary DNA, nCaIL-12p40 987.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Canis familiaris.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 4; SEQ ID NO 60; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the canine single chain IL-12p40 subunit full-length
CC complementary DNA.
XX
SQ Sequence 987 BP; 216 A; 248 C; 244 G; 279 T; 0 U; 0 Other;

Query Match 6.7%; Score 66; DB 14; Length 987;
Best Local Similarity 100.0%; Pred. No. 2.4e-22;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy 597 CTGCCC 602
||||||
Db 391 CTGCCC 386

RESULT 37
ADV34710
ID ADV34710 standard; cDNA; 987 BP.
XX
AC ADV34710;
XX
DT 24-FEB-2005 (first entry)
XX
DE Canine single chain IL-12p40 full-length cDNA, nCaIL-12p40 987.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; gene; ss.
XX
OS Canis familiaris.
XX
FH Key Location/Qualifiers
FT CDS 1. .987
FT /*tag= a
FT /product= "PCaIL-12P40-329 protein"
FT /partial
FT /note= "No stop codon"
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
DR P-PSDB; ADV34711.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 4; SEQ ID NO 58; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the canine single chain IL-12p40 subunit protein
CC encoding full-length cDNA.
XX
SQ Sequence 987 BP; 279 A; 244 C; 248 G; 216 T; 0 U; 0 Other;

```
  Query Match             6.7%;  Score 66;  DB 14;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 38
AAV13816
ID   AAV13816 standard; cDNA to mRNA; 990 BP.
XX
AC   AAV13816;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P40 subunit cDNA.
XX
KW   Canine; interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour;
KW   antiviral; vaccine adjuvant; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
FT                   /product= "interleukin-12_P40_subunit"
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-00296789.
XX
PR   08-NOV-1995;   95JP-00289729.
PR   23-MAY-1996;   96JP-00128104.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   P-PSDB; AAW41790.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected.
XX
PS   Claim 8; Page 8; 12pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin-12 (IL-12) P40 subunit.
CC   A canine IL-12 comprising a P40 and P35 subunit is capable of inducing an
CC   antiviral activating factor and the expression of class II MHC molecules
CC   in canine tumour cells, stimulating proliferation of canine blastogenic
CC   lymphocytes and activating canine leukocytes to inhibit canine tumour
CC   cells. The canine IL-12 can be used in veterinary medicines, e.g.
CC   antitumour, antivirus and vaccine adjuvant activities are expected
XX
SQ   Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 39
AAV13817
ID   AAV13817 standard; cDNA to mRNA; 990 BP.
XX
AC   AAV13817;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P40 subunit cDNA.
XX
KW   Canine; interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour;
KW   antiviral; vaccine adjuvant; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
FT                   /product= "interleukin-12_P40_subunit"
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-00296789.
XX
PR   08-NOV-1995;   95JP-00289729.
PR   23-MAY-1996;   96JP-00128104.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   P-PSDB; AAW41791.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected.
XX
PS   Claim 10; Page 10-11; 12pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin-12 (IL-12) P40 subunit.
CC   A canine IL-12 comprising a P40 and P35 subunit is capable of inducing an
CC   antiviral activating factor and the expression of class II MHC molecules
CC   in canine tumour cells, stimulating proliferation of canine blastogenic
CC   lymphocytes and activating canine leukocytes to inhibit canine tumour
CC   cells. The canine IL-12 can be used in veterinary medicines, e.g.
CC   antitumour, antivirus and vaccine adjuvant activities are expected
XX
SQ   Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 40
AAX03162
ID   AAX03162 standard; cDNA to mRNA; 990 BP.
XX
AC   AAX03162;
XX
```

```
DT   30-MAR-1999  (first entry)
XX
DE   Nucleic acid encoding canine interleukin 12.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
FT                   /product= "interleukin_12"
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP002031.
XX
PR   16-MAY-1997;   97JP-00127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   P-PSDB; AAW84373.
XX
PT   New therapeutic and prophylactic agents - comprise genetically-engineered
PT   canine interleukin 12, used to treat, e.g. canine and feline
PT   immunological diseases.
XX
PS   Claim 1; Page 30-32; 45pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin 12 (IL-12) protein. The
CC   IL-12 protein can be used in therapeutic or prophylactic agents. The
CC   agents can be used to prevent and treat canine and feline immunological
CC   diseases including dog and cat tumours, skin diseases, viral infections
CC   and allergic diseases, especially tumours, breast tumour, oesinophilic
CC   granuloma, epidermoid tumour, skin tumour, lipoma, othematoma,
CC   pneumonoedema, skin soft pedicled soft tumour and anal tumour; skin
CC   diseases, otitis externa, dermatitis, eczema, fungal diseases of the
CC   skin, pyoderma, allergic dermatitis, nettle rash, traumatic dermatitis
CC   and hair loss; infections; dog Parvovirus infection and distemper virus,
CC   cat plaque virus infection and feline leukaemia, and allergic diseases,
CC   e.g. pollinosis
XX
SQ   Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 41
AAX03152
ID   AAX03152 standard; cDNA to mRNA; 990 BP.
XX
AC   AAX03152;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Nucleic acid encoding canine interleukin 12.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
FT                   /product= "interleukin_12"
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP002031.
XX
PR   16-MAY-1997;   97JP-00127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   P-PSDB; AAW84371.
XX
PT   New therapeutic and prophylactic agents - comprise genetically-engineered
PT   canine interleukin 12, used to treat, e.g. canine and feline
PT   immunological diseases.
XX
PS   Claim 1; Page 23-25; 45pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin 12 (IL-12) protein. The
CC   IL-12 protein can be used in therapeutic or prophylactic agents. The
CC   agents can be used to prevent and treat canine and feline immunological
CC   diseases including dog and cat tumours, skin diseases, viral infections
CC   and allergic diseases, especially tumours, breast tumour, oesinophilic
CC   granuloma, epidermoid tumour, skin tumour, lipoma, othematoma,
CC   pneumonoedema, skin soft pedicled soft tumour and anal tumour; skin
CC   diseases, otitis externa, dermatitis, eczema, fungal diseases of the
CC   skin, pyoderma, allergic dermatitis, nettle rash, traumatic dermatitis
CC   and hair loss; infections; dog Parvovirus infection and distemper virus,
CC   cat plaque virus infection and feline leukaemia, and allergic diseases,
CC   e.g. pollinosis
XX
SQ   Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 42
AAX35625
```

```
ID   AAX35625 standard; cDNA to mRNA; 990 BP.
XX
AC   AAX35625;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-00133345.
XX
PR   16-MAY-1997;   97JP-00127690.
PR   07-AUG-1997;   97JP-00213755.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   P-PSDB; AAY02342.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) - for
PT   prevention and treatment of dog and cat immune diseases.
XX
PS   Claim 1; Page 14-15; 16pp; Japanese.
XX
CC   The present sequence encodes canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment of dog
CC   and cat immune diseases. The treatment used an agent comprising dog IL-12
CC   (CaIL12) proteins to form a heterodimer. The agent is useful for
CC   preventing and treating dog and cat immune diseases, including tumours,
CC   skin diseases, infectious diseases and allergic diseases
XX
SQ   Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 43
AAX35615
ID   AAX35615 standard; cDNA to mRNA; 990 BP.
XX
AC   AAX35615;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-00133345.
XX
PR   16-MAY-1997;   97JP-00127690.
PR   07-AUG-1997;   97JP-00213755.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   P-PSDB; AAY02339.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) - for
PT   prevention and treatment of dog and cat immune diseases.
XX
PS   Claim 1; Page 12; 16pp; Japanese.
XX
CC   The present sequence encodes canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment of dog
CC   and cat immune diseases. The treatment used an agent comprising dog IL-12
CC   (CaIL12) proteins to form a heterodimer. The agent is useful for
CC   preventing and treating dog and cat immune diseases, including tumours,
CC   skin diseases, infectious diseases and allergic diseases
XX
SQ   Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 44
AAI64378
ID   AAI64378 standard; DNA; 990 BP.
XX
AC   AAI64378;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine coding sequence #1.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
FT                   /product= "Canine protein #1"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .987
FT                   /*tag=  c
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-00292946.
```

```
XX
PR   01-OCT-1999;   99JP-00281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   P-PSDB; AAG66480.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian.
XX
PS   Claim 6; Page 14; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention
XX
SQ   Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 4;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 45
AAI64388
ID   AAI64388 standard; DNA; 990 BP.
XX
AC   AAI64388;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine coding sequence #3.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
FT                   /product= "Canine protein #1"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .987
FT                   /*tag=  c
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-00292946.
XX
PR   01-OCT-1999;   99JP-00281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   P-PSDB; AAG66482.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian.
XX
PS   Claim 6; Page 16-17; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention
XX
SQ   Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 4;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 46
ADZ25698
ID   ADZ25698 standard; cDNA; 990 BP.
XX
AC   ADZ25698;
XX
DT   16-JUN-2005  (first entry)
XX
DE   Canine interleukin 12 P40 encoding cDNA SEQ ID NO:3.
XX
KW   interleukin-12; antiviral; gene; ss.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  b
FT                   /product= "interleukin-12 P40"
FT   sig_peptide     1. .66
FT                   /*tag=  a
FT   mat_peptide     67. .987
FT                   /*tag=  c
FT                   /product= "interleukin-12 P40"
XX
PN   JP2003284585-A.
XX
PD   07-OCT-2003.
XX
PF   28-MAR-2002; 2002JP-00090161.
XX
PR   28-MAR-2002; 2002JP-00090161.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2003-885430/82.
DR   P-PSDB; ADZ25702.
XX
PT   Large scale production of interleukin-12 for pharmaceutical applications,
PT   comprises infecting an insect cell with a recombinant virus containing
PT   gene encoding IL-12, and producing IL-12 by carrying out spinner culture
PT   of insect cell.
XX
PS   Example; SEQ ID NO 3; 8pp; Japanese.
XX
CC   The invention related to the large scale production of interleukin-12 (IL
CC   -12), which involves infecting an insect cell with a recombinant virus
```

```
CC   containing a gene encoding IL-12, and producing IL-12 by carrying out
CC   spinner culture of insect cell. The method is useful for producing IL-12,
CC   preferably canine IL-12. IL-12 has pharmaceutical applications. The
CC   present sequence encodes canine IL-12 P40, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 11;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 47
ABK98967
ID   ABK98967 standard; cDNA; 1533 BP.
XX
AC   ABK98967;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1533 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69314.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 83-85; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 446 A; 368 C; 369 G; 350 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 6;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy        597 CTGCCC 602
              ||||||
Db        531 CTGCCC 536


RESULT 48
ABK98968/c
ID   ABK98968 standard; cDNA; 1533 BP.
XX
AC   ABK98968;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1533 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 86-87; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 6;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
```

```
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy        597 CTGCCC 602
              ||||||
Db       1003 CTGCCC 998


RESULT 49
ADV34718/c
ID   ADV34718 standard; DNA; 1533 BP.
XX
AC   ADV34718;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12 complementary DNA, nCaIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 68; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 complementary DNA.
XX
SQ   Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 14;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy        597 CTGCCC 602
              ||||||
Db       1003 CTGCCC 998


RESULT 50
ADV34716
ID   ADV34716 standard; cDNA; 1533 BP.
XX
AC   ADV34716;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12 protein cDNA, nCaIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1533
FT                   /*tag=  a
FT                   /product= "PCaIL-12 511 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34717.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 66; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1533 BP; 446 A; 368 C; 369 G; 350 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 14;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy        597 CTGCCC 602
              ||||||
Db        531 CTGCCC 536


RESULT 51
ABK98965
ID   ABK98965 standard; cDNA; 1599 BP.
XX
AC   ABK98965;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1599 coding strand.
XX
```

KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69313.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 79-80; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1599 BP; 452 A; 392 C; 383 G; 372 T; 0 U; 0 Other;

Query Match 6.7%; Score 66; DB 6; Length 1599;
Best Local Similarity 100.0%; Pred. No. 2.4e-22;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy 597 CTGCCC 602
||||||
Db 597 CTGCCC 602

RESULT 52
ABK98966/c
ID ABK98966 standard; cDNA; 1599 BP.
XX
AC ABK98966;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12-1599 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 82-83; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1599 BP; 372 A; 383 C; 392 G; 452 T; 0 U; 0 Other;

Query Match 6.7%; Score 66; DB 6; Length 1599;
Best Local Similarity 100.0%; Pred. No. 2.4e-22;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy 597 CTGCCC 602
||||||
Db 1003 CTGCCC 998

RESULT 53
ADV34715/c
ID ADV34715 standard; DNA; 1599 BP.
XX
AC ADV34715;
XX
DT 24-FEB-2005 (first entry)
XX
DE Canine single chain IL-12 complementary DNA, nCaIL-12 1599.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Canis familiaris.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.

```
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 63; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 complementary DNA.
XX
SQ   Sequence 1599 BP; 372 A; 383 C; 392 G; 452 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 14;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy        597 CTGCCC 602
              ||||||
Db       1003 CTGCCC 998


RESULT 54
ADV34713
ID   ADV34713 standard; cDNA; 1599 BP.
XX
AC   ADV34713;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12 protein cDNA, nCaIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1599
FT                   /*tag=  a
FT                   /product= "PCaIL-12 533 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34714.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 61; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1599 BP; 452 A; 392 C; 383 G; 372 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 14;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db       597 CTGCCC 602


RESULT 55
AAX18176
ID   AAX18176 standard; cDNA; 2154 BP.
XX
AC   AAX18176;
XX
DT   07-MAY-1999  (first entry)
XX
DE   Canine full length CLAF p40 subunit coding sequence.
XX
KW   CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW   viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW   canine infectious hepatitis; ds.
XX
OS   Canis sp.
XX
PN   WO9855511-A1.
XX
PD   10-DEC-1998.
XX
PF   26-MAY-1998;   98WO-JP002295.
XX
PR   03-JUN-1997;   97JP-00161936.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Tokiyoshi S,  Eda Y;
XX
DR   WPI; 1999-070260/06.
DR   P-PSDB; AAW74322.
XX
PT   Canine cytokine protein which activates canine cytotoxic T lymphocytes -
PT   is useful for treatment of viral and autoimmune diseases in dogs.
XX
PS   Claim 8; Page 30-31; 51pp; Japanese.
XX
CC   This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC   the invention. CLAF activates lymphocytes, especially canine cytotoxic T
CC   cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC   recognising it may be used in the treatment of viral diseases in dogs
CC   (such as canine distemper, canine parvovirus and canine infectious
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CC   hepatitis). The antibodies may also be used in isolation of CLAF from
CC   culture of the transformant host cells by affinity chromatography. The
CC   p40 homodimer can be used for the treatment of autoimmune diseases in
CC   dogs
XX
SQ   Sequence 2154 BP; 663 A; 448 C; 477 G; 566 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 2;  Length 2154;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 650

Qy        597 CTGCCC 602
              ||||||
Db        651 CTGCCC 656


RESULT 56
ABK99006/c
ID   ABK99006 standard; cDNA; 2267 BP.
XX
AC   ABK99006;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p40-2267 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 4; Page 99-100; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 2267 BP; 591 A; 504 C; 468 G; 704 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 6;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1578 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1519

Qy        597 CTGCCC 602
              ||||||
Db       1518 CTGCCC 1513


RESULT 57
ABK99005
ID   ABK99005 standard; cDNA; 2267 BP.
XX
AC   ABK99005;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p40-2267 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69317.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 4; Page 97-98; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 2267 BP; 704 A; 468 C; 504 G; 591 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 6;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        690 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 749

Qy        597 CTGCCC 602
              ||||||
Db        750 CTGCCC 755


RESULT 58
ADV34757
ID   ADV34757 standard; cDNA; 2267 BP.
XX
AC   ADV34757;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p40 protein cDNA, nCaIL-12p40 2267.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             154. .1143
FT                   /*tag=  a
FT                   /product= "PCaIL-12p40 329 protein"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34758.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 107; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p40 subunit protein
CC   encoding cDNA.
XX
SQ   Sequence 2267 BP; 704 A; 468 C; 504 G; 591 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 14;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 749

Qy        597 CTGCCC 602
              ||||||
Db        750 CTGCCC 755


RESULT 59
ADV34759/c
ID   ADV34759 standard; DNA; 2267 BP.
XX
AC   ADV34759;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p40 complementary DNA, nCaIL-12p35 2267.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 109; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p40 subunit
CC   complementary DNA.
XX
SQ   Sequence 2267 BP; 591 A; 504 C; 468 G; 704 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 14;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1578 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1519

Qy        597 CTGCCC 602
              ||||||
Db       1518 CTGCCC 1513


RESULT 60
AAD15206
ID   AAD15206 standard; DNA; 984 BP.
XX
AC   AAD15206;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p40 encoding DNA from clone B1-81.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
```

```
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p40; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .984
FT                   /*tag=  a
FT                   /product= "Modified p40 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .981
FT                   /*tag=  c
FT                   /product= "Mature modified p40 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08599.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 1; Page 137; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p40 protein encoding
CC   DNA
XX
SQ   Sequence 984 BP; 272 A; 254 C; 247 G; 211 T; 0 U; 0 Other;

  Query Match             6.6%;  Score 65;  DB 5;  Length 984;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        451 GATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGT 510
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGT 510

Qy        511 GGAGC 515
              |||||
Db        511 GGAGC 515


RESULT 61
ADT04849
ID   ADT04849 standard; DNA; 1015 BP.
XX
AC   ADT04849;
XX
DT   13-JAN-2005  (first entry)
XX
DE   Canine interleukin-12 (IL-12) p40 DNA.
XX
KW   gene expression; insect; ds; interleukin-12; IL-12.
XX
OS   Canis familiaris.
XX
PN   JP2004290182-A.
XX
PD   21-OCT-2004.
XX
PF   06-FEB-2004; 2004JP-00030183.
XX
PR   10-MAR-2003; 2003JP-00062907.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2004-740760/73.
XX
PT   Novel gene vector for expression in insect useful for expression of
PT   foreign gene such as dog interleukin 12 gene, comprises two promoters.
XX
PS   Claim 4; SEQ ID NO 5; 13pp; Japanese.
XX
CC   The invention relates to a novel gene vector for expression in an insect
CC   comprising at least two promoters, particularly the polyhedrin promoter
CC   and p10 promoter. The vector contains at least two types of foreign
CC   protein expression gene and the gene product of the vector is produced
CC   using a gene recombinant baculovirus, particularly a recombinant silkworm
CC   nuclear polyhedrosis virus. The baculovirus is proliferated in a
CC   silkworm. The vector of the invention may be useful for expression of a
CC   foreign gene, such as canine interleukin 12. Within the vector, two types
CC   of foreign protein expression genes are integrated simultaneously for
CC   their simultaneous expression. The current sequence is that of the canine
CC   interleukin-12 (IL-12) p40 DNA of the invention.
XX
SQ   Sequence 1015 BP; 285 A; 251 C; 254 G; 225 T; 0 U; 0 Other;

  Query Match             6.4%;  Score 63;  DB 13;  Length 1015;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-21;
  Matches   63;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         88 GTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACC 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 GTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACC 147

Qy        148 TGC 150
              |||
Db        148 TGC 150


RESULT 62
AAD15204
ID   AAD15204 standard; DNA; 984 BP.
XX
AC   AAD15204;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p40 encoding DNA from clone B8-96.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p40; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .984
FT                   /*tag=  a
FT                   /product= "Modified p40 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .981
```

```
FT                   /*tag=  c
FT                   /product= "Mature modified p40 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08597.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 1; Page 136; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p40 protein encoding
CC   DNA
XX
SQ   Sequence 984 BP; 270 A; 249 C; 259 G; 206 T; 0 U; 0 Other;

  Query Match             6.2%;  Score 61;  DB 5;  Length 984;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-20;
  Matches   61;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        673 ACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTG 732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        673 ACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTG 732

Qy        733 A 733
              |
Db        733 A 733


RESULT 63
AAD15205
ID   AAD15205 standard; DNA; 984 BP.
XX
AC   AAD15205;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p40 encoding DNA from clone B2-52.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p40; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .984
FT                   /*tag=  a
FT                   /product= "Modified p40 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .981
FT                   /*tag=  c
FT                   /product= "Mature modified p40 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08598.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 1; Page 136-137; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p40 protein encoding
CC   DNA
XX
SQ   Sequence 984 BP; 267 A; 246 C; 254 G; 217 T; 0 U; 0 Other;

  Query Match             6.1%;  Score 60;  DB 5;  Length 984;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-19;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAAC 723
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAAC 723


RESULT 64
AAD15208
ID   AAD15208 standard; DNA; 975 BP.
XX
AC   AAD15208;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p40 encoding DNA from clone A16-94.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p40; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .975
FT                   /*tag=  a
FT                   /product= "Modified p40 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .972
```

```
FT                   /*tag=  c
FT                   /product= "Mature modified p40 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08601.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 1; Page 137; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p40 protein encoding
CC   DNA
XX
SQ   Sequence 975 BP; 261 A; 250 C; 255 G; 209 T; 0 U; 0 Other;

  Query Match             5.4%;  Score 53;  DB 5;  Length 975;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-16;
  Matches   53;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        895 GTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTA 947
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 GTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTA 926


RESULT 65
AAQ04701
ID   AAQ04701 standard; DNA; 906 BP.
XX
AC   AAQ04701;
XX
DT   25-MAR-2003  (revised)
DT   11-OCT-1990  (first entry)
XX
DE   Sequence encoding natural killer cell stimulatory factor (NKSF).
XX
KW   Natural killer cell stimulatory factor; NKSF; cancer; leukopaenia;
KW   anaemia; radiation; bone marrow transplantation; ds.
XX
OS   Homo sapiens.
XX
PN   WO9005147-A.
XX
PD   17-MAY-1990.
XX
PF   10-NOV-1988;   88US-00269945.
XX
PR   10-NOV-1988;   88US-00269945.
PR   07-FEB-1989;   89US-00307817.
XX
PA   (GEMY ) GENETICS INST INC.
PA   (WIST-) WISTAR INST.
XX
PI   Trinchieri G,  Perussia B,  Kobayashi M,  Clark SC,  Wong GG;
XX
DR   WPI; 1990-178800/23.
DR   P-PSDB; AAR05171.
XX
PT   New natural killer cell stimulatory factor - useful for treating cancer
PT   and e.g. leukopenia, bacterial and viral infections, anaemia and B or T
PT   cell deficiencies.
XX
PS   Claim 16; Page 60; 69pp; English.
XX
CC   Natural killer cell stimulatory factor (NKSF) is useful in treating
CC   cancer and other disease states which respond to NK cell activity. Such
CC   states may arise from immune or haematopoietic-cell deficiency following
CC   a bone marrow translpantation, exposure to radiation and disease.
CC   (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
CC   correct PA field.)
XX
SQ   Sequence 906 BP; 244 A; 220 C; 238 G; 204 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 2;  Length 906;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        693 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 736


RESULT 66
AAD15207
ID   AAD15207 standard; DNA; 969 BP.
XX
AC   AAD15207;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p40 encoding DNA from clone A3-48.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p40; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .969
FT                   /*tag=  a
FT                   /product= "Modified p40 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .966
FT                   /*tag=  c
FT                   /product= "Mature modified p40 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08599.
```

```
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 1; Page 137; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p40 protein encoding
CC   DNA
XX
SQ   Sequence 969 BP; 263 A; 249 C; 251 G; 206 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 5;  Length 969;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        649 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 692


RESULT 67
AAQ12149
ID   AAQ12149 standard; DNA; 979 BP.
XX
AC   AAQ12149;
XX
DT   10-SEP-1991  (first entry)
XX
DE   Cytotoxic lymphocyte maturation factor (40 kD subunit) gene.
XX
KW   Cytotoxic lymphocyte maturation factor; CLMF; probe; antitumour;
KW   monoclonal antibodies; T cell; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             41. .979
FT                   /*tag=  a
FT                   /product= "CLMF"
FT   sig_peptide     41. .106
FT                   /*tag=  b
FT                   /note= "hydrophobic signal peptide"
FT   mat_peptide     107. .979
FT                   /*tag=  c
XX
PN   EP433827-A.
XX
PD   26-JUN-1991.
XX
PF   09-DEC-1990;   90EP-00123670.
XX
PR   22-DEC-1989;   89US-00455708.
PR   09-MAY-1990;   90US-00520935.
PR   27-AUG-1990;   90US-00572284.
XX
PA   (HOFF ) HOFFMANN-LA ROCHE AG.
XX
PI   Chizzonite RA,  Gately MK,  Gubler UA,  Hulmes JD,  Pan YCE;
PI   Podlaski FJ,  Stern AS;
XX
DR   WPI; 1991-186715/26.
DR   P-PSDB; AAR12493.
XX
PT   New cytotoxic lymphocyte maturation factor - used as antitumour agent and
PT   monoclonal antibodies used in transplantation to block proliferation and
PT   activation of cytotoxic T cells.
XX
PS   Disclosure; Fig 25 (a-c); 90pp; English.
XX
CC   The natural CLMF protein is a 75 kD heterodimer comprising two
CC   polypeptide subunits, a 40 kD and a 35 kD subunit (AAQ12150). The
CC   subunits are bonded together via one or more disulfide bonds. The CLMF
CC   can interact with IL-2 to synergistically induce the cytolytic activity
CC   of Lymphokine Activated Killer (LAK) cells. It is also capable of
CC   stimulating T-cell growth. It can be used for the prepn. of LAK- and T-
CC   cell activator and antitumour compsns. and for stimulating Natural Killer
CC   (NK) cells
XX
SQ   Sequence 979 BP; 261 A; 245 C; 257 G; 216 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 2;  Length 979;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        701 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 744


RESULT 68
AAT50759
ID   AAT50759 standard; cDNA; 984 BP.
XX
AC   AAT50759;
XX
DT   17-OCT-2003  (revised)
DT   24-SEP-1997  (first entry)
XX
DE   Sequence of ovine IL-12 40 kD sununit cDNA.
XX
KW   Cytokine; ovine; sheep; interleukin-5; interleukin-12; IL-5; IL-12;
KW   livestock; cow; stress; transport; vaccine adjuvant; veterinary; cancer;
KW   immunosuppression; allergy; reproductive system; growth; early maturity;
KW   antibody; diagnosis; immunopotentiator;
KW   early haematopoietic progenitor cell; cytotoxic cell; thymocyte;
KW   secretion; IgM; IgA; bacterial endotoxin; gamma-interferon; ss.
XX
OS   Ovis aries.
XX
PN   WO9700321-A1.
XX
PD   03-JAN-1997.
XX
PF   14-JUN-1996;   96WO-AU000360.
XX
PR   14-JUN-1995;   95AU-00003502.
PR   27-OCT-1995;   95AU-00006244.
XX
PA   (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
PI   Seow H,  Wood P;
XX
DR   WPI; 1997-077528/07.
DR   P-PSDB; AAW08483.
XX
PT   Nucleic acid encoding ovine interleukin-5 or -12 - used as vaccine
PT   adjuvants and to treat or prevent microbial infections in livestock.
XX
PS   Claim 10; Page 49-51; 78pp; English.
XX
CC   The sequences given in AAT50757-59 encode ovine interleukin-12 (IL-12) 35
CC   kD subunit (partial and full length sequence) and the 40 kD subunit.
CC   Ovine IL-5 or IL-12 are used to treat and/or prevent infections in
CC   livestock (esp. cows and sheep), particularly where the animals are
CC   stressed, e.g. during transport. IL-5 and IL-12 can also be used as
CC   adjuvants in vaccines for veterinary use (partic. weakly immunogenic
CC   subunit or synthetic peptide vaccines). They may also be used to treat
```

```
CC   cancer, immunosuppression and allergy, to enhance/suppress the
CC   reproductive system and to promote growth or early maturity. Optionally
CC   interleukin can be delivered from constructs or delivery cells and
CC   antibodies are useful in enzyme immunoassays for rapid diagnosis of
CC   infection. The interleukins are immunopotentiators, especially IL-5
CC   promotes growth of early haematopoietic progenitor cells and generation
CC   of cytotoxic cells from thymocytes, also it stimulates production and
CC   secretion of IgM and IgA (in synergism with bacterial endotoxin). IL-12
CC   induces production of gamma-interferon by, and proliferation of, T and NK
CC   cells and increases the (non-)specific cytolytic lymphocyte response. The
CC   genetic constructs can also be used for in vitro production of IL-5 or -
CC   12. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ   Sequence 984 BP; 273 A; 243 C; 253 G; 215 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 2;  Length 984;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707


RESULT 69
ADG39430
ID   ADG39430 standard; DNA; 984 BP.
XX
AC   ADG39430;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human CLMF 40 kDa subunit DNA.
XX
KW   human; cytotoxic lymphocyte maturation factor; CLMF;
KW   activated T-cell stimulator; natural killer cell stimulator;
KW   immunoenhancer; antitumour; tumour; cancer; ds; gene.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             67. .984
FT                   /*tag=  a
FT                   /partial
FT                   /product= "CLMF 40 kDa subunit"
FT                   /note= "No start or stop codon given"
XX
PN   US2003204059-A1.
XX
PD   30-OCT-2003.
XX
PF   08-OCT-2002; 2002US-00267565.
XX
PR   22-DEC-1989;   89US-00455708.
PR   09-MAY-1990;   90US-00520935.
PR   27-AUG-1990;   90US-00572284.
PR   24-MAR-1992;   92US-00857023.
PR   02-MAR-1994;   94US-00205011.
PR   02-JUN-1995;   95US-00459151.
PR   22-SEP-1999;   99US-00401839.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CIE SA F.
XX
PI   Gately MK,  Gubler UA,  Hulmes JD,  Podlaski FJ,  Stern AS;
PI   Chizzonite RA,  Pan YE;
XX
DR   WPI; 2004-010534/01.
DR   P-PSDB; ADG39429.
XX
PT   Novel protein comprising cytotoxic lymphocyte maturation factor in
PT   substantially pure form or protein which exhibits cytotoxic lymphocyte
PT   maturation factor activity, useful as antitumor and immunoenhancing
PT   agent.
XX
PS   Claim 17; Page 28-29; 74pp; English.
XX
CC   The invention relates to a protein which comprises a cytotoxic lymphocyte
CC   maturation factor (CLMF). The protein is useful for stimulating activated
CC   T-cells which involves treating T-cells with the protein. The method
CC   further involves treating the activated T-cells with IL2 or its
CC   biologically active fragment. The protein is useful for stimulating
CC   natural killer cells which involves treating the natural killer cells
CC   with the protein. The protein has immunoenhancing and antitumour effects
CC   when used as single therapeutic agent in vivo. The present sequence is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 984 BP; 263 A; 243 C; 258 G; 220 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 12;  Length 984;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 70
ADK98707
ID   ADK98707 standard; DNA; 985 BP.
XX
AC   ADK98707;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human interleukin-12 (IL-12) P40 subunit DNA.
XX
KW   human; recombinant interleukin-12; IL-12; P35 subunit; P40 subunit; ds.
XX
OS   Homo sapiens.
XX
PN   CN1408727-A.
XX
PD   09-APR-2003.
XX
PF   29-SEP-2001; 2001CN-00126923.
XX
PR   29-SEP-2001; 2001CN-00126923.
XX
PA   (ZHON-) ZHONGXIN GUOJIAN PHARM CO LTD SHANGHAI.
XX
PI   Wan G,  Li C;
XX
DR   WPI; 2003-664076/63.
XX
PT   Method for efficiently expressing recombinant human interleukin 12 in
PT   eukaryotic cell.
XX
PS   Example 2; SEQ ID NO 2; 14pp; Chinese.
XX
CC   The invention describes the process of producing human recombinant
CC   interleukin-12 (IL-12) includes: providing a nucleotide sequence
CC   corresponding to the P35 subunit with the first signal peptide and a
CC   nucleotide sequence corresponding to the P40 subunit; inserting the
CC   nucleotide sequences into an expression vector; converting the eukaryotic
CC   cell with the expression vector; and culturing the transfected eukaryotic
CC   cell in condition suitable for recombinant human IL-12 expression. The
CC   process balances the expression amount of both P35 and P40 subunits and
CC   thus raises the expression amount of IL-12 with bioactivity via raising
CC   the expression strength of P35 subunit. This sequence represents the
CC   human interleukin-12 (IL-12) P40 subunit polynucleotide.
XX
SQ   Sequence 985 BP; 264 A; 242 C; 258 G; 221 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 10;  Length 985;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
```

```
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        659 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 702


RESULT 71
AAQ97484
ID   AAQ97484 standard; cDNA; 987 BP.
XX
AC   AAQ97484;
XX
DT   25-MAR-2003  (revised)
DT   22-DEC-1995  (first entry)
XX
DE   Human interleukin-12 40 kD subunit.
XX
KW   Interleukin-12; IL-12; cytokine; gamma-interferon; T cell;
KW   natural killer cell; graft vs. host disease; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .987
FT                   /*tag=  a
XX
PN   WO9519786-A1.
XX
PD   27-JUL-1995.
XX
PF   20-JAN-1995;   95WO-US000879.
XX
PR   21-JAN-1994;   94US-00186529.
XX
PA   (GEMY ) GENETICS INST INC.
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Wolf SF,  Sykes M;
XX
DR   WPI; 1995-269273/35.
DR   P-PSDB; AAR79186.
XX
PT   Control of graft versus host disease using interleukin 12 - partic.
PT   admin. at the time of bone marrow transplant.
XX
PS   Disclosure; Page 21-22; 32pp; English.
XX
CC   AAQ97484 and AAQ97485 are from human lymphoblast cell line RMPI 8866. IL-
CC   12 is a heterodimeric cytokine which was originally identified as a
CC   factor which induces gamma-interferon from T cells and natural killer
CC   cells as set forth in PCT/US91/06332, published April 2 1992, and
CC   incorporated by reference. EP 433827, published June 26 1991, disclosed
CC   IL-12 as a cytotoxin lymphocyte maturation factor. In the patent, IL-12
CC   is defined as a heterodimeric glycoprotein comprised of two covalently
CC   linked subunits having mol. wts of about 40 kD and 35 kD. The two
CC   subunits may be disulfide-bonded. IL-12 is administered to prevent or
CC   ameliorate GVHD. Dosage is 1 ng-0.1 mg (esp. 1.0 ng-1 microg)/kg daily
CC   for 3 days, the first dose given 1 hr. after transplant. IL-12 can be
CC   used as the native heterodimer or as subunits. (Updated on 25-MAR-2003 to
CC   correct PN field.)
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 72
AAV07273
ID   AAV07273 standard; cDNA; 987 BP.
XX
AC   AAV07273;
XX
DT   25-SEP-1998  (first entry)
XX
DE   Human Interleukin-12 p40 gene.
XX
KW   IL-12 subunit; expression construct; treatment; asthma;
KW   microbial infection; viral infection; cancer; Human; Interleukin; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .987
FT                   /*tag=  a
FT                   /product= "IL-12 p40"
XX
PN   WO9817689-A2.
XX
PD   30-APR-1998.
XX
PF   10-OCT-1997;   97WO-US018779.
XX
PR   18-OCT-1996;   96US-0028676P.
XX
PA   (GENE-) GENEMEDICINE INC.
XX
PI   Nordstrom J,  Freimark B,  Deshpande D;
XX
DR   WPI; 1998-261428/23.
DR   P-PSDB; AAW51311.
XX
PT   Constructs for expression of interleukin-12 sub-units - are used for
PT   delivery of IL-12 sub-units for treating e.g. asthma, microbial or viral
PT   infections and certain cancers.
XX
PS   Claim 1; Page 34; 80pp; English.
XX
CC   The IL-12 subunits AAV07273 and AAV07274 can be expressed using an
CC   appropriate expression construct engineered into a plasmid. The plasmids
CC   can provide for efficient expression of IL-12 subunits. The products can
CC   be used for the treatment of asthma, microbial and viral infections and
CC   certain cancers
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 73
AAV07217
ID   AAV07217 standard; DNA; 987 BP.
XX
AC   AAV07217;
XX
DT   12-AUG-1998  (first entry)
XX
DE   DNA encoding human interleukin-12 40kDa subunit.
XX
KW   Interleukin-12; IL-12; graft-versus-host disease;
KW   GVHD. bone marrow transplantation; graft-versus-leukemia; ss.
XX
OS   Homo sapiens.
XX
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FH   Key             Location/Qualifiers
FT   CDS             1. .987
FT                   /*tag= a
FT                   /product= "Interleukin-12_40kDa_subunit"
XX
PN   US5756085-A.
XX
PD   26-MAY-1998.
XX
PF   30-APR-1996;   96US-00640386.
XX
PR   21-JAN-1994;   94US-00186529.
XX
PA   (GEMY ) GENETICS INST INC.
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Sykes M,  Wolf SF;
XX
DR   WPI; 1998-321459/28.
DR   P-PSDB; AAW51221.
XX
PT   Therapy of graft-versus-host disease - by administration of interleukin-
PT   12 to maintain and/or promote graft-versus-leukaemia effects.
XX
PS   Disclosure; Col 17-20; 20pp; English.
XX
CC   The invention relates to a method for the treatment or prevention of
CC   graft-versus-host disease (GVHD) which comprises the administration of
CC   interleukin-12 (IL-12) at the time of bone-marrow transplantation to
CC   maintain or promote graft-versus-leukaemia effects. Preferably, dosage is
CC   0.001-100 (preferably 1-100) mu g/kg for 3 days starting on the day of
CC   the bone marrow transplant. IL-12 is administered daily until there is an
CC   improvement in the condition. Administration is oral, cutaneous,
CC   subcutaneous, intravenous or by inhalation preferably subcutaneous, or
CC   intravenous. The present sequence encodes the human interleukin-12 40kDa
CC   subunit
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 74
AAZ40404
ID   AAZ40404 standard; DNA; 987 BP.
XX
AC   AAZ40404;
XX
DT   15-FEB-2000  (first entry)
XX
DE   Human interleukin 12 p40 subunit wild type coding sequence.
XX
KW   Wild type; human; interferon-alpha; plasmid; cytomegalovirus; CMV;
KW   promoter; growth hormone; untranslated region; UTR; mammal; disease;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9947678-A2.
XX
PD   23-SEP-1999.
XX
PF   12-MAR-1999;   99WO-US005394.
XX
PR   19-MAR-1998;   98US-0078654P.
XX
PA   (GENE-) GENEMEDICINE INC.
XX
PI   Nordstrom J,  Pericle F,  Rolland A,  Ralston R;
XX
DR   WPI; 1999-562116/47.
DR   P-PSDB; AAY42487.
XX
PT   New plasmids containing an interferon-alpha coding sequence, used for the
PT   treatment of a mammalian condition or disease, particularly cancer.
XX
PS   Claim 11; Page 43-45; 137pp; English.
XX
CC   This sequence represents the wild type coding region for the human
CC   interleukin 12 p40 subunit. The invention relates to a novel plasmid
CC   comprising a cytomegalovirus (CMV) promoter transcriptionally linked with
CC   an interferon alpha (IFN-alpha) coding sequence, and a growth hormone 3'-
CC   untranslated region (UTR). The plasmids can be used for treating a
CC   mammalian condition or disease, particularly cancer
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 75
AAV83199
ID   AAV83199 standard; DNA; 987 BP.
XX
AC   AAV83199;
XX
DT   02-MAR-1999  (first entry)
XX
DE   Interleukin (IL)-12B cDNA.
XX
KW   Mouse; immunodeficient; pathogen; tumour; lymphocyte; antigen;
KW   immunomodulator; vector; vaccine; cancer; HIV; Leishmania; Mycobacterium;
KW   Listeria; Plasmodium; retrovirus; evaluation;
KW   human immunodeficiency virus; ds.
XX
OS   Homo sapiens.
XX
PN   WO9844788-A2.
XX
PD   15-OCT-1998.
XX
PF   09-APR-1998;   98WO-US006944.
XX
PR   09-APR-1997;   97US-00838702.
PR   01-MAY-1997;   97US-00848760.
PR   09-DEC-1997;   97US-0069163P.
XX
PA   (CHAN/) CHANG L.
XX
PI   Chang L;
XX
DR   WPI; 1999-024005/02.
XX
PT   Use of immunodeficient mice comprising human cells - particularly
PT   SCTD/beige mice comprising human immune cells for evaluating vaccines
PT   against cancers or human pathogens, e.g. HIV.
XX
PS   Example 10(c)(i); Page 110; 154pp; English.
XX
CC   Immunodeficient mice comprising human cells can be used for exposure to
CC   human pathogens and/or their components or human tumour cells and human
CC   peripheral blood lymphocytes. Also claimed is a vaccine comprising a cell
CC   modified to express an antigen and an immune-modulating protein, this is
CC   preferably an expression vector comprising a polynucleotide sequence that
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CC   encodes the antigen and immune-modulating protein. Such vectors can be
CC   used to treat a subject having a tumour by transferring the expression
CC   vector into the tumour so that the antigen and the immune-modulator are
CC   expressed by at least the tumour. The methods can be used for producing
CC   and evaluating vaccines including cancer vaccines and vaccines directed
CC   against human pathogens, e.g. HIV, Leishmania, Mycobacterium, Listeria or
CC   Plasmodium. Two primers (AAV83197, AAV83198) were used to amplify the IL-
CC   12B for insertion into expression vectors of the invention
XX
SQ   Sequence 987 BP; 264 A; 245 C; 257 G; 221 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 76
AAD15210
ID   AAD15210 standard; DNA; 987 BP.
XX
AC   AAD15210;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Human cytokine p40 DNA.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p40; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .987
FT                   /*tag=  a
FT                   /product= "p40 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .984
FT                   /*tag=  c
FT                   /product= "Mature p40 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08603.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 5; Page 142; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is human p40 protein encoding DNA
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 5;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 77
ACC47592
ID   ACC47592 standard; DNA; 987 BP.
XX
AC   ACC47592;
XX
DT   12-JUN-2003  (first entry)
XX
DE   Human interleukin 12 (hIL-12) P40 subunit gene.
XX
KW   Human; interleukin 12; hIL-12; baculovirus vector;
KW   recombinant production; AcNPV-hIL12;
KW   Autographa california nuclear polyhedrosis virus; tumour; cancer;
KW   infection; bacterial; viral; cytostatic; P40 subunit; gene; ds.
XX
OS   Homo sapiens.
XX
PN   CN1357622-A.
XX
PD   10-JUL-2002.
XX
PF   02-NOV-2001; 2001CN-00133631.
XX
PR   02-NOV-2001; 2001CN-00133631.
XX
PA   (UYWU-) UNIV WUHAN.
XX
PI   Meng X,  Xu J,  Yu Z;
XX
DR   WPI; 2002-741792/81.
XX
PT   Human interleukin-12 recombinant insect virus strain and its preparation.
XX
PS   Claim 5; Fig 7; 17pp; Chinese.
XX
CC   The invention relates to a recombinant baculovirus comprising DNA
CC   encoding human interleukin 12 (hIL-12) and methods for its preparation.
CC   The recombinant baculovirus strain is designated Autographa california
CC   nuclear polyhedrosis virus AcNPV-hIL12 (CCTCC No. 2 V200108). This strain
CC   contains two human IL-12 subunit genes, the IL-12 P35 subunit gene
CC   (ACC47589) and the IL-12 P40 subunit gene (ACC47592) which are
CC   respectively under the control of the viral polyhedrin and P10 promoters.
CC   The baculovirus can be used in the recombinant production of human IL-12
CC   which is suitable for treating tumours and bacterial, viral and other
CC   infections. The present sequence represents the human IL-12 P40 subunit
CC   gene used in construction of the baculovirus vector of the invention
XX
SQ   Sequence 987 BP; 264 A; 245 C; 257 G; 221 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 6;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704
```

```
RESULT 78
ADF77276
ID   ADF77276 standard; DNA; 987 BP.
XX
AC   ADF77276;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human IL-12 p40 subunit DNA.
XX
KW   ds; human; interferon alpha expression plasmid; tumour; IL-12.
XX
OS   Homo sapiens.
XX
PN   US2003181405-A1.
XX
PD   25-SEP-2003.
XX
PF   29-APR-2002; 2002US-00136837.
XX
PR   12-MAR-1999;   99US-00268135.
XX
PA   (NORD/) NORDSTROM J L.
PA   (PERI/) PERICLE F.
PA   (ROLL/) ROLLAND A.
PA   (RALS/) RALSTON R O.
XX
PI   Nordstrom JL,  Pericle F,  Rolland A,  Ralston RO;
XX
DR   WPI; 2004-020834/02.
XX
PT   A mammalian interferon alpha expression plasmid is useful in gene therapy
PT   to deliver interferon alpha to cells to modulate tumor activity in the
PT   treatment of cancer.
XX
PS   Disclosure; Page 14-15; 65pp; English.
XX
CC   The invention relates to a mammalian interferon alpha expression plasmid,
CC   comprising a promoter and a synthetic 5' intron transcriptionally linked
CC   with an interferon alpha coding sequence and a 3' untranslated region.
CC   The mammalian interferon alpha expression plasmid is useful for treating
CC   tumour growth. The present sequence is used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 987 BP; 264 A; 243 C; 258 G; 221 T; 0 U; 1 Other;

  Query Match             4.5%;  Score 44;  DB 12;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 79
ADO07653
ID   ADO07653 standard; DNA; 987 BP.
XX
AC   ADO07653;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Human interleukin-12 40kDa coding sequence.
XX
KW   cytostatic; virucide; anti-HIV; hepatotropic; neuroprotective;
KW   immunostimulant; expression cassette; viral vector; interleukin-12;
KW   co-stimulatory protein; cancer; infection; ds; gene; human.
XX
OS   Homo sapiens.
XX
PN   WO2004035799-A2.
XX
PD   29-APR-2004.
XX
PF   10-OCT-2003; 2003WO-EP011252.
XX
PR   11-OCT-2002; 2002DE-01048141.
XX
PA   (UYHA-) UNIV HAMBURG-EPPENDORF KLINIKUM.
XX
PI   Waehler R,  Schnieders F;
XX
DR   WPI; 2004-357221/33.
XX
PT   Viral vector that expresses single-chain interleukin-12 and costimulator,
PT   useful for treatment of tumors, viral infections, e.g. human
PT   immunodeficiency virus, and prion diseases.
XX
PS   Claim 4; Fig 19; 129pp; German.
XX
CC   The present invention relates to a viral vector that includes a nucleic
CC   acid encoding a single-chain interleukin-12 (IL-12) and a co-stimulatory
CC   protein. Viral vectors and virus particles derived from them are useful
CC   for treatment of tumours, infectious diseases (e.g. HIV, hepatitis A, B
CC   or C, cytomegalovirus or human papilloma virus), or prion diseases. The
CC   present sequence is a human interleukin-12 coding sequence used in the
CC   exemplification of the invention.
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 12;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 80
ADS00006
ID   ADS00006 standard; DNA; 987 BP.
XX
AC   ADS00006;
XX
DT   16-DEC-2004  (first entry)
XX
DE   Human interleukin-23 (IL-23) p40 subunit DNA.
XX
KW   tumour; interleukin-23; IL-23; cytostatic; immunostimulant; cancer;
KW   p40 subunit; ds; gene.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .987
FT                   /*tag=  a
FT                   /product= "Human interleukin-23 (IL-23) p40 subunit
FT                   protein"
XX
PN   JP2004262797-A.
XX
PD   24-SEP-2004.
XX
PF   28-FEB-2003; 2003JP-00052999.
XX
PR   28-FEB-2003; 2003JP-00052999.
XX
PA   (CHIB-) CHIBA PREFECTURE.
XX
DR   WPI; 2004-665614/65.
DR   P-PSDB; ADS00010.
XX
PT   Novel anti-tumor agent comprising interleukin-23 gene, or cell transduced
```

```
PT   with interleukin-23 gene, as active ingredient, useful for activating
PT   anti-tumor immune response and treating tumor.
XX
PS   Disclosure; SEQ ID NO 2; 23pp; Japanese.
XX
CC   The invention relates to a novel anti-tumour agent comprising an
CC   interleukin-23 (IL-23) gene, or a cell transduced with an IL-23 gene, as
CC   an active ingredient. The molecules of the invention demonstrate
CC   cytostatic and immunostimulant activities and may be useful within an
CC   anti-tumour agent which activates an anti-tumour immune response. The
CC   agent is safe when used in cancer treatment, may be combined with other
CC   treatments and induces tumour-specific acquired immunity. The current
CC   sequence is that of the human interleukin-23 (IL-23) p40 subunit DNA of
CC   the invention.
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 13;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 81
ADV42753
ID   ADV42753 standard; cDNA; 987 BP.
XX
AC   ADV42753;
XX
DT   10-MAR-2005  (first entry)
XX
DE   Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 381.
XX
KW   microarray; psychoneuroendocrinimmune; chronic fatigue;
KW   non-insulin dependent diabetes; allergy; immune disorder; inflammation;
KW   cancer; neoplasm; infection; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO2004108899-A2.
XX
PD   16-DEC-2004.
XX
PF   04-JUN-2004; 2004WO-US017686.
XX
PR   04-JUN-2003; 2003US-0475915P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Nicholson A,  Vernon SD;
XX
DR   WPI; 2005-031682/03.
XX
PT   New microarray comprising probes for genes involved in
PT   psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a
PT   condition associated with PNI activity, e.g., inflammatory or infectious
PT   diseases.
XX
PS   Claim 1; SEQ ID NO 381; 254pp; English.
XX
CC   The invention relates to a new microarray which comprises probes for
CC   genes involved in psychoneuroendocrinimmune (PNI) activity. The
CC   microarray is useful in diagnosing a condition associated with PNI
CC   activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
CC   cancer and infection. The present sequence represents a
CC   psychoneuroendocrinimmune gene expressed sequence tag. Note the
CC   specificatio mentions SEQ ID NO of up to 3314 but only sequences up to
CC   SEQ ID NO 1829 are provided.
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 14;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 82
ADW97242
ID   ADW97242 standard; DNA; 987 BP.
XX
AC   ADW97242;
XX
DT   19-MAY-2005  (first entry)
XX
DE   Human p40 gene that inhibits IL-23 immune response Seq 1a.
XX
KW   immune inhibition; transplant rejection; immune disorder;
KW   autoimmune disease; allergy; immunosuppressive; antiallergic; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .987
FT                   /*tag=  a
FT                   /product= "P40 protein"
XX
PN   JP2005060313-A.
XX
PD   10-MAR-2005.
XX
PF   13-AUG-2003; 2003JP-00292937.
XX
PR   13-AUG-2003; 2003JP-00292937.
XX
PA   (CHIB-) CHIBA PREFECTURE.
XX
DR   WPI; 2005-200132/21.
DR   P-PSDB; ADW97244.
XX
PT   Pharmaceutical formulation for inhibiting immune response generated by
PT   interleukin-23 (IL-23) and treating e.g. autoimmune diseases, comprises
PT   p40 molecules or gene encoding p40 molecules.
XX
PS   Claim 3; SEQ ID NO 1; 12pp; Japanese.
XX
CC   This invention relates to a novel pharmaceutical formulation used for
CC   inhibiting the immune response generated by interleukin-23 (IL-23).
CC   Specifically, it refers to a formulation comprising the p40 protein or
CC   the gene encoding this protein thereof. The present invention describes
CC   the p40 gene contained in the form of a viral or non-viral vector that is
CC   capable of expressing and secreting the p40 protein. This vector can be
CC   introduced into a cell such that it can in turn inhibit the immune
CC   response generated by the production of IL-23. Accordingly, this method
CC   is useful for suppressing organ transplant rejection or treating
CC   immunological disorders associated with abnormal immune response with
CC   regard to IL-23. Furthermore, it can be used to treat autoimmune diseases
CC   and allergy. As such, compositions exhibit immunosuppressive and
CC   antiallergic activities. This polynucleotide sequence is the human p40
CC   gene of the invention.
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 14;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704
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RESULT 83
AEB48822
ID   AEB48822 standard; cDNA to mRNA; 987 BP.
XX
AC   AEB48822;
XX
DT   22-SEP-2005  (first entry)
XX
DE   Human interleukin-12 p40 domain coding sequence.
XX
KW   Interleukin-12; cytokine; lymphokine; cancer; tumor; glioblastoma;
KW   neoplasm; neurological disease; cytostatic; therapy; immunoconjugate;
KW   fusion protein; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .987
FT                   /*tag=  b
FT   sig_peptide     1. .66
FT                   /*tag=  a
FT   mat_peptide     67. .984
FT                   /*tag=  c
FT                   /product= "Mature interleukin-12 p40 subunit"
XX
PN   WO2005066348-A2.
XX
PD   21-JUL-2005.
XX
PF   05-JAN-2005; 2005WO-GB000007.
XX
PR   05-JAN-2004; 2004US-0534307P.
XX
PA   (EMDL-) EMD LEXIGEN RES CENT CORP.
PA   (ANTI-) ANTISOMA PLC.
XX
PI   Gillies S,  Lo K,  Lan Y,  Verma R;
XX
DR   WPI; 2005-512669/52.
XX
PT   Novel compound comprising target specific portion having monoclonal
PT   antibody having specificity for oncofetal fibronectin and effector
PT   portion having interleukin-12, useful for treating cancer e.g.
PT   glioblastoma.
XX
PS   Claim 36; SEQ ID NO 10; 83pp; English.
XX
CC   The invention provides a compound comprising a target specific portion
CC   and an effector portion, in which the target specific portion comprises
CC   or consists of a monoclonal antibody having specificity for oncofetal
CC   fibronectin, or its fragment or variant which retains the antigen binding
CC   specificity of the parent monoclonal antibody, and the effector portion
CC   comprises or consists of interleukin-12, or its functional fragment or
CC   variant. The monoclonal antibody binds to a region of oncofetal
CC   fibronectin other than the extra-domain B region. Preferably, the
CC   compound comprises a target specific portion that is capable of binding
CC   to an amino acid sequence present in fibronectin expressed in both fetal
CC   and normal adult tissue, especially the repeat 7 domain of fibronectin,
CC   and is preferably specific for human oncofetal fibronectin. The
CC   monoclonal antibody is preferably a BC1 antibody. The invention also
CC   provides nucleic acids encoding the compounds of the invention and
CC   methods of their use in the production of these compounds, as well as
CC   methods of using the compounds in medicine, especially for the treatment
CC   of cancer in a patient, where the patient is a mammal, preferably a
CC   human, and the patient has a solid tumor. The cancer is a glioblastoma
CC   (claimed) or ovarian, gastric, colorectal or pancreatic cancer. The
CC   present sequence is the coding sequence of the p40 domain of human
CC   interleukin-12. In a claimed compound, the effector portion consists of a
CC   single chain interleukin-12 comprising or consisting of an interleukin-12
CC   p40 domain conjugated to the interleukin-12 and p35 domain AEB48815 via a
CC   disulfide bond. A further claimed compound comprises the p40 sequence
CC   linked by disulfide bond to a fusion protein AEB48818 comprising the BC1
CC   heavy chain fused to human interleukin-12 p35.
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 14;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 84
AAD18585
ID   AAD18585 standard; DNA; 1007 BP.
XX
AC   AAD18585;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human interleukin-12 (IL-12) p40 subunit DNA.
XX
KW   Human; interleukin-12; IL-12; p40 subunit; cytostatic; virucide; AIDS;
KW   Acquired Immune Deficiency Syndrome; immunisation; hepatitis; malaria;
KW   tuberculosis; vaccine; gene therapy; cancer; influenza; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             7. .993
FT                   /*tag=  a
FT                   /product= "Human IL-12p40 subunit protein"
XX
PN   WO200168802-A2.
XX
PD   20-SEP-2001.
XX
PF   15-MAR-2001; 2001WO-KR000408.
XX
PR   15-MAR-2000; 2000KR-00013133.
PR   13-MAR-2001; 2001KR-00012987.
XX
PA   (UYPO-) UNIV POHANG SCI & TECHNOLOGY.
PA   (PROG-) PROGEN CO LTD.
XX
PI   Sung YC,  Lee SH,  Ha SJ,  Song MK,  Chang J;
XX
DR   WPI; 2001-596904/67.
DR   P-PSDB; AAE11198.
XX
PT   Novel human or mouse interleukin (IL)-12p40 subunit mutant genes, that
PT   inhibit secretion of IL-12p40, but normally secrete IL-12p70, useful as
PT   adjuvant for DNA vaccination and gene therapy to AIDS, cancer, malaria.
XX
PS   Claim 1; Page 89-90; 103pp; English.
XX
CC   The invention relates to mutant interleukin (IL)-12p40 subunit genes
CC   which produces highly active human or mouse IL-12p40 sequence. IL-12p40
CC   DNA is useful for DNA immunisation or gene therapy for treating diseases
CC   such as cancer, AIDS, hepatitis C, hepatitis B or influenza, malaria or
CC   tuberculosis, as an therapeutic or prophylactic adjuvant. IL-12p40 DNA
CC   induces immune response by increasing the hydrolysis activity of
CC   cytotoxic T lymphocytes when IL-12p40 subunit gene is injected with the
CC   DNA vaccine, or increasing secretion of interferon (IFN)-gamma from T
CC   helper cells or CD8+ T cells when IL-12p40 subunit gene is injected with
CC   DNA vaccine. IL-12p40 DNA is useful in gene therapy and as a DNA vaccine.
CC   The present sequence is a DNA encoding human Interleukin (IL)-12p40
CC   subunit protein
XX
SQ   Sequence 1007 BP; 270 A; 247 C; 265 G; 225 T; 0 U; 0 Other;
```

```
  Query Match             4.5%;  Score 44;  DB 5;  Length 1007;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        667 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 710


RESULT 85
AAQ67879
ID   AAQ67879 standard; DNA; 1018 BP.
XX
AC   AAQ67879;
XX
DT   25-MAR-2003  (revised)
DT   23-MAR-1995  (first entry)
XX
DE   EPV 42 kD promoter/Human IL-12 p40 subunit expression cassette.
XX
KW   Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant;
KW   murine; interleukin-2; IL-2; pRW825; pmut-1; pBS-SK; pMM151; TK vector;
KW   plasmid; vaccinia; H6 promoter; amplify; primer; antigenic response;
KW   polymerase chain reaction; poxvirus; pSD542; immunological response;
KW   pathogen; human; interferon; IFN; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   promoter        1. .31
FT                   /*tag=  a
FT                   /note= "EPV 42 kD promoter"
FT   CDS             32. .1018
FT                   /*tag=  b
FT                   /product= "Human IL-12 p40"
XX
PN   WO9416716-A1.
XX
PD   04-AUG-1994.
XX
PF   21-JAN-1994;   94WO-US000888.
XX
PR   21-JAN-1993;   93US-00007115.
PR   19-JAN-1994;   94US-00184009.
XX
PA   (VIRO-) VIROGENETICS CORP.
XX
PI   Paoletti E,  Tartaglia J,  Cox WI;
XX
DR   WPI; 1994-263767/32.
XX
PT   Attenuated recombinant virus used for cancer therapy - comprises DNA
PT   encoding cytokine and/or tumour associated antigen.
XX
PS   Example 27; Fig 33; 232pp; English.
XX
CC   The sequences given in AAQ67879-80 are expression cassettes which contain
CC   the p40 and p35 subunits of human interleukin-12 (IL-12) under the
CC   control of the entomopox virus (EPV) promoter and the vaccinia E3L
CC   promoter, respectively. These sequences were used in the construction of
CC   an ALVAC-based recombinant virus containing the genes for the two
CC   subunits of human IL-12. The p40 subunit was amplified using primers
CC   JP202 and JP189 and placed under the control of the entomopox virus (EPV)
CC   42 kD promoter in plasmid PBSHIL12p40II. The p35 subunit was amplified
CC   using primers JP186 and JP201 and placed under the control of the
CC   vaccinia E3L promoter using primers JP218 and JP220. The expression
CC   cassette was isolated and ligated with pBSSK+ generating plasmid
CC   PBSHIL12p35II. The p35 and p40 expression cassettes were excised and
CC   assembled in pBSSK+ to give PBSHIL12 in which the two expression
CC   cassettes are orientated head-to-head relative to each other. The
CC   combination casette containing the poxvirus promoted genes for both IL-12
CC   subunits was excised from PBSHIL12 and cloned in to ALVAC C6 vector
CC   plasmid pC6L to give pC6HIL12. Recombination between this donor plasmid
CC   and ALVAC rescuing virus produced recombinant virus ALVAC+IL12, which
CC   contains both the human IL-12 genes in the C6 locus. The resulting virus
CC   may be used in a composition for inducing an antigenic or immunological
CC   response, ie. for immunisation against pathogens. (Updated on 25-MAR-2003
CC   to correct PN field.)
XX
SQ   Sequence 1018 BP; 283 A; 245 C; 260 G; 230 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 2;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 86
AAZ08510
ID   AAZ08510 standard; DNA; 1018 BP.
XX
AC   AAZ08510;
XX
DT   19-OCT-1999  (first entry)
XX
DE   EPV 42 kDa/human IL-12 P40 expression cassette.
XX
KW   Attenuated recombinant virus; cytokine; tumour associated antigen;
KW   NYVAC recombinant virus; ALVAC recombinant virus; gene therapy; rabies;
KW   cancer; tumour necrosis factor; nuclear phosphoprotein; p53; IL-2; GMCSF;
KW   interleukin; interferon; IFN-gamma; IL-4; melanoma associated antigen;
KW   carcinoembryonic antigen; immunisation; antigenic; poxvirus; influenza;
KW   immunological response; immunotherapy; vaccine; Newcastle Disease; ss.
XX
OS   Synthetic.
OS   pox virus.
OS   Homo sapiens.
OS   Unidentified.
XX
PN   US5942235-A.
XX
PD   24-AUG-1999.
XX
PF   02-JUN-1995;   95US-00458356.
XX
PR   24-DEC-1981;   81US-00334456.
PR   08-DEC-1982;   82US-00446824.
PR   19-JUN-1984;   84US-00622135.
PR   27-AUG-1987;   87US-00090209.
PR   28-AUG-1987;   87US-00090711.
PR   20-OCT-1987;   87US-00110335.
PR   25-APR-1988;   88US-00186054.
PR   23-AUG-1988;   88US-00234390.
PR   14-JUN-1990;   90US-00537882.
PR   14-JUN-1990;   90US-00537890.
PR   16-DEC-1991;   91US-00805567.
PR   03-MAR-1992;   92US-00847977.
PR   06-MAR-1992;   92US-00847951.
PR   04-MAY-1992;   92US-00881995.
PR   22-JUL-1992;   92US-00918278.
PR   20-JAN-1993;   93US-00007115.
PR   19-JAN-1994;   94US-00184009.
PR   14-APR-1994;   94US-00228926.
PR   13-SEP-1994;   94US-00306259.
XX
PA   (HEAL-) HEALTH RES INC.
XX
PI   Paoletti E;
XX
DR   WPI; 1999-493494/41.
XX
PT   Recombinant poxviruses comprising exogenous DNA encoding antigenic
PT   determinants useful in immunotherapy to immunize against cancers and
```

```
PT   other diseases such as influenza, Newcastle Disease and rabies.
XX
PS   Example 27; Fig 33; 163pp; English.
XX
CC   The present invention describes a recombinant poxvirus (I), comprising
CC   exogenous DNA encoding an antigenic determinant of a pathogen which is
CC   then expressed in vivo in infected host cells after administration to a
CC   patient and therefore induces an immunological response. (I) may be used
CC   to vaccinate patients against a wide range of diseases and disorders
CC   depending on the type of antigen encoded by the exogenous DNA. (I) may be
CC   used to vaccinate against diseases such as rabies, influenza and
CC   Newcastle Disease. It is particularly useful for immunising against
CC   cancers. The poxvirus (I) also provides a means of manipulating
CC   lymphocytes and tumour cells for use in cell-based immunotherapeutic
CC   modalities for cancer. (I) also have enhanced safety compared to
CC   unattenuated viruses (attenuation reduces the virulence of the viruses)
CC   and known recombinant poxvirus vaccines. This increased level of safety
CC   reduces the possibility of a 'runaway' infection in the host and reduces
CC   the chance of transmission from vaccinated to unvaccinated individuals
CC   and contamination of the environment. The present sequence represents a
CC   EPV 42 kDa/human IL-12 P40 expression cassette used in the
CC   exemplification of the present invention
XX
SQ   Sequence 1018 BP; 283 A; 245 C; 260 G; 230 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 2;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 87
ADR21886
ID   ADR21886 standard; DNA; 1018 BP.
XX
AC   ADR21886;
XX
DT   04-NOV-2004  (first entry)
XX
DE   EPV 42kDa/human IL-12 expression cassette.
XX
KW   Cytostatic; Vaccine; recombinant poxvirus; nonessential region;
KW   attenuated avipox Virus; carcinoembryonic antigen; B7 protein;
KW   cancer therapy; ds; human; IL-12; EPV 42kDa; expression cassette.
XX
OS   Heliothis armigera entomopoxvirus.
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US6780407-B1.
XX
PD   24-AUG-2004.
XX
PF   15-SEP-2000; 2000US-00663667.
XX
PR   08-MAR-1989;   89US-00320471.
PR   14-FEB-1990;   90US-00478179.
PR   07-JAN-1991;   91US-00638080.
PR   07-MAR-1991;   91US-00666056.
PR   11-JUN-1991;   91US-00713967.
PR   16-DEC-1991;   91US-00805567.
PR   03-MAR-1992;   92US-00847977.
PR   06-MAR-1992;   92US-00847951.
PR   21-JAN-1993;   93US-00007115.
PR   19-JAN-1994;   94US-00184009.
PR   30-AUG-1995;   95US-00521016.
XX
PA   (AVET ) AVENTIS PASTEUR.
XX
PI   Paoletti E,  Tartaglia J,  Cox WI;
XX
DR   WPI; 2004-601998/58.
XX
PT   New recombinant poxvirus which is an attenuated avipox Virus that
PT   expresses an exogenous DNA encoding carcinoembryonic antigen and an
PT   exogenous DNA encoding B7 protein, useful for cancer therapy.
XX
PS   Example 27; SEQ ID NO 194; 181pp; English.
XX
CC   The invention describes a recombinant poxvirus containing exogenous DNA
CC   in a nonessential region of the poxvirus, where the poxvirus is an
CC   attenuated avipox Virus that expresses an exogenous DNA encoding
CC   carcinoembryonic antigen and an exogenous DNA encoding B7 protein. Also
CC   described are: a composition comprising a poxvirus above in admixture
CC   with a carrier; and expressing carcinoembryonic antigen and B7 protein in
CC   vivo comprising administering to a mammal the composition above.
CC   Disclosed are: making recombinant poxvirus defined above; recombinant
CC   poxvirus vaccine having an increased level of safety compared to known
CC   recombinant poxvirus vaccines; and a modified vector for expressing a
CC   gene product in a host. The recombinant poxvirus is useful for providing
CC   a recombinant poxvirus vaccine having an increased level of safety
CC   compared to known recombinant poxvirus vaccines. The recombinant poxvirus
CC   is useful for cancer therapy. This sequence represents a human IL-12
CC   expression cassette used in the creation of NYVAC rescue virus and
CC   canarypox virus vector ALVAC comprising the human IL-12 gene.
XX
SQ   Sequence 1018 BP; 283 A; 245 C; 260 G; 230 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 13;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 88
AAA70709
ID   AAA70709 standard; DNA; 1019 BP.
XX
AC   AAA70709;
XX
DT   15-DEC-2000  (first entry)
XX
DE   Bovine interleukin-12 p40 subunit gene.
XX
KW   Antiinfective; bovine; interleukin 12; IL12; heterodimer; infection; ss.
XX
OS   Bos taurus.
XX
FH   Key             Location/Qualifiers
FT   CDS             12. .995
FT                   /*tag=  a
FT                   /product= "IL-12 p40 subunit"
XX
PN   JP2000157274-A.
XX
PD   13-JUN-2000.
XX
PF   20-NOV-1998;   98JP-00331052.
XX
PR   20-NOV-1998;   98JP-00331052.
XX
PA   (DAUC ) DAIICHI PHARM CO LTD.
XX
DR   WPI; 2000-468201/41.
DR   P-PSDB; AAB15391.
XX
PT   Preparation of bovine interleukin 12 comprising using a vector containing
PT   the gene encoding it, useful for the prevention and treatment of chronic
PT   and opportunistic infections.
XX
```

```
PS   Example 1; Page 8-9; 11pp; Japanese.
XX
CC   The invention relates to a method for the preparation of bovine
CC   interleukin 12 (BoIL12). BoIL12 consists of a heterodimer of p35 and p40
CC   subunits. BoIL12 is produced by introducing into a host cell, recombinant
CC   vectors containing genes encoding the p35 and p40 subunits. This sequence
CC   represents the coding region for the bovine IL12 p40 subunit. Interleukin
CC   12 is used for the prevention and treatment of chronic infections and
CC   opportunistic infections
XX
SQ   Sequence 1019 BP; 273 A; 248 C; 271 G; 227 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 3;  Length 1019;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        675 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 718


RESULT 89
ADP88402
ID   ADP88402 standard; cDNA; 1029 BP.
XX
AC   ADP88402;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human interleukin-12 beta chain coding sequence.
XX
KW   antiinflammatory; antiasthmatic; antiallergic; immunosuppressive;
KW   antibacterial; protozoacide; gene therapy; expression vector;
KW   interleukin; ecdysone-inducible promoter; ss; gene; interleukin-12;
KW   human.
XX
OS   Homo sapiens.
XX
PN   WO2004052929-A2.
XX
PD   24-JUN-2004.
XX
PF   08-DEC-2003; 2003WO-IB006404.
XX
PR   06-DEC-2002; 2002GB-00028465.
XX
PA   (UYBE-) UNIV QUEENS BELFAST.
XX
PI   Vandenbroeck K,  Alloza I;
XX
DR   WPI; 2004-487887/46.
XX
PT   New expression vector comprising DNA encoding a subunit of a dimeric form
PT   of interleukin under transcriptional control of an ecdysone-inducible
PT   promoter, useful in preparing a composition for treating e.g.,
PT   inflammatory disease.
XX
PS   Disclosure; Page 86-87; 87pp; English.
XX
CC   The present invention relates to an expression vector comprising DNA
CC   encoding a subunit of a dimeric form of interleukin under transcriptional
CC   control of an ecdysone-inducible promoter. The expression vector is
CC   useful in preparing a composition for treating a disease having a
CC   pathogenesis which includes endogenous production of cytokine IL-12, IL-
CC   23 or IL-27, e.g., infectious diseases, bacterial, protozoal or virus-
CC   induced inflammation, epithelial airway inflammation such as asthma,
CC   allergic disease, or autoimmune disease such as multiple sclerosis or
CC   inflammatory bowel disease. The present sequence is the coding sequence
CC   of the human interleukin-12 beta chain used in the exemplification of the
CC   invention.
XX
SQ   Sequence 1029 BP; 275 A; 261 C; 267 G; 226 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 12;  Length 1029;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        676 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 719


RESULT 90
AAF76880
ID   AAF76880 standard; DNA; 1389 BP.
XX
AC   AAF76880;
XX
DT   15-MAY-2001  (first entry)
XX
DE   Human p40-IL-2 coding sequence.
XX
KW   Human; p40-IL-2; interleukin-2; IL-2; antiviral; antibacterial;
KW   antifungal; cytostatic; antiparasitic; vaccine; gene therapy;
KW   fusion protein; protein complex; cytokine; immunoglobulin; cancer;
KW   infection; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200110912-A1.
XX
PD   15-FEB-2001.
XX
PF   09-AUG-2000; 2000WO-US021715.
XX
PR   09-AUG-1999;   99US-0147924P.
XX
PA   (LEXI-) LEXIGEN PHARM CORP.
XX
PI   Gillies SD,  Lo KM;
XX
DR   WPI; 2001-191523/19.
XX
PT   Novel multifunctional fusion protein or protein complexes useful for
PT   treating cancer and viral infections, comprise two different cytokine
PT   molecules and a targeting group.
XX
PS   Example 1; Page 75-76; 90pp; English.
XX
CC   The present sequence is given in a specification relating to
CC   multifunctional fusion proteins and protein complexes comprising at least
CC   two different cytokine molecules and a targeting group such as an
CC   immunoglobulin. The fusion proteins and protein complexes are useful for
CC   treating cancers, and bacterial, viral, fungal and parasitic infections.
CC   They are also useful in gene therapy and as vaccines to prevent or treat
CC   various diseases
XX
SQ   Sequence 1389 BP; 413 A; 325 C; 327 G; 324 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 4;  Length 1389;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 91
AAT77849
ID   AAT77849 standard; DNA; 1397 BP.
XX
AC   AAT77849;
XX
DT   25-MAR-2003  (revised)
```

```
DT   18-MAR-1998  (first entry)
XX
DE   40 kDa subunit of human cytotoxic lymphocyte maturation factor DNA.
XX
KW   Cytotoxic lymphocyte maturation factor; CLMF; 40 kDa subunit;
KW   interleukin-2; T-cell growth; antibody; lymphokine activated killer cell;
KW   CLMF bioactivity inhibition; affinity ligand; transplantation;
KW   cytotoxic T cell proliferation; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             41. .1027
FT                   /*tag=  a
XX
PN   EP790255-A2.
XX
PD   20-AUG-1997.
XX
PF   09-DEC-1990;   97EP-00104656.
XX
PR   22-DEC-1989;   89US-00455708.
PR   09-MAY-1990;   90US-00520935.
PR   27-AUG-1990;   90US-00572284.
PR   09-DEC-1990;   90EP-00123670.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Chizzonite RA,  Gately MK,  Gubler UA,  Hulmes JD,  Pan YE;
PI   Podlanski FJ,  Stern AS;
XX
DR   WPI; 1997-404698/38.
DR   P-PSDB; AAW24235.
XX
PT   Antibodies to cytotoxic lymphocyte maturation factor protein - useful as
PT   affinity ligands, assay reagents and medicaments.
XX
PS   Disclosure; Fig 25; 80pp; English.
XX
CC   The present DNA sequence encodes the 40 kDa subunit of cytotoxic
CC   lymphocyte maturation factor (CLMF) protein. The natural CLMF protein is
CC   a 75 kDa heterodimer, where the 2 subunits (see AAT77850 for the 35 kDa
CC   subunit) are bonded together via one or more disulphide bonds. CLMF
CC   protein is produced by a human B lyphoblastoid cell line. CLMF
CC   synergistically induces, in the presence of interleukin-2, the cytolytic
CC   activity of lymphokine activated killer cells. CLMF is also capable of
CC   stimulating T-cell growth. A novel antibody directed against an epitope
CC   of CLMF protein (see AAW24237 for epitope) is capable of neutralising
CC   and/or inhibiting CLMF bioactivity. This antibody may be used as an
CC   affinity ligand for purifying the CLMF protein. The antibody can also be
CC   used as an assay reagent for detecting the CLMF protein, and as a
CC   medicament for selectively blocking the proliferation and activation of
CC   cytotoxic T cells, e.g. in transplantation. (Updated on 25-MAR-2003 to
CC   correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 1397 BP; 390 A; 307 C; 333 G; 367 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 2;  Length 1397;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        701 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 744


RESULT 92
AAT97969
ID   AAT97969 standard; DNA; 1397 BP.
XX
AC   AAT97969;
XX
DT   25-MAR-2003  (revised)
DT   18-MAR-1998  (first entry)
XX
DE   40 kDa subunit of human cytotoxic lymphocyte maturation factor DNA.
XX
KW   Cytotoxic lymphocyte maturation factor; CLMF; 40 kDa subunit;
KW   interleukin-2; T-cell growth; antibody; lymphokine activated killer cell;
KW   CLMF bioactivity inhibition; affinity ligand; transplantation;
KW   cytotoxic T cell proliferation; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             41. .1027
FT                   /*tag=  a
XX
PN   EP790308-A1.
XX
PD   20-AUG-1997.
XX
PF   09-DEC-1990;   97EP-00104682.
XX
PR   22-DEC-1989;   89US-00455708.
PR   09-MAY-1990;   90US-00520935.
PR   27-AUG-1990;   90US-00572284.
PR   09-DEC-1990;   90EP-00123670.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Chizzonite RA,  Gately MK,  Gubler UA,  Hulmes JD,  Pan YE;
PI   Podlanski FJ,  Stern AS;
XX
DR   WPI; 1997-404733/38.
DR   P-PSDB; AAW36939.
XX
PT   Sub-unit of cytotoxic lymphocyte maturation factor protein - useful for
PT   producing protein and as antitumour agent.
XX
PS   Disclosure; Fig 25; 83pp; English.
XX
CC   The present DNA sequence encodes a 40 kDa subunit of cytotoxic lymphocyte
CC   maturation factor (CLMF) protein. The natural CLMF protein is a 75 kDa
CC   heterodimer, where the 2 subunits (see AAT97970 for the 35 kDa subunit)
CC   are bonded together via one or more disulphide bonds. CLMF protein is
CC   produced by a human B lyphoblastoid cell line. CLMF synergistically
CC   induces, in the presence of interleukin-2, the cytolytic activity of
CC   lymphokine activated killer cells. CLMF is also capable of stimulating T-
CC   cell growth. The subunits may be used for preparing the CLMF protein and
CC   for preparing medicants for antitumour therapy. (Updated on 25-MAR-2003
CC   to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 1397 BP; 390 A; 307 C; 333 G; 367 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 2;  Length 1397;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        701 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 744


RESULT 93
AAV00401
ID   AAV00401 standard; DNA; 1397 BP.
XX
AC   AAV00401;
XX
DT   25-MAR-2003  (revised)
DT   18-MAR-1998  (first entry)
XX
DE   40 kDa subunit of human cytotoxic lymphocyte maturation factor DNA.
XX
KW   Cytotoxic lymphocyte maturation factor; CLMF; 40 kDa subunit;
```

```
KW   interleukin-2; T-cell growth; antibody; lymphokine activated killer cell;
KW   CLMF bioactivity inhibition; affinity ligand; transplantation;
KW   cytotoxic T cell proliferation; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             41. .1027
FT                   /*tag=  a
XX
PN   EP790309-A1.
XX
PD   20-AUG-1997.
XX
PF   09-DEC-1990;   97EP-00104860.
XX
PR   22-DEC-1989;   89US-00455708.
PR   09-MAY-1990;   90US-00520935.
PR   27-AUG-1990;   90US-00572284.
PR   09-DEC-1990;   90EP-00123670.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Chizzonite RA,  Gately MK,  Gubler UA,  Hulmes J,  Pan YE;
PI   Podlanski FJ,  Stern AS,  Witte H;
XX
DR   WPI; 1997-404734/38.
DR   P-PSDB; AAW36941.
XX
PT   Sub-unit of cytotoxic lymphocyte maturation factor protein - useful for
PT   producing CLMF protein and as an antitumour agent.
XX
PS   Disclosure; Fig 25; 83pp; English.
XX
CC   The present DNA sequence encodes a novel 40 kDa subunit of cytotoxic
CC   lymphocyte maturation factor (CLMF) protein. The natural CLMF protein is
CC   a 75 kDa heterodimer, where the 2 subunits (see AAV00402 for the 35 kDa
CC   subunit) are bonded together via one or more disulphide bonds. CLMF
CC   protein is produced by a human B lyphoblastoid cell line. CLMF
CC   synergistically induces, in the presence of interleukin-2, the cytolytic
CC   activity of lymphokine activated killer cells. CLMF is also capable of
CC   stimulating T-cell growth. The subunits may be used for preparing the
CC   CLMF protein and for preparing medicants for antitumour therapy. (Updated
CC   on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC   PR field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 1397 BP; 390 A; 307 C; 333 G; 367 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 2;  Length 1397;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        701 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 744


RESULT 94
AAV37767
ID   AAV37767 standard; cDNA; 1397 BP.
XX
AC   AAV37767;
XX
DT   17-SEP-1998  (first entry)
XX
DE   Cytotoxic lymphocyte maturation factor 40 kD subunit encoding cDNA.
XX
KW   Cytotoxic lymphocyte maturation factor; CLMF; cytokine; synergize;
KW   interleukin 2; IL-2; human; lymphoblastoid cell; detection; purifying;
KW   proliferation; cytotoxic T cell; transplantation; antibody; ss.
XX
OS   Homo sapiens.
XX
```

```
FH   Key             Location/Qualifiers
FT   CDS             41. .1027
FT                   /*tag=  a
FT                   /product= "CLMF 40 kD subunit"
XX
PN   US5780597-A.
XX
PD   14-JUL-1998.
XX
PF   02-JUN-1995;   95US-00460061.
XX
PR   22-DEC-1989;   89US-00455708.
PR   09-MAY-1990;   90US-00520935.
PR   27-AUG-1990;   90US-00572284.
PR   24-MAR-1992;   92US-00857023.
PR   02-MAR-1994;   94US-00205011.
XX
PA   (HOFF ) HOFFMANN LA ROCHE INC.
XX
PI   Podlaski FJ,  Stern AS,  Gately MK,  Pan YE,  Hulmes JD;
PI   Chizzonite RA,  Gubler UA;
XX
DR   WPI; 1998-413150/35.
DR   P-PSDB; AAW58725.
XX
PT   New antibodies to cytotoxic lymphocyte maturation factor - useful for
PT   detecting, purifying, and/or blocking proliferation and activation of
PT   cytotoxic T cells, such as in transplantation(s).
XX
PS   Example 10; Fig 25; 71pp; English.
XX
CC   An isolated antibody has been developed which binds specifically to
CC   cytotoxic lymphocyte maturation factor (CLMF) and neutralises CLMF
CC   induced proliferation by more than 50% in a CLMF dependent T cell growth
CC   assay and/or inhibits binding of at least 60% of the factor to
CC   phytohaemagglutinin (PHA) activated peripheral blood lymphocyte (PBL)
CC   blasts as determined in a CLMF receptor binding assay. CLMF is a
CC   heterodimeric protein having a molecular weight band of 75 kD, determined
CC   by sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE)
CC   under non-reducing and/or reducing conditions, providing a first subunit
CC   having a molecular weight band of 40 kD and a second subunit having a
CC   molecular weight of 35 kD. The present sequence encodes the CLMF 40 kD
CC   subunit, from an example of the present invention. The antibody can be
CC   used for the purification and/or detection of CLMF. It is also used in
CC   therapeutic treatments which require selective blocking of proliferation
CC   and activation of cytotoxic T cells (CTLs) such as in transplantation
XX
SQ   Sequence 1397 BP; 390 A; 309 C; 333 G; 365 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 2;  Length 1397;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        701 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 744


RESULT 95
ADG39387
ID   ADG39387 standard; DNA; 1397 BP.
XX
AC   ADG39387;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human cytotoxic lymphocyte maturation factor, CLMF, 40 kDa subunit DNA.
XX
KW   ds; gene; human; cytotoxic lymphocyte maturation factor; CLMF;
KW   activated T-cell stimulator; natural killer cell stimulator;
KW   immunoenhancer; antitumour; tumour; cancer.
XX
OS   Homo sapiens.
```

```
XX
FH   Key             Location/Qualifiers
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FT                   /*tag=  a
FT                   /product= "CLMF 40 kDa subunit"
XX
PN   US2003204059-A1.
XX
PD   30-OCT-2003.
XX
PF   08-OCT-2002; 2002US-00267565.
XX
PR   22-DEC-1989;   89US-00455708.
PR   09-MAY-1990;   90US-00520935.
PR   27-AUG-1990;   90US-00572284.
PR   24-MAR-1992;   92US-00857023.
PR   02-MAR-1994;   94US-00205011.
PR   02-JUN-1995;   95US-00459151.
PR   22-SEP-1999;   99US-00401839.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CIE SA F.
XX
PI   Gately MK,  Gubler UA,  Hulmes JD,  Podlaski FJ,  Stern AS;
PI   Chizzonite RA,  Pan YE;
XX
DR   WPI; 2004-010534/01.
DR   P-PSDB; ADG39388.
XX
PT   Novel protein comprising cytotoxic lymphocyte maturation factor in
PT   substantially pure form or protein which exhibits cytotoxic lymphocyte
PT   maturation factor activity, useful as antitumor and immunoenhancing
PT   agent.
XX
PS   Disclosure; Fig 25; 74pp; English.
XX
CC   The invention relates to a protein which comprises a cytotoxic lymphocyte
CC   maturation factor (CLMF). The protein is useful for stimulating activated
CC   T-cells which involves treating T-cells with the protein. The method
CC   further involves treating the activated T-cells with IL2 or its
CC   biologically active fragment. The protein is useful for stimulating
CC   natural killer cells which involves treating the natural killer cells
CC   with the protein. The protein has immunoenhancing and antitumour effects
CC   when used as single therapeutic agent in vivo. The present sequence is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 1397 BP; 390 A; 309 C; 333 G; 365 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 12;  Length 1397;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 96
ADO03758
ID   ADO03758 standard; cDNA; 1397 BP.
XX
AC   ADO03758;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human CLMF 40kDa subunit cDNA.
XX
KW   pharmaceutical composition; T cell growth factor assay; cytokine;
KW   cytokine lymphocyte maturation factor; CLMF; interleukin-12; IL-12;
KW   NC-37 B lymphoblastoid cell; T-cell growth stimulator; human; gene; ss;
KW   40 kDa subunit.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             41. .1027
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FT                   /product= "CLMF 40 kDa subunit"
FT                   /note= "Cytotoxic Lymphocyte Maturation Factor"
FT   sig_peptide     41. .106
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FT   mat_peptide     107. .1024
FT                   /*tag=  c
FT                   /note= "Mature CLMF 40 kDa subunit"
XX
PN   US6683046-B1.
XX
PD   27-JAN-2004.
XX
PF   02-JUN-1995;   95US-00459151.
XX
PR   22-DEC-1989;   89US-00455708.
PR   09-MAY-1990;   90US-00520935.
PR   27-AUG-1990;   90US-00572284.
PR   24-MAR-1992;   92US-00857023.
PR   02-MAR-1994;   94US-00205011.
XX
PA   (HOFF ) HOFFMANN LA ROCHE INC.
XX
PI   Gately MK,  Gubler UA,  Hulmes JD,  Podlaski FJ,  Stern AS;
PI   Chizzonite RA,  Pan YE;
XX
DR   WPI; 2004-118577/12.
DR   P-PSDB; ADO03759, ADO03795.
XX
PT   Pharmaceutical composition useful for activating T cell growth factors in
PT   assays comprises heterodimeric protein comprising first and second
PT   subunits and carrier.
XX
PS   Disclosure; Fig 25; 72pp; English.
XX
CC   The invention describes a pharmaceutical composition active in a T cell
CC   growth factor assay. The pharmaceutical composition comprises a
CC   heterodimeric protein having a molecular weight of 75 kDa as determined
CC   by Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE)
CC   under non-reducing conditions, and under reducing conditions, providing a
CC   first subunit having a molecular weight of 40 kDa as determined by (SDS-
CC   PAGE), and having a fully defined sequence of 306 amino acids as given in
CC   the specification, and second subunit having a molecular weight of 35 kDa
CC   as determined by (SDS-PAGE). Also described are: a novel cytokine protein
CC   called Cytokine lymphocyte maturation factor (CLMF) or interleukin-12 (IL
CC   -12) synthesised by mammalian cells, particularly human NC-37 B
CC   lymphoblastoid cells, and capable of stimulating T-cell growth; and
CC   monoclonal antibodies directed against (CLMF). (I) is useful as a
CC   pharmaceutical composition which is active in a T cell growth factor
CC   assay. This sequence encodes human cytotoxic lymphocyte maturation factor
CC   (CLMF) 40 kDa subunit.
XX
SQ   Sequence 1397 BP; 390 A; 309 C; 333 G; 365 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 12;  Length 1397;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        701 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 744


RESULT 97
AAZ40021
ID   AAZ40021 standard; DNA; 1399 BP.
XX
AC   AAZ40021;
XX
DT   14-FEB-2000  (first entry)
XX
```

DE Human p40 coding sequence.
XX
KW Interleukin-12; IL-12; fusion protein; IL-12 p35 subunit; B7 protein;
KW IL-12 p40 subunit; gene therapy; tumour; leukaemia; ss.
XX
OS Homo sapiens.
XX
PN US5994104-A.
XX
PD 30-NOV-1999.
XX
PF 08-NOV-1996; 96US-00751767.
XX
PR 08-NOV-1996; 96US-00751767.
XX
PA (UNLO) ROYAL FREE HOSPITAL SCHOOL MED.
XX
PI Anderson RJ, Prentice HG, Macdonald ID;
XX
DR WPI; 2000-038261/03.
DR P-PSDB; AAY54919.
XX
PT Nucleic acid constructs encoding interleukin-12 fusion proteins useful
PT for treating leukemia and other cancers.
XX
PS Example; Fig 9; 73pp; English.
XX
CC This sequence encodes the human p40 protein sequence. The invention
CC relates to an isolated nucleic acid construct (I) comprising a region
CC encoding an interleukin-12 (IL-12) fusion protein (comprising an IL-12
CC p35 subunit, an IL-12 p40 subunit and a linker peptide (joining the
CC subunits)) and a region encoding a B7 protein. (I) may be used to produce
CC IL-12 fusion proteins according to standard recombinant DNA
CC methodologies. The fusion proteins may be produced either in vitro in a
CC fermentation culture or in vivo as part of a gene therapy protocol (in
CC this case (I) is used to transform a patients cells, which then secrete
CC the functional polypeptide to supplement the patients own production of
CC IL-12 or to rectify mutations which lead to the expression of inactive
CC polypeptides). The fusion proteins produced in this way may be used to
CC treat any disease which responds to IL-12 such as tumours (both solid and
CC dispersed of the kidney, breast, colon, ovarian and cervical tumours and
CC melanomas) and in particular, tumours of the blood such as leukaemia.
CC Alternatively, the polypeptides may be used as antigens in the production
CC of antibodies to IL-12 and to assay for agonists and antagonists of its
CC activity. The antibodies and antagonists may be used to inhibit the
CC activity of IL-12. (I) may also be used diagnostically as a probe which
CC hybridizes to sequences encoding IL-12 and the antibodies may be used to
CC detect the presence of IL-12 polypeptides in samples. They may be used
CC diagnostically to quantitate the expression of the polypeptide by
CC patients and hence which subjects may be in need of restorative therapy
XX
SQ Sequence 1399 BP; 390 A; 310 C; 333 G; 366 T; 0 U; 0 Other;

Query Match 4.5%; Score 44; DB 3; Length 1399;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 703 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 746

RESULT 98
ADY86632
ID ADY86632 standard; DNA; 1399 BP.
XX
AC ADY86632;
XX
DT 02-JUN-2005 (first entry)
XX
DE Human interleukin-12 40 kDa (IL-12 p40) subunit gene.
XX
KW Gene expression; screening; multiple sclerosis; neuroprotective;
KW immune disorder; neurological disease; DNA microarray; gene; ds;
KW interleukin-12; lymphokine; cytokine.
XX
OS Homo sapiens.
XX
PN US2005064483-A1.
XX
PD 24-MAR-2005.
XX
PF 30-AUG-2004; 2004US-00929182.
XX
PR 28-AUG-2003; 2003US-0498731P.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Zang JZ, Hong J;
XX
DR WPI; 2005-252668/26.
DR GENBANK; M65272.
XX
PT Monitoring multiple sclerosis patient taking beta-interferon or
PT glatiramer acetate to predict treatment response by determining
PT expression profile of inflammatory nucleic acids using RNA of patient and
PT comparing to control.
XX
PS Claim 1; SEQ ID NO 22; 73pp; English.
XX
CC The present invention relates to gene expression profiling technology to
CC quantatively measure the expression profiles of genes selected based on
CC their role in inflammation and their susceptibility to regulation by
CC current multiple sclerosis (MS) treatment agents by isolating RNA from
CC peripheral blood mononuclear cells (PBMC) of patient. The invention is
CC particularly useful for monitoring a multiple sclerosis patient taking
CC interferon-beta (IFN-beta) or glatiramer acetate (GA) in order to predict
CC treatment response. The present sequence is human interleukin-12 40 kDa
CC (IL-12 p40) subunit gene. This gene is used to illustrate the evaluation
CC of PBMC responses to in Vitro treatment with IFN-beta or GA agents by
CC gene expression profiling technology.
XX
SQ Sequence 1399 BP; 390 A; 310 C; 333 G; 366 T; 0 U; 0 Other;

Query Match 4.5%; Score 44; DB 14; Length 1399;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 703 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 746

RESULT 99
ADQ14472
ID ADQ14472 standard; DNA; 1580 BP.
XX
AC ADQ14472;
XX
DT 07-OCT-2004 (first entry)
XX
DE DNA encoding human hyperkine protein.
XX
KW Wound healing; agonist; antagonist; interleukin-23; IL-23; vulnerary;
KW cytokine; human; hyperkine; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 7. .1572
FT /*tag= a
FT /product= "Human hyperkine protein"
XX
PN WO2004058178-A2.
XX
PD 15-JUL-2004.

XX
PF 18-DEC-2003; 2003WO-US040937.
XX
PR 23-DEC-2002; 2002US-0436274P.
XX
PA (SCHE) SCHERING CORP.
XX
PI Bowman EP, Chen S, Cua DJ;
XX
DR WPI; 2004-525781/50.
DR P-PSDB; ADQ14473.
XX
PT Treating inflammatory skin disorders or improving wound healing comprises
PT administering to a subject an agonist or antagonist of Interleukin-23.
XX
PS Example; SEQ ID NO 7; 52pp; English.
XX
CC The invention relates to a novel method for treating or improving wound
CC healing. The method comprises administering to a subject an agonist or
CC antagonist of interleukin (IL)-23. The invention further comprises: an
CC agonist of IL-23 derived from the binding site of an antibody that
CC specifically binds to an IL-23 receptor; and a kit comprising the agonist
CC and a compartment or instructions for use or disposal. The interleukin-23
CC agents have vulnerary activity. The method is useful for treating or
CC improving wound healing. This polynucleotide sequence represents the
CC nucleic acid encoding a hyperkine protein used in the wound healing
CC method of the invention.
XX
SQ Sequence 1580 BP; 399 A; 411 C; 426 G; 344 T; 0 U; 0 Other;

Query Match 4.5%; Score 44; DB 12; Length 1580;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
||||||||||||||||||||||||||||||||||||||||||||
Db 673 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 716

RESULT 100
AAA92406
ID AAA92406 standard; cDNA; 2300 BP.
XX
AC AAA92406;
XX
DT 15-JAN-2001 (first entry)
XX
DE Human interleukin 2 encoding p35 and p40 proteins.
XX
KW Human; interleukin 2; IL-2; p35; p40; immune response; tumour;
KW infectious disease; bacteria; virus; parasite; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 19. .678
FT /*tag= a
FT /product= "p35"
FT CDS 1304. .2290
FT /*tag= b
FT /product= "p40"
XX
PN CN1258740-A.
XX
PD 05-JUL-2000.
XX
PF 31-DEC-1998; 98CN-00126748.
XX
PR 31-DEC-1998; 98CN-00126748.
XX
PA (HUAC-) HUACHEN BIOLOGICAL TECHNOLOGY INST SHANG.
XX
PI Cao X, Zhang W, Ju D;
XX
DR WPI; 2000-558956/52.
DR P-PSDB; AAB23795, AAB23796.
XX
PT Recombinant adenovirus expressing human interleukin-12 and its
PT preparation and use.
XX
PS Example 3; Fig 4; 27pp; Chinese.
XX
CC The present invention describes a recombinant adenovirus and its
CC preparation and use, as well as medicine composite containing the
CC recombinant adenovirus. The recombinant adenovirus is used clinically,
CC has the advantages of low cost, easy use and high efficiency and is
CC especially suitable for immune treatment of tumour and infectious
CC diseases caused by bacteria, virus and parasite. The present sequence
CC represents human interleukin 2 (IL-2) cDNA which encodes the p35 and p40
CC proteins, which is used in an example from the present invention
XX
SQ Sequence 2300 BP; 598 A; 591 C; 571 G; 540 T; 0 U; 0 Other;

Query Match 4.5%; Score 44; DB 3; Length 2300;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	6	44	4.5	766	5	CD559449	CD559449 AGENCOURT
c	7	44	4.5	772	5	CD559450	CD559450 AGENCOURT
c	8	44	4.5	785	5	CD559448	CD559448 AGENCOURT
	9	41	4.2	772	5	CD559604	CD559604 AGENCOURT
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	22	29	2.9	387	4	BY167742	BY167742 BY167742
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	24	29	2.9	423	4	BY218447	BY218447 BY218447
	25	29	2.9	432	4	BY154173	BY154173 BY154173
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	30	28	2.8	535	11	AZ441303	AZ441303 1M0232M24
c	31	27	2.7	668	14	AG079702	AG079702 Pan trogl
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c	33	24	2.4	414	13	CW885638	CW885638 RPCI42_10
c	34	21	2.1	330	13	CW047416	CW047416 104_285_1
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c	37	21	2.1	509	5	CF059708	CF059708 QCS15g07.
c	38	21	2.1	509	5	CF060247	CF060247 QCS5b05.y
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c	41	21	2.1	523	1	AI491671	AI491671 486020E06
c	42	21	2.1	553	7	AW566435	AW566435 660074D12
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	82	20	2.0	563	1	AL956562	AL956562 AL956562
	83	20	2.0	564	2	BJ030774	BJ030774 BJ030774
	84	20	2.0	570	1	AI666909	AI666909 fd16d08.x
	85	20	2.0	571	2	BJ032049	BJ032049 BJ032049
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	88	20	2.0	633	1	AL900775	AL900775 AL900775
c	89	20	2.0	646	12	CE454520	CE454520 tigr-gss-
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93	20	2.0	667	14	CT167835	CT167835 Sus scrof
c 94	20	2.0	681	12	CC008436	CC008436 PUDHR12TD
c 95	20	2.0	690	11	AZ424475	AZ424475 1M0204A12
c 96	20	2.0	696	11	BZ240832	BZ240832 CH230-272
97	20	2.0	698	2	BG740695	BG740695 602631544
c 98	20	2.0	701	10	DT267303	DT267303 JGI_CAAV1
99	20	2.0	701	10	DT267304	DT267304 JGI_CAAV1
c 100	20	2.0	719	10	DT283860	DT283860 JGI_CAAV1
c 101	20	2.0	724	13	CZ313704	CZ313704 ZMMBF0012
c 102	20	2.0	742	9	CX704941	CX704941 gmrtDrNS0
103	20	2.0	752	9	CX474004	CX474004 JGI_XZG49
104	20	2.0	760	9	CX401138	CX401138 JGI_XZT49
105	20	2.0	777	12	CG222535	CG222535 OG0DT06TH
c 106	20	2.0	777	14	AG472962	AG472962 Mus muscu
107	20	2.0	778	12	CE021855	CE021855 tigr-gss-
108	20	2.0	782	9	CX515114	CX515114 JGI_XZG45
109	20	2.0	790	14	DE263787	DE263787 Oryzias l
c 110	20	2.0	794	12	CC526964	CC526964 CH240_401
111	20	2.0	815	9	CX966008	CX966008 JGI_CAAP1
112	20	2.0	819	12	CG433498	CG433498 ZMMBBc004
113	20	2.0	837	12	CG424739	CG424739 ZMMBBc004
114	20	2.0	862	9	CX490517	CX490517 JGI_XZG33
115	20	2.0	866	4	BX719908	BX719908 BX719908
116	20	2.0	876	11	BZ274756	BZ274756 CH230-450
c 117	20	2.0	879	3	BU134895	BU134895 603121826
118	20	2.0	879	12	CG419488	CG419488 ZMMBBc002
119	20	2.0	881	8	CR579278	CR579278 CR579278
120	20	2.0	884	12	CG152443	CG152443 PUFQD62TB
121	20	2.0	885	9	CX414760	CX414760 JGI_XZT55
122	20	2.0	890	9	CX375663	CX375663 JGI_XZT59
123	20	2.0	893	4	CA792037	CA792037 AGENCOURT
124	20	2.0	893	12	CC969890	CC969890 ZUAGO82TV
c 125	20	2.0	897	11	BZ169807	BZ169807 CH230-463
c 126	20	2.0	900	12	CC001138	CC001138 PUEAP48TD
127	20	2.0	905	7	BE533710	BE533710 601232852
c 128	20	2.0	926	8	CX116780	CX116780 EI106B21
129	20	2.0	927	14	DX042542	DX042542 KBrB042P0
130	20	2.0	947	12	CG701262	CG701262 ZMMBBc017
c 131	20	2.0	956	10	DW611860	DW611860 CLJ265-F0
c 132	20	2.0	960	12	CG152445	CG152445 PUFQD62TD
133	20	2.0	965	13	CL304216	CL304216 ZMMBBb009
c 134	20	2.0	985	10	DW657589	DW657589 CLJ397-G1
c 135	20	2.0	998	14	DU878040	DU878040 279669 To
c 136	20	2.0	1003	12	CG222548	CG222548 OG0DT06TV
137	20	2.0	1048	12	CG698770	CG698770 ZMMBBc011
138	20	2.0	1049	10	DW611861	DW611861 CLJ265-F0
139	20	2.0	1082	12	CC175278	CC175278 ZMMBBc029
c 140	20	2.0	1204	9	DN661975	DN661975 CFW06-B07
141	20	2.0	1595	2	BG256021	BG256021 602367310
c 142	19	1.9	224	12	BZ779302	BZ779302 ih87h11.g
143	19	1.9	234	4	CD131385	CD131385 MG1-0012T
c 144	19	1.9	236	8	CO314283	CO314283 EK235626.
c 145	19	1.9	255	8	CV827114	CV827114 EST001412
146	19	1.9	293	3	BP949628	BP949628 BP949628
c 147	19	1.9	300	1	AA714194	AA714194 nw05h05.s
c 148	19	1.9	328	14	CNS00P65	AL084107 Arabidops
c 149	19	1.9	346	2	BJ694940	BJ694940 BJ694940
c 150	19	1.9	368	3	BU661053	BU661053 c167c12.z
151	19	1.9	369	8	CO362672	CO362672 RTK1_5_D0
152	19	1.9	369	11	AZ884788	AZ884788 RPCI-23-1
c 153	19	1.9	373	5	CK045056	CK045056 51163rsic
154	19	1.9	377	4	CA362220	CA362220 636256 NC
c 155	19	1.9	378	2	BI594826	BI594826 As_tgz_44
156	19	1.9	381	1	AL964966	AL964966 AL964966
157	19	1.9	382	8	CN921966	CN921966 000409AEL
c 158	19	1.9	384	4	BY282227	BY282227 BY282227
c 159	19	1.9	394	7	AW042400	AW042400 614028B11
160	19	1.9	394	9	DR059212	DR059212 RTNIT1_16
161	19	1.9	413	9	DR177926	DR177926 RTMNUT1_8
c 162	19	1.9	415	5	CF917109	CF917109 Bflor498.
163	19	1.9	429	14	CR204657	CR204657 Reverse s
c 164	19	1.9	434	4	CB793439	CB793439 AMGNNUC:S
c 165	19	1.9	434	4	CB793440	CB793440 AMGNNUC:S
166	19	1.9	434	12	CE700465	CE700465 tigr-gss-
c 167	19	1.9	439	2	BI385075	BI385075 BFLG2_003
168	19	1.9	444	9	CX646589	CX646589 COLD1_10_
c 169	19	1.9	448	5	CI357610	CI357610 CI357610
170	19	1.9	493	8	CN619918	CN619918 TgESTzym9
171	19	1.9	496	1	AI871624	AI871624 we28d11.x
c 172	19	1.9	505	11	AZ635629	AZ635629 1M0493D09
173	19	1.9	510	10	DR446638	DR446638 AR1034E03
c 174	19	1.9	511	12	CG991849	CG991849 CH240_151
c 175	19	1.9	512	5	CK057894	CK057894 61316rsic
c 176	19	1.9	512	13	CL955283	CL955283 OsIRUA000
c 177	19	1.9	517	10	DR787178	DR787178 ZM_BFb000
178	19	1.9	523	14	AG956728	AG956728 Drosophil
c 179	19	1.9	526	8	CO783019	CO783019 BL016D_D1
180	19	1.9	530	13	CL259985	CL259985 ZMMBBb061
c 181	19	1.9	533	5	CI183750	CI183750 CI183750
182	19	1.9	534	5	CK737831	CK737831 TgESTzyj8
183	19	1.9	535	2	BF922172	BF922172 MR4-NT014
184	19	1.9	536	7	AW073130	AW073130 wy94a10.x
185	19	1.9	537	7	BF394460	BF394460 UI-R-CA0-
186	19	1.9	541	3	BP949994	BP949994 BP949994
187	19	1.9	543	9	DA100433	DA100433 DA100433
188	19	1.9	543	9	DA100435	DA100435 DA100435
c 189	19	1.9	543	14	CT107392	CT107392 Sus scrof
190	19	1.9	551	4	BW536306	BW536306 BW536306
c 191	19	1.9	555	8	CO700056	CO700056 DG32-170e
c 192	19	1.9	562	2	BJ692987	BJ692987 BJ692987
193	19	1.9	566	3	BQ906981	BQ906981 M023C03 O
194	19	1.9	571	2	BJ524824	BJ524824 BJ524824
195	19	1.9	573	9	DA674546	DA674546 DA674546
196	19	1.9	577	14	AG961043	AG961043 Drosophil
197	19	1.9	582	3	BP280239	BP280239 BP280239
198	19	1.9	583	3	BP280282	BP280282 BP280282
c 199	19	1.9	587	10	DR787069	DR787069 ZM_BFb000
200	19	1.9	588	14	AG071104	AG071104 Pan trogl

ALIGNMENTS

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RESULT 1
CE093997
LOCUS       CE093997                700 bp    DNA     linear   GSS 24-SEP-2003
DEFINITION  tigr-gss-dog-17000359883851 Dog Library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION   CE093997
VERSION     CE093997.1  GI:35160844
KEYWORDS    GSS.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 700)
  AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
            Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
            Venter,J.C.
  TITLE     The dog genome: survey sequencing and comparative analysis
  JOURNAL   Science 301 (5641), 1898-1903 (2003)
   PUBMED   14512627
COMMENT     Contact: Kirkness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirknes@tigr.org
            Class: shotgun.
FEATURES             Location/Qualifiers
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                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /strain="Standard Poodle"
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                     /db_xref="taxon:9615"
                     /clone_lib="Dog Library"
                     /note="Site_1: BstXI; Libraries were prepared from
                     peripheral blood"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 3.6e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
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Db        360 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 419

Qy        597 CTGCCC 602
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Db        420 CTGCCC 425


RESULT 2
CD559454/c
LOCUS       CD559454                725 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14497089 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971868 5', mRNA sequence.
ACCESSION   CD559454
VERSION     CD559454.2  GI:38453478
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 725)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585522.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: g  column: 11
            High quality sequence start: 13
            High quality sequence stop: 573.
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971868"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match              4.5%;  Score 44;  DB 5;  Length 725;
  Best Local Similarity   100.0%;  Pred. No. 5.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db        426 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 383


RESULT 3
CD559605
LOCUS       CD559605                735 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496534 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971870 5', mRNA sequence.
ACCESSION   CD559605
VERSION     CD559605.2  GI:38558937
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 735)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585673.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 01
            High quality sequence stop: 709.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971870"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
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                    a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             4.5%;  Score 44;  DB 5;  Length 735;
  Best Local Similarity   100.0%;  Pred. No. 5.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db        677 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 720


RESULT 4
CD559453/c
LOCUS       CD559453                736 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14497154 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971869 5', mRNA sequence.
ACCESSION   CD559453
VERSION     CD559453.2  GI:38453475
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 736)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585521.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: g  column: 12
            High quality sequence stop: 683.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971869"
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                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             4.5%;  Score 44;  DB 5;  Length 736;
  Best Local Similarity   100.0%;  Pred. No. 5.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db        401 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 358


RESULT 5
CD559451/c
LOCUS       CD559451                762 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496580 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971871 5', mRNA sequence.
ACCESSION   CD559451
VERSION     CD559451.2  GI:38453471
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585519.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 02
            High quality sequence start: 38
            High quality sequence stop: 761.
FEATURES             Location/Qualifiers
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                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             4.5%;  Score 44;  DB 5;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 5.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db        422 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 379


RESULT 6
CD559449/c
LOCUS       CD559449                766 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496649 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971873 5', mRNA sequence.
ACCESSION   CD559449
VERSION     CD559449.2  GI:38453467
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 766)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585517.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 04
            High quality sequence stop: 641.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
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                     /clone="IMAGE:6971873"
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                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             4.5%;  Score 44;  DB 5;  Length 766;
  Best Local Similarity   100.0%;  Pred. No. 5.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db        414 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 371


RESULT 7
CD559450/c
LOCUS       CD559450                772 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496612 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971872 5', mRNA sequence.
ACCESSION   CD559450
VERSION     CD559450.2  GI:38453469
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 772)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585518.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 03
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FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
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                     /clone="IMAGE:6971872"
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                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             4.5%;  Score 44;  DB 5;  Length 772;
  Best Local Similarity   100.0%;  Pred. No. 5.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db        425 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 382


RESULT 8
CD559448/c
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LOCUS       CD559448                785 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496712 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971874 5', mRNA sequence.
ACCESSION   CD559448
VERSION     CD559448.2  GI:38453466
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 785)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585516.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 05
            High quality sequence stop: 696.
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                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             4.5%;  Score 44;  DB 5;  Length 785;
  Best Local Similarity   100.0%;  Pred. No. 5.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        416 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 373


RESULT 9
CD559604
LOCUS       CD559604                772 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496598 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971872 5', mRNA sequence.
ACCESSION   CD559604
VERSION     CD559604.2  GI:38558934
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 772)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585672.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 03
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                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             4.2%;  Score 41;  DB 5;  Length 772;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-10;
  Matches   41;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAA 704
              |||||||||||||||||||||||||||||||||||||||||
Db        698 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAA 738


RESULT 10
CD559603
LOCUS       CD559603                724 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496630 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971873 5', mRNA sequence.
ACCESSION   CD559603
VERSION     CD559603.2  GI:38558932
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 724)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585671.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 04
            High quality sequence stop: 525.
FEATURES             Location/Qualifiers
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                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             4.0%;  Score 39;  DB 5;  Length 724;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-09;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        400 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 438
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Db        413 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 451


RESULT 11
CD559602
LOCUS       CD559602                 745 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496684 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971874 5', mRNA sequence.
ACCESSION   CD559602
VERSION     CD559602.2  GI:38558930
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 745)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585670.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 05
            High quality sequence start: 2
            High quality sequence stop: 644.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             4.0%;  Score 39;  DB 5;  Length 745;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-09;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        400 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 438
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Db        405 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 443


RESULT 12
CD559607
LOCUS       CD559607                 747 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14497061 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971868 5', mRNA sequence.
ACCESSION   CD559607
VERSION     CD559607.2  GI:38558941
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 747)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
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  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585675.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: g  column: 11
            High quality sequence start: 14
            High quality sequence stop: 671.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971868"
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                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             4.0%;  Score 39;  DB 5;  Length 747;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-09;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        400 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 438
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Db        428 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 466


RESULT 13
CD559452/c
LOCUS       CD559452                754 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496548 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971870 5', mRNA sequence.
ACCESSION   CD559452
VERSION     CD559452.2  GI:38453473
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 754)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585520.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 01
            High quality sequence start: 130
            High quality sequence stop: 572.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971870"
                     /tissue_type="mixed"
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                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             4.0%;  Score 39;  DB 5;  Length 754;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-09;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        400 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 438
              |||||||||||||||||||||||||||||||||||||||
Db        682 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 644


RESULT 14
CK130264
LOCUS       CK130264                756 bp    mRNA    linear   EST 02-DEC-2003
DEFINITION  AGENCOURT_14496566 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971871 5', mRNA sequence.
ACCESSION   CK130264
VERSION     CK130264.1  GI:38622200
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 756)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
```

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            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 02
            High quality sequence start: 5
            High quality sequence stop: 731.
FEATURES             Location/Qualifiers
     source          1. .756
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971871"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             4.0%;  Score 39;  DB 5;  Length 756;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-09;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        400 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 438
              |||||||||||||||||||||||||||||||||||||||
Db        433 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 471


RESULT 15
CD559606
LOCUS       CD559606                1042 bp    mRNA    linear   EST 11-JUN-2003
DEFINITION  AGENCOURT_14497125 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971869 5', mRNA sequence.
ACCESSION   CD559606
VERSION     CD559606.1  GI:31585674
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1042)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: g  column: 12
            High quality sequence stop: 386.
FEATURES             Location/Qualifiers
     source          1. .1042
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971869"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             4.0%;  Score 39;  DB 5;  Length 1042;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-09;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        400 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 438
              |||||||||||||||||||||||||||||||||||||||
Db        403 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 441


RESULT 16
DV799576
LOCUS       DV799576                252 bp    mRNA    linear   EST 23-NOV-2005
DEFINITION  est_t_truncatus2262 HML_TuTr_IL-2_PBL Tursiops truncatus cDNA, mRNA
            sequence.
ACCESSION   DV799576
VERSION     DV799576.1  GI:82652485
KEYWORDS    EST.
SOURCE      Tursiops truncatus (bottlenosed dolphin)
  ORGANISM  Tursiops truncatus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
            Odontoceti; Delphinidae; Tursiops.
REFERENCE   1  (bases 1 to 252)
  AUTHORS   Mancia,A., Gefroh,H.A., Lundqvist,M.L., Romano,T.A., Almeida,J.S.,
            Chen,Y., McKillen,D.J., Trent,H.F., Wu,S. and Warr,G.W.
  TITLE     Construction and validation of T. truncatus immunospecific cDNA
            microarray at marinegenomics.org
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Annalaura Mancia
            Hollings Marine Lab
            Medical University of South Carolina
            Hollings Marine Lab, 331 Ft. Johnson Rd., Charleston, SC 29412, USA
            Tel: (843) 762 8962
            Fax: (843) 762 8737
            Email: mancia@musc.edu.
FEATURES             Location/Qualifiers
     source          1. .252
                     /organism="Tursiops truncatus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9739"
```

/tissue_type="PBL"
/cell_type="PBL"
/clone_lib="HML_TuTr_IL-2_PBL"
/note="Vector: pCR2.1TOPO; Site_1: GAATTC"
ORIGIN

Query Match 3.4%; Score 33; DB 10; Length 252;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 320 AGGAAGATGGAATTTGGTCCACTGATATCTTAA 352
||||||||||||||||||||||||||||||||||
Db 1 AGGAAGATGGAATTTGGTCCACTGATATCTTAA 33

RESULT 17
AK162981
LOCUS AK162981 1839 bp mRNA linear HTC 21-SEP-2005
DEFINITION Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430014H12 product:interleukin 12b, full insert sequence.
ACCESSION AK162981
VERSION AK162981.1 GI:74188061
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
CONSRTM RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
PUBMED 11217851
REFERENCE 5
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
CONSRTM FANTOM Consortium
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420 (6915), 563-573 (2002)
PUBMED 12466851
REFERENCE 6
AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M.,

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            Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M.,
            Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K.,
            Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.
  CONSRTM   FANTOM Consortium
  TITLE     The transcriptional landscape of the mammalian genome
  JOURNAL   Science 309 (5740), 1559-1563 (2005)
   PUBMED   16141072
REFERENCE   7
  AUTHORS   Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M.,
            Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H.,
            Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T.,
            Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L.,
            Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A.,
            Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and
            Wahlestedt,C.
  CONSRTM   RIKEN Genome Exploration Research Group
  TITLE     Antisense transcription in the mammalian transcriptome
  JOURNAL   Science 309 (5740), 1564-1566 (2005)
   PUBMED   16141073
REFERENCE   8  (bases 1 to 1839)
  AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K.,
            Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S.,
            Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N.,
            Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D.,
            Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
     source          1. .1839
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM_DB:A430014H12"
                     /db_xref="taxon:10090"
                     /clone="A430014H12"
                     /tissue_type="thymus"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="0 day neonate"
     CDS             58. .1065
                     /note="unnamed protein product; interleukin 12b
                     (MGD|MGI:96540 GB|M86671, evidence: BLASTN, 100%,
                     match=1816)
                     putative"
                     /codon_start=1
                     /protein_id="BAE37146.1"
                     /db_xref="GI:74188062"
                     /translation="MCPQKLTISWFAIVLLVSPLMAMWELEKDVYVVEVDWTPDAPGE
                     TVNLTCDTPEEDDITWTSDQRHGVIGSGKTLTITVKEFLDAGQYTCHKGGETLSHSHL
                     LLHKKENGIWSTEILKNFKNKTFLKCEAPNYSGRFTCSWLVQRNMDLKFNIKSSSSSP
                     DSRAVTCGMASLSAEKVTLDQRDYEKYSVSCQEDVTCPTAEETLPIELALEARQQNKY
                     ENYSTSFFIRDIIKPDPPKNLQMKPLKNSQVEVSWEYPDSWSTPHSYFSLKFFVRIQR
                     KKEKMKETEEGCNQKGAFLVEKTSTEVQCKGGNVCVQAQDRYYNSSCSKWACVPCRVR
                     S"
ORIGIN

  Query Match             3.0%;  Score 30;  DB 6;  Length 1839;
  Best Local Similarity   100.0%;  Pred. No. 0.00032;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||
Db        726 CAGCTTCTTCATCAGGGACATCATCAAACC 755


RESULT 18
AK155593
LOCUS       AK155593               2908 bp    mRNA    linear   HTC 21-SEP-2005
DEFINITION  Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN
            full-length enriched library, clone:F730005O03 product:interleukin
            12b, full insert sequence.
ACCESSION   AK155593
VERSION     AK155593.1  GI:74212721
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
            Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
            Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
            Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
            Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
            Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
            Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
            Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
            Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  CONSRTM   RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
   PUBMED   11217851
REFERENCE   5
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
```

Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420 (6915), 563-573 (2002)

PUBMED 12466851

REFERENCE 6

AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE The transcriptional landscape of the mammalian genome

JOURNAL Science 309 (5740), 1559-1563 (2005)

PUBMED 16141072

REFERENCE 7

AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.

CONSRTM RIKEN Genome Exploration Research Group

TITLE Antisense transcription in the mammalian transcriptome

JOURNAL Science 309 (5740), 1564-1566 (2005)

PUBMED 16141073

REFERENCE 8 (bases 1 to 2908)

AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

source 1. .2908
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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/clone="F730005O03"
/cell_type="B6-derived CD11 +ve dendritic cells"
/clone_lib="RIKEN full-length enriched mouse cDNA library"

misc_feature 1. .2908
/note="interleukin 12b (MGD|MGI:96540 GB|M86671, evidence: BLASTN, 99%, match=1807)
putative"

ORIGIN

Query Match 3.0%; Score 30; DB 6; Length 2908;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db       1130 CAGCTTCTTCATCAGGGACATCATCAAACC 1159
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RESULT 19
BY164658
LOCUS BY164658 346 bp mRNA linear EST 10-DEC-2002
DEFINITION BY164658 RIKEN full-length enriched, bone marrow macrophage Mus musculus cDNA clone I830052P21 5', mRNA sequence.
ACCESSION BY164658
VERSION BY164658.1 GI:26301304
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 346)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by David A. Hume (Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane,Q 4072 Australia) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
FEATURES Location/Qualifiers
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/clone_lib="RIKEN full-length enriched, bone marrow macrophage"
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.00096;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 214 CCTGAAGAAGATGACATCACCTGGACCTC 242

RESULT 20
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LOCUS BY221814 355 bp mRNA linear EST 10-DEC-2002
DEFINITION BY221814 RIKEN full-length enriched, activated spleen Mus musculus cDNA clone F830223O08 5', mRNA sequence.
ACCESSION BY221814
VERSION BY221814.1 GI:26402917
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 355)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,

Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

```
FEATURES             Location/Qualifiers
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                     /tissue_type="activated spleen"
                     /clone_lib="RIKEN full-length enriched, activated spleen"
ORIGIN

  Query Match             2.9%;  Score 29;  DB 4;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 0.00096;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        157 CCTGAAGAAGATGACATCACCTGGACCTC 185
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Db        213 CCTGAAGAAGATGACATCACCTGGACCTC 241


RESULT 21
BY222535
LOCUS       BY222535                375 bp    mRNA    linear   EST 10-DEC-2002
DEFINITION  BY222535 RIKEN full-length enriched, activated spleen Mus musculus
            cDNA clone F830228K06 5', mRNA sequence.
ACCESSION   BY222535
VERSION     BY222535.1  GI:26403638
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 375)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
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            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
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            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
            Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
            Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
            Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
            Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
            Hayashizaki,Y. Direct Submission
            Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
            Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
            RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
            Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
            Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
            Trust/MRC building Addenbrookes Hospital Cambridge) whose
            assistance we gratefully acknowledge.
            Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
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Db        213 CCTGAAGAAGATGACATCACCTGGACCTC 241
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ACCESSION BY167742
VERSION BY167742.1 GI:26304388
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 387)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by David A. Hume (Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane,Q 4072 Australia) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
FEATURES Location/Qualifiers
source 1. .387
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/mol_type="mRNA"
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/clone="I830068I17"
/tissue_type="bone marrow"
/cell_type="macrophage"
/clone_lib="RIKEN full-length enriched, bone marrow macrophage"
ORIGIN

Query Match 2.9%; Score 29; DB 4; Length 387;
Best Local Similarity 100.0%; Pred. No. 0.00097;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 157 CCTGAAGAAGATGACATCACCTGGACCTC 185
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RESULT 23
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LOCUS CO949904 417 bp mRNA linear EST 09-SEP-2004
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ACCESSION CO949904
VERSION CO949904.1 GI:51326849
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 417)
AUTHORS Jiang,H., Whitworth,K.M., Bivens,N.J., Ries,J.E., Woods,R.J., Forrester,L.J., Springer,G.K., Mathialagan,N., Agca,C., Prather,R.S. and Lucy,M.C.
TITLE Large-scale Generation and Analysis of Expressed Sequence Tags from Porcine Ovary
JOURNAL Unpublished (2004)
COMMENT Contact: DNA Core Facility (Swine Project)
Animal Science - RS Prather
University of Missouri-Columbia
M616 Medical Sciences Bldg., Columbia, MO 65212, USA
Tel: (573)882-0428
Fax: (573)884-5552
Email: porcine@rnet.missouri.edu
POLYA=No.
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/note="Vector: T3T7PAC; Funding: A grant from the Monsanto Company to the University of Missouri. Genetic Source: Ovarian tissue (whole ovary, dissected follicles, or corpora lutea) was collected from crossbred pigs (Sus scrofa domestica), frozen in liquid nitrogen shortly after collection, and stored at -80 degrees Celsius until RNA

extraction. The tissue from several individual pigs was pooled for the purpose of RNA extraction. The specific tissues collected were fetal whole ovary; neonatal whole ovary; prepubutal whole ovary; 2, 4, 6 and 8 mm growing follicles; Day 0 follicles; Day 5 small antral follicles and corpora lutea; Day 12 corpora lutea and Day 12 follicles. More information regarding the methods can be found at:
http://genome.rnet.missouri.edu/Swine/Methods.html.
Library Construction (Standard Protocol): All procedures discussed in this section have been described in detail elsewhere (Soares et al., 1994; Bonaldo et al., 1996; Jiang et al., 2001). Total cellular RNA from each sample was isolated by using STAT-60 reagent (Tel-Test, Friendswood, TX) and the poly(A)+ RNA was obtained by two rounds of purification with the Oligotex mRNA isolation kit (Qiagen) according to the manufacturer's instructions. The libraries were constructed essentially as described by the manufacturer's instructions provided with the SuperScript Plasmid System (Invitrogen, cat. no. 18248-013). Briefly, 1mg of poly(A)+ RNA will be annealed at 37 degrees Celsius with 10mg of NotI-tag-dT18 oligonucleotide (GCTGCTCGCGGCCGC-tag-T18) and reverse transcribed at 37 degrees Celsius with SuperScript II (Invitrogen) reverse transcriptase (Jiang et al., 2001). The 'tag' represents a tissue/stage-specific ten-base sequence identifier (http://genome.uiowa.edu/pubsoft/software.html) present in the oligonucleotide used to prime first-strand synthesis. Second strand synthesis was performed with T4 DNA polymerase in the presence of DNA ligase and RNase H. After second strand synthesis, the double-stranded cDNAs was ligated to SalI adapters (Invitrogen-Life Technologies) and digested with NotI. The cDNAs will be size selected by passage through cDNA size fractionation columns (Invitrogen-Life technologies). The cDNAs derived from each developmental stage of a particular tissue were mixed on an equimolar basis and ligated directionally into the NotI and SalI sites of the pSPORT1 vector (Invitrogen). After ligation of the inserts, the plasmids will be electroporated into DH10B bacteria. Preliminary Library Characterization: Randomly chosen clones from each library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (~4 96-well plates) to confirm library quality [e.g. the presence of short polyA+ tails, genomic DNA contamination (must be <1%), ribosomal RNA clones (must be <1%), etc.] and to provide a sequence database representing the predominant clones in each library. The clones were sequenced at the University of Missouri-Columbia DNA Core Facility. Bioinformatics work was performed by GK Springer's bioinformatics group (WG Spollen, JE Ries, A Guillen, AA Khambati, RV Patel, CM Topinka, SB Bhuiyan) in Computer Science and Health Management and Informatics Departments at the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri DNA Core facility at: porcine@rnet.missouri.edu. Citations: 1. Bonaldo MF, Lennon G, Soares MB. Normalization and Subtraction: Two approaches to facilitate gene discovery. Genome Res, 1996; 6:791-806. 2. Jiang H, Bivens NJ, Ries JE, Whitworth KM, Green JA, Forrester LJ, Springer GK, Didion BA, Mathialagan N, Prather RS, Lucy MC (2001) Constructing cDNA libraries with fewer clones that contain long poly(dA) tails. Biotechniques 31:38-42. 3. Soares MB, MF Banaldo, P Jelene, L Su, L Lawton, A Efstrantiadis. 1994. Construction and characterization of a normalized cDNA library. Proc Natl Acad Sci, 91:9228-9232.
TAG_TISSUE=Day 12 Corpus Luteum
TAG_SEQ=Not found"

ORIGIN

Query Match 2.9%; Score 29; DB 8; Length 417;
Best Local Similarity 100.0%; Pred. No. 0.00098;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      201 CCTGAAGAAGATGACATCACCTGGACCTC 229
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RESULT 24
BY218447
LOCUS BY218447 423 bp mRNA linear EST 10-DEC-2002
DEFINITION BY218447 RIKEN full-length enriched, activated spleen Mus musculus cDNA clone F830107N16 5', mRNA sequence.
ACCESSION BY218447
VERSION BY218447.1 GI:26399344
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 423)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

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                     /tissue_type="activated spleen"
                     /clone_lib="RIKEN full-length enriched, activated spleen"
ORIGIN

  Query Match             2.9%;  Score 29;  DB 4;  Length 423;
  Best Local Similarity   100.0%;  Pred. No. 0.00098;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        157 CCTGAAGAAGATGACATCACCTGGACCTC 185
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RESULT 25
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ACCESSION   BY154173
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KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
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            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 432)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
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            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
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            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
            Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
            Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
            Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
            Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
            Hayashizaki,Y. Direct Submission
            Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
            Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
            RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
            Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Tissues were provided by David A. Hume ( Depts. of Biochemistry
            and Microbiology/Parasitology Institute for Molecular Bioscience
            University of Queensland Brisbane,Q 4072 Australia ) whose
            assistance we gratefully acknowledge.
            Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .432
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="G530005B20"
                     /tissue_type="bone marrow"
                     /cell_type="macrophage"
                     /clone_lib="RIKEN full-length enriched, bone marrow
                     macrophage"
ORIGIN

  Query Match             2.9%;  Score 29;  DB 4;  Length 432;
  Best Local Similarity   100.0%;  Pred. No. 0.00098;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        157 CCTGAAGAAGATGACATCACCTGGACCTC 185
              ||||||||||||||||||||||||||||||
Db        214 CCTGAAGAAGATGACATCACCTGGACCTC 242


RESULT 26
BF704417
LOCUS       BF704417                475 bp    mRNA    linear   EST 22-DEC-2000
DEFINITION  MI-P-E6-acc-g-09-1-UM.s1 MI-P-E6 Sus scrofa cDNA clone
            MI-P-E6-acc-g-09-1-UM 3', mRNA sequence.
ACCESSION   BF704417
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VERSION     BF704417.1  GI:11989825
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 475)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
   PUBMED   8889548
COMMENT     Contact: Tuggle CK
            Molecular Genetics Laboratory, Department of Animal Science
            Iowa State University
            201 Kildee Hall, Ames, IA 50011-3150, USA
            Tel: 5152944252
            Fax: 5152942401
            Email: cktuggle@iastate.edu
            Oligo-dT track not found, Not I site shown in beginning of sequence
            is likely internal to the message. cDNA Library Preparation: RJ
            Woods, JA Green, RS Prather S142 Animal Science Research Center,
            Department of Animal Science, University of Missouri-Columbia,
            65211 Clone distribution: clones will be available through Research
            Genetics (www.resgen.com)
            Seq primer: M13 Forward
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .475
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /strain="crossbreed"
                     /db_xref="taxon:9823"
                     /clone="MI-P-E6-acc-g-09-1-UM"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="MI-P-E6"
                     /note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: EcoRI;
                     The MI-P-E6 library is derived from fetus at gestational
                     day 20.  For a detailed description of the  library from
                     which this clone was derived, please visit our web site at
                     http://pigest.genome.iastate.edu/.
                     TAG_SEQ=None found"
ORIGIN

  Query Match             2.9%;  Score 29;  DB 7;  Length 475;
  Best Local Similarity   100.0%;  Pred. No. 0.00099;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        157 CCTGAAGAAGATGACATCACCTGGACCTC 185
              |||||||||||||||||||||||||||||
Db        202 CCTGAAGAAGATGACATCACCTGGACCTC 230


RESULT 27
AZ853726/c
LOCUS       AZ853726                569 bp    DNA     linear   GSS 21-FEB-2001
DEFINITION  2M0157M01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0157M01 F, genomic survey sequence.
ACCESSION   AZ853726
VERSION     AZ853726.1  GI:13042136
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 569)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0157  row: M  column: 01
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 569.
FEATURES             Location/Qualifiers
     source          1. .569
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0157M01"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             2.9%;  Score 29;  DB 11;  Length 569;
  Best Local Similarity   100.0%;  Pred. No. 0.001;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        157 CCTGAAGAAGATGACATCACCTGGACCTC 185
              |||||||||||||||||||||||||||||
Db        214 CCTGAAGAAGATGACATCACCTGGACCTC 186


RESULT 28
CJ134671
LOCUS       CJ134671                649 bp    mRNA    linear   EST 23-SEP-2005
DEFINITION  CJ134671 RIKEN full-length enriched mouse cDNA library, C57BL/6J
            bone marrow macrophage Mus musculus cDNA clone G530135F14 5', mRNA
            sequence.
ACCESSION   CJ134671
VERSION     CJ134671.1  GI:76234999
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 649)
  AUTHORS   The FANTOM Consortium and RIKEN Genome Exploration Research Group
            and Genome Science Group (Genome Network Project Core Group).
  TITLE     The transcriptional landscape of the mammalian genome
```

```
  JOURNAL   Science 309 (5740), 1559-1563 (2005)
   PUBMED   16141072
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. Tissues were provided by David A. Hume (
            Depts. of Biochemistry and Microbiology/Parasitology Institute for
            Molecular Bioscience University of Queensland Brisbane,Q 4072
            Australia ) whose assistance we gratefully acknowledge.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/.
FEATURES             Location/Qualifiers
     source          1. .649
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="G530135F14"
                     /tissue_type="bone marrow"
                     /cell_type="macrophage"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library,
                     C57BL/6J bone marrow macrophage"
ORIGIN

  Query Match             2.9%;  Score 29;  DB 5;  Length 649;
  Best Local Similarity   100.0%;  Pred. No. 0.001;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        157 CCTGAAGAAGATGACATCACCTGGACCTC 185
              ||||||||||||||||||||||||||||||
Db        214 CCTGAAGAAGATGACATCACCTGGACCTC 242


RESULT 29
BY749553
LOCUS       BY749553                 666 bp    mRNA    linear   EST 17-DEC-2002
DEFINITION  BY749553 RIKEN full-length enriched, B6-derived CD11 +ve dendritic
            cells Mus musculus cDNA clone F730005O03 5', mRNA sequence.
ACCESSION   BY749553
VERSION     BY749553.1  GI:27179008
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
            Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
            Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
            Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
            Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
            Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
            Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
            Direct Submission
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
             cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
             Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
            Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
            Trust/MRC building Addenbrookes Hospital Cambridge) whose
            assistance we gratefully acknowledge.
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="F730005O03"
                     /cell_type="B6-derived CD11 +ve dendritic cells"
                     /clone_lib="RIKEN full-length enriched, B6-derived CD11
                     +ve dendritic cells"
ORIGIN

  Query Match             2.9%;  Score 29;  DB 4;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 0.001;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        157 CCTGAAGAAGATGACATCACCTGGACCTC 185
              ||||||||||||||||||||||||||||||
Db        614 CCTGAAGAAGATGACATCACCTGGACCTC 642
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RESULT 30
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LOCUS       AZ441303                 535 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0232M24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0232M24 R, genomic survey sequence.
ACCESSION   AZ441303
VERSION     AZ441303.1  GI:10565316
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 535)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0232  row: M  column: 24
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 535.
FEATURES             Location/Qualifiers
     source          1. .535
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0232M24"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             2.8%;  Score 28;  DB 11;  Length 535;
  Best Local Similarity   100.0%;  Pred. No. 0.0036;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        158 CTGAAGAAGATGACATCACCTGGACCTC 185
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Db        157 CTGAAGAAGATGACATCACCTGGACCTC 184
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RESULT 31
AG079702/c
LOCUS       AG079702                 668 bp    DNA     linear   GSS 03-NOV-2001
DEFINITION  Pan troglodytes DNA, clone: PTB-075I07.R, genomic survey sequence.
ACCESSION   AG079702
VERSION     AG079702.1  GI:16631504
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     BAC end sequences of Library PTB
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 668)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the chimpanzee BAC library PTB This BAC end
            was generated during the R&D process and may have higher chance of
            clone tracking errors.
             PRIMERS
                 Sequencing: M13Rev
             LIBRARY
                 Vector    : pKS145
                 R.Site 1  : SacI
                 R.Site 2  : SacI.
FEATURES             Location/Qualifiers
     source          1. .668
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
                     /clone="PTB-075I07.R"
                     /sex="male"
                     /cell_type="lymphoblast"
                     /clone_lib="PTB Chimpanzee Male BAC Library"
ORIGIN

  Query Match             2.7%;  Score 27;  DB 14;  Length 668;
  Best Local Similarity   100.0%;  Pred. No. 0.013;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        412 GGACGTTTCACCTGCTGGTGGCTGACG 438
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Db        494 GGACGTTTCACCTGCTGGTGGCTGACG 468
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RESULT 32
DU179885
LOCUS       DU179885                 672 bp    DNA     linear   GSS 03-OCT-2005
DEFINITION  1098553497457 CHORI-243 Ovis aries genomic clone CH243-410B4,
            genomic survey sequence.
ACCESSION   DU179885
VERSION     DU179885.1  GI:76820406
KEYWORDS    GSS.
SOURCE      Ovis aries (sheep)
  ORGANISM  Ovis aries
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Caprinae; Ovis.
REFERENCE   1  (bases 1 to 672)
  AUTHORS   Kirkness,E., Shetty,J., de Jong,P., McEwan,J.C., Oddy,H. and
            Cockett,N.
  TITLE     Ovine BAC End Sequences from Library CHORI-243
```

```
  JOURNAL   Unpublished (2004)
COMMENT     Other_GSSs: 1098553723711
            Contact: Ewen Kirkness
            The Institute for Genomic Research (TIGR; www.tigr.org)
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-795-7536
            Email: ekirknes@tigr.org
            Sequences generated at the J. Craig Venter Institute Joint
            Technology Center (JCVIJTC; http://www.venterinstitute.org/).
            Original Trace: 1098553497457 Trace TI: gnl|ti|918706746
            Insert Length: 184000   Std Error: 0.00  row: B  column: 4
            Seq primer: SP6
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .672
                     /organism="Ovis aries"
                     /mol_type="genomic DNA"
                     /strain="Texel breed"
                     /db_xref="taxon:9940"
                     /clone="CH243-410B4"
                     /sex="Male"
                     /cell_type="Blood"
                     /clone_lib="CHORI-243"
                     /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
                     The CHORI-243 sheep (M) (Ovis aries) BAC library produced
                     by Pieter de Jong's lab at CHORI
                     http://bacpac.chori.org/library.php?id=162"
ORIGIN

  Query Match             2.6%;  Score 26;  DB 13;  Length 672;
  Best Local Similarity   100.0%;  Pred. No. 0.047;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         26 CCTGGTTTTCCCTGGTTTTGCTGGCA 51
              |||||||||||||||||||||||||
Db        108 CCTGGTTTTCCCTGGTTTTGCTGGCA 133


RESULT 33
CW885638/c
LOCUS       CW885638                414 bp    DNA     linear   GSS 08-DEC-2004
DEFINITION  RPCI42_102G16.TV RPCI-42 Bos taurus genomic clone RPCI42_102G16,
            genomic survey sequence.
ACCESSION   CW885638
VERSION     CW885638.1  GI:56424578
KEYWORDS    GSS.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 414)
  AUTHORS   Larkin,D.M., Donthu,K., LeDuc,R., Ryan,K., Liu,L., de Jong,P.J. and
            Lewin,H.A.
  TITLE     End sequencing of Holstein BAC library RPCI-42
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Harris Lewin
            Department of Animal Sciences
            University of Illinois at Urbana Champaign
            1201 W. Gregory Dr., Urbana, IL 61801, USA
            Tel: 217 333 5998
            Fax: 217 244 5617
            Email: h-lewin@uiuc.edu
            Clones are derived from the bovine BAC library RPCI-42
            (http://bacpac.chori.org/mbovine42.htm). For BAC library
            availability, please contact Pieter de Jong
            (pdejong@mail.cho.org).Clones may be purchased from BACPAC
            Resources (http://www.chori.org/bacpac/ordering_information.htm).
            Funding was provided in part by grant no. AG2004-34480-14417 from
            USDA-CSREES (Livestock Genome Sequencing Initiative) and
            AG58-5438-2-313 from USDA-ARS
            Plate: 102  row: G  column: 16
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .414
                     /organism="Bos taurus"
                     /mol_type="genomic DNA"
                     /strain="Holstein"
                     /db_xref="taxon:9913"
                     /clone="RPCI42_102G16"
                     /sex="male"
                     /cell_type="blood"
                     /clone_lib="RPCI-42"
                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     RPCI-42 Bovine BAC library (Male) produced by Pieter de
                     Jong"
ORIGIN

  Query Match             2.4%;  Score 24;  DB 13;  Length 414;
  Best Local Similarity   100.0%;  Pred. No. 0.57;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        709 GACCCACCCAAGAACCTGCAACTG 732
              ||||||||||||||||||||||||
Db         24 GACCCACCCAAGAACCTGCAACTG 1


RESULT 34
CW047416/c
LOCUS       CW047416                330 bp    DNA     linear   GSS 28-OCT-2004
DEFINITION  104_285_10512716_115_30217 Sorghum methylation filtered library
            (LibID: 104) Sorghum bicolor genomic clone 10512716, genomic survey
            sequence.
ACCESSION   CW047416
VERSION     CW047416.1  GI:54724146
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 330)
  AUTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
            Martienssen,R.A.
  TITLE     Sorghum genome sequencing by methylation filtration
  JOURNAL   PLoS Biol. 3 (1), e13 (2005)
   PUBMED   15660154
COMMENT     Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: 285  row: e  column: 18
            Seq primer: M13/pUC Reverse
            Class: methylation filtered
            High quality sequence stop: 330.
FEATURES             Location/Qualifiers
     source          1. .330
                     /organism="Sorghum bicolor"
                     /mol_type="genomic DNA"
                     /cultivar="ATx623"
                     /db_xref="taxon:4558"
                     /clone="10512716"
                     /clone_lib="Sorghum methylation filtered library (LibID:
                     104)"
                     /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                     prepared from purified nuclei was randomly sheared,
                     end-repaired, size fractionated to enrich for the 0.5 to 5
                     kb fraction, ligated into HincII-digested pBCSK(-) vector
                     and electroporated into E. coli cells. This is a
                     methylation filtered library."
```

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ORIGIN

  Query Match             2.1%;  Score 21;  DB 13;  Length 330;
  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        441 AATCAGTACCGATTTGAAATT 461
              |||||||||||||||||||||
Db        100 AATCAGTACCGATTTGAAATT 80


RESULT 35
T99581/c
LOCUS       T99581                   374 bp    mRNA    linear   EST 31-MAR-1995
DEFINITION  ye65d08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone
            IMAGE:122607 5', mRNA sequence.
ACCESSION   T99581
VERSION     T99581.1  GI:749318
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 374)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 954
            High qality sequence stops: 243 Source: IMAGE Consortium, LLNL This
            clone is available royalty-free through LLNL ; contact the IMAGE
            Consortium (info@image.llnl.gov) for further information.
            Insert Length: 954   Std Error: 0.00
            Seq primer: M13RP1
            High quality sequence stop: 243.
FEATURES             Location/Qualifiers
     source          1. .374
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:475152"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:122607"
                     /sex="male"
                     /dev_stage="20 week-post conception fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares fetal liver spleen 1NFLS"
                     /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                     with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                     1st strand cDNA was primed with a Pac I - oligo(dT) primer
                     [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Pac I and cloned into the Pac I
                     and Eco RI sites of the modified pT7T3 vector.  Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
ORIGIN

  Query Match             2.1%;  Score 21;  DB 10;  Length 374;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        387 AAAATGTGAGGCAAAGAATTA 407
              |||||||||||||||||||||
Db         84 AAAATGTGAGGCAAAGAATTA 64


RESULT 36
CN071927/c
LOCUS       CN071927                 508 bp    mRNA    linear   EST 30-MAR-2004
DEFINITION  1021022B08.x2 1021 - Unigene II from Maize Genome Project Zea mays
            cDNA, mRNA sequence.
ACCESSION   CN071927
VERSION     CN071927.1  GI:45847984
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 508)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 1021022  row: B  column: 08.
FEATURES             Location/Qualifiers
     source          1. .508
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /db_xref="dbEST:949071E08.x1"
                     /db_xref="taxon:4577"
                     /clone_lib="1021 - Unigene II from Maize Genome Project"
                     /note="This library represents the unique genes found in
                     the second round of EST sequencing at Stanford University
                     for the maize genome project. Sequences are present from
                     library 949. Contigs were assembled using ZmDBAssembler
                     and 2 representatives from each contig were selected for
                     the Unigene set. All singlets were also selected. Library
                     947, also part of Unigene II, was submitted under NAME
                     '1020 - Unigene II from Maize Genome Project'."
ORIGIN

  Query Match             2.1%;  Score 21;  DB 8;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        314 TACTCCTGAAGAAGATGACAT 294


RESULT 37
CF059708/c
LOCUS       CF059708                 509 bp    mRNA    linear   EST 21-JUL-2003
DEFINITION  QCS15g07.yg QCS Zea mays cDNA clone QCS15g07, mRNA sequence.
ACCESSION   CF059708
VERSION     CF059708.1  GI:33099748
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 509)
  AUTHORS   Genoplante.
  TITLE     Genoplante, a major partnership french program in plant genomics
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Genoplante
            Genoplante
```

```
            93, rue Henri Rochefort 91025 EVRY CEDEX France
            Tel: 33 1 69 47 54 00
            Fax: 33 1 69 47 54 10
            This sequence has been generated in the framework of the french
            plant genomics programme 'Genoplante' (http://www.genoplante.com
            and http://genoplante-info.infobiogen.fr).
FEATURES              Location/Qualifiers
     source           1. .509
                      /organism="Zea mays"
                      /mol_type="mRNA"
                      /cultivar="F2"
                      /db_xref="taxon:4577"
                      /clone="QCS15g07"
                      /tissue_type="whole plant"
                      /clone_lib="QCS"
ORIGIN

  Query Match             2.1%;  Score 21;  DB 5;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        362 TACTCCTGAAGAAGATGACAT 342


RESULT 38
CF060247/c
LOCUS       CF060247                509 bp    mRNA    linear   EST 21-JUL-2003
DEFINITION  QCS5b05.yg QCS Zea mays cDNA clone QCS5b05, mRNA sequence.
ACCESSION   CF060247
VERSION     CF060247.1  GI:33100287
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 509)
  AUTHORS   Genoplante.
  TITLE     Genoplante, a major partnership french program in plant genomics
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Genoplante
            Genoplante
            93, rue Henri Rochefort 91025 EVRY CEDEX France
            Tel: 33 1 69 47 54 00
            Fax: 33 1 69 47 54 10
            This sequence has been generated in the framework of the french
            plant genomics programme 'Genoplante' (http://www.genoplante.com
            and http://genoplante-info.infobiogen.fr).
FEATURES              Location/Qualifiers
     source           1. .509
                      /organism="Zea mays"
                      /mol_type="mRNA"
                      /cultivar="F2"
                      /db_xref="taxon:4577"
                      /clone="QCS5b05"
                      /tissue_type="whole plant"
                      /clone_lib="QCS"
ORIGIN

  Query Match             2.1%;  Score 21;  DB 5;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        362 TACTCCTGAAGAAGATGACAT 342


RESULT 39
CF059885/c
LOCUS       CF059885                510 bp    mRNA    linear   EST 21-JUL-2003
DEFINITION  QCS18b04.yg QCS Zea mays cDNA clone QCS18b04, mRNA sequence.
ACCESSION   CF059885
VERSION     CF059885.1  GI:33099925
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 510)
  AUTHORS   Genoplante.
  TITLE     Genoplante, a major partnership french program in plant genomics
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Genoplante
            Genoplante
            93, rue Henri Rochefort 91025 EVRY CEDEX France
            Tel: 33 1 69 47 54 00
            Fax: 33 1 69 47 54 10
            This sequence has been generated in the framework of the french
            plant genomics programme 'Genoplante' (http://www.genoplante.com
            and http://genoplante-info.infobiogen.fr).
FEATURES              Location/Qualifiers
     source           1. .510
                      /organism="Zea mays"
                      /mol_type="mRNA"
                      /cultivar="F2"
                      /db_xref="taxon:4577"
                      /clone="QCS18b04"
                      /tissue_type="whole plant"
                      /clone_lib="QCS"
ORIGIN

  Query Match             2.1%;  Score 21;  DB 5;  Length 510;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        363 TACTCCTGAAGAAGATGACAT 343


RESULT 40
BI431328/c
LOCUS       BI431328                521 bp    mRNA    linear   EST 20-AUG-2001
DEFINITION  949071E08.x1 949 - Juvenile leaf and shoot cDNA from Steve Moose
            Zea mays cDNA, mRNA sequence.
ACCESSION   BI431328
VERSION     BI431328.1  GI:15215523
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 521)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 949071  row: E  column: 08.
FEATURES              Location/Qualifiers
     source           1. .521
                      /organism="Zea mays"
                      /mol_type="mRNA"
                      /cultivar="W64A"
                      /db_xref="taxon:4577"
```

```
                     /tissue_type="immature leaf primordium and vegetative
                     meristem"
                     /dev_stage="4 stages from 3-13 days after imbibing"
                     /lab_host="E. coli XLOLR"
                     /clone_lib="949 - Juvenile leaf and shoot cDNA from Steve
                     Moose"
                     /note="Organ: juvenile vegetative shoots; Vector:
                     pAD-GAL4-2.1; Site_1: EcoRI; Site_2: XhoI; Equal amounts
                     of total RNA by weight from 4 tissue sources (see below)
                     were pooled, polyA+ RNA isolated, and cDNA synthesized for
                     EcoRI (5') and XhoI (3') directional cloning into lambda
                     Hybrizap vector from Stratagene. Tissue Sources: 1. Whole
                     shoots 3 days after sowing/imbibing in wet soil. 2. Basal
                     1.5 cm shoots 6 days after sowing - includes yellow
                     portions of developing leaves 1-5, primordia from 6-8, and
                     the vegetative apex. 3. Non-green portions of developing
                     leaves 4-5 and the vegetative apex,  including adult leaf
                     primordia, 9 days after sowing. 4. Partially expanded and
                     greening leaves 4-5 at 13 days after sowing."
ORIGIN

  Query Match             2.1%;  Score 21;  DB 2;  Length 521;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        351 TACTCCTGAAGAAGATGACAT 331


RESULT 41
AI491671/c
LOCUS       AI491671                523 bp    mRNA    linear   EST 22-APR-1999
DEFINITION  486020E06.x2 486 - leaf primordia cDNA library from Hake lab Zea
            mays cDNA, mRNA sequence.
ACCESSION   AI491671
VERSION     AI491671.2  GI:4646526
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 523)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     On Mar 8, 1999 this sequence version replaced gi:4388499.
            Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 486020  row: E  column: 06.
FEATURES             Location/Qualifiers
     source          1. .523
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="B73"
                     /db_xref="taxon:4577"
                     /tissue_type="leaf primordia"
                     /dev_stage="P7-P11 leaf"
                     /lab_host="E.coli XL1-Blue MFR'"
                     /clone_lib="486 - leaf primordia cDNA library from Hake
                     lab"
                     /note="Organ: shoot; Vector: Lambda zap; Hake lab cDNA
                     library."
ORIGIN

  Query Match             2.1%;  Score 21;  DB 1;  Length 523;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        408 TACTCCTGAAGAAGATGACAT 388


RESULT 42
AW566435/c
LOCUS       AW566435                553 bp    mRNA    linear   EST 10-MAR-2000
DEFINITION  660074D12.x1 660 - Mixed stages of anther and pollen Zea mays cDNA,
            mRNA sequence.
ACCESSION   AW566435
VERSION     AW566435.1  GI:7227794
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 553)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 660074  row: D  column: 12.
FEATURES             Location/Qualifiers
     source          1. .553
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="Ohio43"
                     /db_xref="taxon:4577"
                     /tissue_type="whole premieotic anthers to pollen shed"
                     /dev_stage="premieotic anthers to pollen shed"
                     /lab_host="XLOLR"
                     /clone_lib="660 - Mixed stages of anther and pollen"
                     /note="Organ: anthers; Vector: Lambda Zap; Site_1: EcoRI;
                     Site_2: XhoI; Anther and pollen cDNA library.
                     Directionally sequenced with 5' end at the EcoRI site.
                     Created by Amie Franklin."
ORIGIN

  Query Match             2.1%;  Score 21;  DB 7;  Length 553;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        324 TACTCCTGAAGAAGATGACAT 304


RESULT 43
BQ294193
LOCUS       BQ294193                566 bp    mRNA    linear   EST 15-MAY-2002
DEFINITION  1091026G08.y2 1091 - Immature ear with common ESTs screened by
            Schmidt lab Zea mays cDNA, mRNA sequence.
ACCESSION   BQ294193
VERSION     BQ294193.1  GI:20803143
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 566)
```

```
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 1091026  row: G  column: 08.
FEATURES             Location/Qualifiers
     source          1. .566
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="OH43"
                     /db_xref="taxon:4577"
                     /tissue_type="Inflorescence meristem - floral organ
                     primordia"
                     /dev_stage="0.5 cm to 2 cm"
                     /lab_host="Stratagene XLOLR"
                     /clone_lib="1091 - Immature ear with common ESTs screened
                     by Schmidt lab"
                     /note="Organ: Immature ear; Vector: pAD-GAL4; Site_1:
                     EcoRI; Site_2: XhoI; RNA from library 606 was filtered for
                     common ESTs found in 606."
ORIGIN

  Query Match             2.1%;  Score 21;  DB 3;  Length 566;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        500 TACTCCTGAAGAAGATGACAT 520


RESULT 44
CA627255/c
LOCUS       CA627255                588 bp    mRNA    linear   EST 23-NOV-2002
DEFINITION  w11n.pk154.e4 w11n Triticum aestivum cDNA clone w11n.pk154.e4 5'
            end, mRNA sequence.
ACCESSION   CA627255
VERSION     CA627255.1  GI:25205551
KEYWORDS    EST.
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 588)
  AUTHORS   Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,
            Miao,G., Caraher,N. and Hanafey,M.K.
  TITLE     DuPont Wheat cDNA Sequence
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Scott V. Tingey
            Crop Genetics
            E. I. DuPont de Nemours and Company
            1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
            Tel: 302-631-2602
            Fax: 302-631-2607
            Email: Scott.V.Tingey@USA.dupont.com
            Seq primer: M13.
FEATURES             Location/Qualifiers
     source          1. .588
                     /organism="Triticum aestivum"
                     /mol_type="mRNA"
                     /db_xref="taxon:4565"
                     /clone="w11n.pk154.e4"
                     /tissue_type="leaf"
                     /clone_lib="w11n"
                     /note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
                     XhoI; Wheat (Triticum aestivum L.) leaf 7 day old
                     seedling, light grown (normalized)"
ORIGIN

  Query Match             2.1%;  Score 21;  DB 4;  Length 588;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        357 TACTCCTGAAGAAGATGACAT 337


RESULT 45
AW573354
LOCUS       AW573354                594 bp    mRNA    linear   EST 13-MAR-2000
DEFINITION  660074D12.y1 660 - Mixed stages of anther and pollen Zea mays cDNA,
            mRNA sequence.
ACCESSION   AW573354
VERSION     AW573354.1  GI:7238132
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 594)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 660074  row: D  column: 12.
FEATURES             Location/Qualifiers
     source          1. .594
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="Ohio43"
                     /db_xref="taxon:4577"
                     /tissue_type="whole premieotic anthers to pollen shed"
                     /dev_stage="premieotic anthers to pollen shed"
                     /lab_host="XLOLR"
                     /clone_lib="660 - Mixed stages of anther and pollen"
                     /note="Organ: anthers; Vector: Lambda Zap; Site_1: EcoRI;
                     Site_2: XhoI; Anther and pollen cDNA library.
                     Directionally sequenced with 5' end at the EcoRI site.
                     Created by Amie Franklin."
ORIGIN

  Query Match             2.1%;  Score 21;  DB 7;  Length 594;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        336 TACTCCTGAAGAAGATGACAT 356


RESULT 46
BI478972
LOCUS       BI478972                599 bp    mRNA    linear   EST 27-AUG-2001
DEFINITION  949071E08.y1 949 - Juvenile leaf and shoot cDNA from Steve Moose
            Zea mays cDNA, mRNA sequence.
ACCESSION   BI478972
VERSION     BI478972.1  GI:15313824
KEYWORDS    EST.
SOURCE      Zea mays
```

```
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 599)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 949071  row: E  column: 08.
FEATURES             Location/Qualifiers
     source          1. .599
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="W64A"
                     /db_xref="taxon:4577"
                     /tissue_type="immature leaf primordium and vegetative
                     meristem"
                     /dev_stage="4 stages from 3-13 days after imbibing"
                     /lab_host="E. coli XLOLR"
                     /clone_lib="949 - Juvenile leaf and shoot cDNA from Steve
                     Moose"
                     /note="Organ: juvenile vegetative shoots; Vector:
                     pAD-GAL4-2.1; Site_1: EcoRI; Site_2: XhoI; Equal amounts
                     of total RNA by weight from 4 tissue sources (see below)
                     were pooled, polyA+ RNA isolated, and cDNA synthesized for
                     EcoRI (5') and XhoI (3') directional cloning into lambda
                     Hybrizap vector from Stratagene. Tissue Sources: 1. Whole
                     shoots 3 days after sowing/imbibing in wet soil. 2. Basal
                     1.5 cm shoots 6 days after sowing - includes yellow
                     portions of developing leaves 1-5, primordia from 6-8, and
                     the vegetative apex. 3. Non-green portions of developing
                     leaves 4-5 and the vegetative apex,  including adult leaf
                     primordia, 9 days after sowing. 4. Partially expanded and
                     greening leaves 4-5 at 13 days after sowing."
ORIGIN

  Query Match             2.1%;  Score 21;  DB 2;  Length 599;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        471 TACTCCTGAAGAAGATGACAT 491


RESULT 47
CA293522/c
LOCUS       CA293522                632 bp    mRNA    linear   EST 26-SEP-2003
DEFINITION  SCSGLV1005G05.g LV1 Saccharum officinarum cDNA clone SCSGLV1005G05
            5', mRNA sequence.
ACCESSION   CA293522
VERSION     CA293522.1  GI:36054204
KEYWORDS    EST.
SOURCE      Saccharum officinarum
  ORGANISM  Saccharum officinarum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
            complex.
REFERENCE   1  (bases 1 to 632)
  AUTHORS   Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
  TITLE     The libraries that made SUCEST
  JOURNAL   Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT     Contact: Arruda P
            Centro de Biologia Molecular e Engenharia Genetica
            Universidade Estadual de Campinas
            Caixa Postal 6010, 13083-970, Campinas SP, Brazil
            Tel: 55 19 3788 1137
            Fax: 55 19 3788 1089
            Email: parruda@unicamp.br
            Clone distribution: clone distribution information can be found
            through the Brazilian Clone Collection Center (BCCC) at
            http://www.bcccenter.fcav.unesp.br
            Plate: 005  row: G  column: 05
            Seq primer: T7 Promoter Primer.
FEATURES             Location/Qualifiers
     source          1. .632
                     /organism="Saccharum officinarum"
                     /mol_type="mRNA"
                     /db_xref="taxon:4547"
                     /clone="SCSGLV1005G05"
                     /lab_host="DH10B"
                     /clone_lib="LV1"
                     /note="Organ: Etiolated leaves from in vitro grown
                     sedlings; Vector: pSport1; Site_1: SalI; Site_2: NotI; An
                     unidirectional cDNA library generated from [Etiolated
                     leaves from in  vitro grown sedlings]. cDNA was prepared
                     from polyA+ mRNA using  SuperScript Plasmid System Kit
                     (Invitrogen). The double-strand cDNAs were  fractionated
                     in a sepharose CL-2B 40cm-columns and fragments sizing
                     between 0.8 and 1.5 Kb were directionally cloned into the
                     vector. Details  of each source of RNA and library
                     construction can be obtained at
                     http://sucest.lad.ic.unicamp.br/public"
ORIGIN

  Query Match             2.1%;  Score 21;  DB 4;  Length 632;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        441 AATCAGTACCGATTTGAAATT 461
              |||||||||||||||||||||
Db        620 AATCAGTACCGATTTGAAATT 600


RESULT 48
DN207344/c
LOCUS       DN207344                633 bp    mRNA    linear   EST 28-FEB-2005
DEFINITION  MEST847_H05.T7-1 UGA-ZmSAM-XZ2 Zea mays cDNA, mRNA sequence.
ACCESSION   DN207344
VERSION     DN207344.1  GI:60340371
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 633)
  AUTHORS   Chen,H.D., Zhang,X., Zhou,R.L., Arias L,A.C., Shendelman,J.M.,
            Zazubovits,N., Borsuk,L.A., Emrich,S.J., Ashlock,D.A., Scanlon,M.J.
            and Schnable,P.S.
  TITLE     Expressed Sequence Tags from B73 Maize Shoot Apical Meristems
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Patrick S. Schnable
            Schnable Laboratory
            Iowa State University
            2035B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA
            Tel: 515-294-0975
            Fax: 515-294-5256
            Email: schnable@iastate.edu.
FEATURES             Location/Qualifiers
     source          1. .633
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="inbred B73"
                     /db_xref="taxon:4577"
                     /tissue_type="Vegetative Shoot Apical Meristem (SAM) and
                     leaf primordia staged P1-P4"
```

/lab_host="XL1-Blue"
/clone_lib="UGA-ZmSAM-XZ2"
/note="Organ: Shoot apex; Vector: Uni-Zap XR; Site_1: EcoRI; Site_2: XhoI; This library was constructed by Xiaolan Zhang. Vegetative Shoot Apical Meristem (SAM) and leaf primordia staged P1-P4 from 14-17 day-after germination seedlings were quickly dissected into dry ice under a light microscope. Total RNA was isolated using Trizol and mRNA was purified with Dynal Oligo-DT25. ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with an XhoI oligo-dT primer (5'-GAGAGAGAGAGAGAGAGAACTAGTCTCGAGTTTTTTTTTTTTTTTT). The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with XhoI and size-selected to be >600 bp. The resulting molecules were directionally cloned into the EcoRI and XhoI sites of the Uni-Zap XR vector. The lambda library was packaged with Gigapack III Gold packaging extract and was mass excised by XL1-Blue cells and ExAssist helper phage. Excised phagemids were titered in SOLR cells and plated onto LB-ampicillin agar plates. Base calling was conducted using Phred. Trimming was performed using Lucy with the following criteria: (-minimum 200 -error 0.01 0.01 -bracket 10 0.01). A low complexity filter was applied and additional trimming was conducted to remove E. coli, vector, and organelle contamination. After processing ~30% of the sequences contained a minimum of 10 Ts at the beginning of the sequence. For reasons that are not understood many of the clones in this library lack an XhoI site at their 3' ends."
ORIGIN

Query Match 2.1%; Score 21; DB 9; Length 633;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        456 TACTCCTGAAGAAGATGACAT 436
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RESULT 49
BQ294192/c
LOCUS BQ294192 637 bp mRNA linear EST 15-MAY-2002
DEFINITION 1091026G08.x2 1091 - Immature ear with common ESTs screened by Schmidt lab Zea mays cDNA, mRNA sequence.
ACCESSION BQ294192
VERSION BQ294192.1 GI:20803142
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 637)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 1091026 row: G column: 08.
FEATURES Location/Qualifiers
source 1. .637
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="OH43"
/db_xref="taxon:4577"
/tissue_type="Inflorescence meristem - floral organ primordia"
/dev_stage="0.5 cm to 2 cm"
/lab_host="Stratagene XLOLR"
/clone_lib="1091 - Immature ear with common ESTs screened by Schmidt lab"
/note="Organ: Immature ear; Vector: pAD-GAL4; Site_1: EcoRI; Site_2: XhoI; RNA from library 606 was filtered for common ESTs found in 606."
ORIGIN

Query Match 2.1%; Score 21; DB 3; Length 637;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        359 TACTCCTGAAGAAGATGACAT 339
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RESULT 50
DN222336/c
LOCUS DN222336 692 bp mRNA linear EST 28-FEB-2005
DEFINITION MEST1126_F09.T7-1 UGA-ZmSAM-XZ2 Zea mays cDNA, mRNA sequence.
ACCESSION DN222336
VERSION DN222336.1 GI:60355363
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 692)
AUTHORS Chen,H.D., Zhang,X., Zhou,R.L., Arias L,A.C., Shendelman,J.M., Zazubovits,N., Borsuk,L.A., Emrich,S.J., Ashlock,D.A., Scanlon,M.J. and Schnable,P.S.
TITLE Expressed Sequence Tags from B73 Maize Shoot Apical Meristems
JOURNAL Unpublished (2004)
COMMENT Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
2035B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA
Tel: 515-294-0975
Fax: 515-294-5256
Email: schnable@iastate.edu.
FEATURES Location/Qualifiers
source 1. .692
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="inbred B73"
/db_xref="taxon:4577"
/tissue_type="Vegetative Shoot Apical Meristem (SAM) and leaf primordia staged P1-P4"
/lab_host="XL1-Blue"
/clone_lib="UGA-ZmSAM-XZ2"
/note="Organ: Shoot apex; Vector: Uni-Zap XR; Site_1: EcoRI; Site_2: XhoI; This library was constructed by Xiaolan Zhang. Vegetative Shoot Apical Meristem (SAM) and leaf primordia staged P1-P4 from 14-17 day-after germination seedlings were quickly dissected into dry ice under a light microscope. Total RNA was isolated using Trizol and mRNA was purified with Dynal Oligo-DT25. ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with an XhoI oligo-dT primer (5'-GAGAGAGAGAGAGAGAGAACTAGTCTCGAGTTTTTTTTTTTTTTTT). The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with XhoI and size-selected to be

>600 bp. The resulting molecules were directionally cloned into the EcoRI and XhoI sites of the Uni-Zap XR vector. The lambda library was packaged with Gigapack III Gold packaging extract and was mass excised by XL1-Blue cells and ExAssist helper phage. Excised phagemids were titered in SOLR cells and plated onto LB-ampicillin agar plates. Base calling was conducted using Phred. Trimming was performed using Lucy with the following criteria: (-minimum 200 -error 0.01 0.01 -bracket 10 0.01). A low complexity filter was applied and additional trimming was conducted to remove E. coli, vector, and organelle contamination. After processing ~30% of the sequences contained a minimum of 10 Ts at the beginning of the sequence. For reasons that are not understood many of the clones in this library lack an XhoI site at their 3' ends."

ORIGIN

Query Match 2.1%; Score 21; DB 9; Length 692;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        388 TACTCCTGAAGAAGATGACAT 368
```

RESULT 51
DN220924/c
LOCUS DN220924 693 bp mRNA linear EST 28-FEB-2005
DEFINITION MEST1104_C12.T7-1 UGA-ZmSAM-XZ2 Zea mays cDNA, mRNA sequence.
ACCESSION DN220924
VERSION DN220924.1 GI:60353951
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 693)
AUTHORS Chen,H.D., Zhang,X., Zhou,R.L., Arias L,A.C., Shendelman,J.M., Zazubovits,N., Borsuk,L.A., Emrich,S.J., Ashlock,D.A., Scanlon,M.J. and Schnable,P.S.
TITLE Expressed Sequence Tags from B73 Maize Shoot Apical Meristems
JOURNAL Unpublished (2004)
COMMENT Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
2035B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA
Tel: 515-294-0975
Fax: 515-294-5256
Email: schnable@iastate.edu.
FEATURES Location/Qualifiers
source 1. .693
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="inbred B73"
/db_xref="taxon:4577"
/tissue_type="Vegetative Shoot Apical Meristem (SAM) and leaf primordia staged P1-P4"
/lab_host="XL1-Blue"
/clone_lib="UGA-ZmSAM-XZ2"
/note="Organ: Shoot apex; Vector: Uni-Zap XR; Site_1: EcoRI; Site_2: XhoI; This library was constructed by Xiaolan Zhang. Vegetative Shoot Apical Meristem (SAM) and leaf primordia staged P1-P4 from 14-17 day-after germination seedlings were quickly dissected into dry ice under a light microscope. Total RNA was isolated using Trizol and mRNA was purified with Dynal Oligo-DT25. ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with an XhoI oligo-dT primer (5'-GAGAGAGAGAGAGAGAGAACTAGTCTCGAGTTTTTTTTTTTTTTTT). The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with XhoI and size-selected to be >600 bp. The resulting molecules were directionally cloned into the EcoRI and XhoI sites of the Uni-Zap XR vector. The lambda library was packaged with Gigapack III Gold packaging extract and was mass excised by XL1-Blue cells and ExAssist helper phage. Excised phagemids were titered in SOLR cells and plated onto LB-ampicillin agar plates. Base calling was conducted using Phred. Trimming was performed using Lucy with the following criteria: (-minimum 200 -error 0.01 0.01 -bracket 10 0.01). A low complexity filter was applied and additional trimming was conducted to remove E. coli, vector, and organelle contamination. After processing ~30% of the sequences contained a minimum of 10 Ts at the beginning of the sequence. For reasons that are not understood many of the clones in this library lack an XhoI site at their 3' ends."

ORIGIN

Query Match 2.1%; Score 21; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        359 TACTCCTGAAGAAGATGACAT 339
```

RESULT 52
DN219584/c
LOCUS DN219584 694 bp mRNA linear EST 28-FEB-2005
DEFINITION MEST1083_C10.T7-1 UGA-ZmSAM-XZ2 Zea mays cDNA, mRNA sequence.
ACCESSION DN219584
VERSION DN219584.1 GI:60352611
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 694)
AUTHORS Chen,H.D., Zhang,X., Zhou,R.L., Arias L,A.C., Shendelman,J.M., Zazubovits,N., Borsuk,L.A., Emrich,S.J., Ashlock,D.A., Scanlon,M.J. and Schnable,P.S.
TITLE Expressed Sequence Tags from B73 Maize Shoot Apical Meristems
JOURNAL Unpublished (2004)
COMMENT Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
2035B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA
Tel: 515-294-0975
Fax: 515-294-5256
Email: schnable@iastate.edu.
FEATURES Location/Qualifiers
source 1. .694
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="inbred B73"
/db_xref="taxon:4577"
/tissue_type="Vegetative Shoot Apical Meristem (SAM) and leaf primordia staged P1-P4"
/lab_host="XL1-Blue"
/clone_lib="UGA-ZmSAM-XZ2"
/note="Organ: Shoot apex; Vector: Uni-Zap XR; Site_1: EcoRI; Site_2: XhoI; This library was constructed by Xiaolan Zhang. Vegetative Shoot Apical Meristem (SAM) and leaf primordia staged P1-P4 from 14-17 day-after germination seedlings were quickly dissected into dry ice under a light microscope. Total RNA was isolated using Trizol and mRNA was purified with Dynal Oligo-DT25.

ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with an XhoI oligo-dT primer (5'-GAGAGAGAGAGAGAGAGAACTAGTCTCGAGTTTTTTTTTTTTTTTT). The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with XhoI and size-selected to be >600 bp. The resulting molecules were directionally cloned into the EcoRI and XhoI sites of the Uni-Zap XR vector. The lambda library was packaged with Gigapack III Gold packaging extract and was mass excised by XL1-Blue cells and ExAssist helper phage. Excised phagemids were titered in SOLR cells and plated onto LB-ampicillin agar plates. Base calling was conducted using Phred. Trimming was performed using Lucy with the following criteria: (-minimum 200 -error 0.01 0.01 -bracket 10 0.01). A low complexity filter was applied and additional trimming was conducted to remove E. coli, vector, and organelle contamination. After processing ~30% of the sequences contained a minimum of 10 Ts at the beginning of the sequence. For reasons that are not understood many of the clones in this library lack an XhoI site at their 3' ends."

ORIGIN

Query Match 2.1%; Score 21; DB 9; Length 694;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        456 TACTCCTGAAGAAGATGACAT 436
```

RESULT 53
DV622355/c
LOCUS DV622355 716 bp mRNA linear EST 01-NOV-2005
DEFINITION IV-1091-403D-A11.T7-1 UGIV-1091-Reseq Zea mays cDNA, mRNA sequence.
ACCESSION DV622355
VERSION DV622355.1 GI:78544857
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 716)
AUTHORS Zhou,R.L., Shendelman,J.M., Borsuk,L.A., Chen,H.D., Chen,Y.R. and Schnable,P.S.
TITLE Resequencing Unigene IV-1091 EST set
JOURNAL Unpublished (2005)
COMMENT Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
2035B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA
Tel: 515-294-0975
Fax: 515-294-5256
Email: schnable@iastate.edu.
FEATURES Location/Qualifiers
source 1. .716
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="taxon:4577"
/clone_lib="UGIV-1091-Reseq"

ORIGIN

Query Match 2.1%; Score 21; DB 10; Length 716;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        409 TACTCCTGAAGAAGATGACAT 389
```

RESULT 54
AY112414/c
LOCUS AY112414 724 bp mRNA linear HTC 01-MAR-2005
DEFINITION Zea mays CL8984_1 mRNA sequence.
ACCESSION AY112414
VERSION AY112414.1 GI:21217004
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 724)
AUTHORS Gardiner,J., Schroeder,S., Polacco,M.L., Sanchez-Villeda,H., Fang,Z., Morgante,M., Landewe,T., Fengler,K., Useche,F., Hanafey,M., Tingey,S., Chou,H., Wing,R., Soderlund,C. and Coe,E.H. Jr.
TITLE Anchoring 9,371 maize expressed sequence tagged unigenes to the bacterial artificial chromosome contig map by two-dimensional overgo hybridization
JOURNAL Plant Physiol. 134 (4), 1317-1326 (2004)
PUBMED 15020742
REFERENCE 2 (bases 1 to 724)
AUTHORS Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 3 (bases 1 to 724)
AUTHORS Coe,E.H.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.
FEATURES Location/Qualifiers
source 1. .724
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="MaizeGDB:633032"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Cornsensus Library"
/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
ORIGIN

Query Match 2.1%; Score 21; DB 6; Length 724;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        391 TACTCCTGAAGAAGATGACAT 371
```

RESULT 55
CL163765/c
LOCUS CL163765 743 bp DNA linear GSS 06-JAN-2004
DEFINITION 104_357_10807387_116_31813_139 Sorghum methylation-filtered library (LibID: 104) Sorghum bicolor genomic clone 10807387, genomic survey

```
            sequence.
ACCESSION   CL163765
VERSION     CL163765.1  GI:40671650
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 743)
  AUTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
            Martienssen,R.A.
  TITLE     Sorghum genome sequencing by methylation filtration
  JOURNAL   PLoS Biol. 3 (1), e13 (2005)
   PUBMED   15660154
COMMENT     Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: 357  row: f  column: 19
            Seq primer: T3 Reverse
            Class: methylation filtered
            High quality sequence stop: 743.
FEATURES             Location/Qualifiers
     source          1. .743
                     /organism="Sorghum bicolor"
                     /mol_type="genomic DNA"
                     /cultivar="ATx623"
                     /db_xref="taxon:4558"
                     /clone="10807387"
                     /clone_lib="Sorghum methylation-filtered library (LibID:
                     104)"
                     /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                     prepared from purified nuclei was randomly sheared,
                     end-repaired, size fractionated to enrich for the 0.5 to 5
                     kb fraction, ligated into HincII-digested pBCSK(-) vector
                     and electroporated into E. coli cells. This is a
                     methylation-filtered library."
ORIGIN

  Query Match             2.1%;  Score 21;  DB 12;  Length 743;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        441 AATCAGTACCGATTTGAAATT 461
              |||||||||||||||||||||
Db         77 AATCAGTACCGATTTGAAATT 57


RESULT 56
AG462380
LOCUS       AG462380                755 bp    DNA     linear   GSS 22-DEC-2004
DEFINITION  Mus musculus molossinus DNA, clone:MSMg01-350N23.T7, genomic survey
            sequence.
ACCESSION   AG462380
VERSION     AG462380.1  GI:48159636
KEYWORDS    GSS.
SOURCE      Mus musculus molossinus (Japanese wild mouse)
  ORGANISM  Mus musculus molossinus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T.,
            Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and
            Shiroishi,T.
  TITLE     Contribution of Asian mouse subspecies Mus musculus molossinus to
            genomic constitution of strain C57BL/6J, as defined by BAC-end
            sequence-SNP analysis
  JOURNAL   Genome Res. 14 (12), 2439-2447 (2004)
   PUBMED   15574823
REFERENCE   2  (bases 1 to 755)
  AUTHORS   Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
            (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the mouse BAC library MSMg01. For BAC
            library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
            Tsukuba Institude, Bio Resource Center,
            The Institute of Physical and Chemical Research (RIKEN) 3-1-1
            Koyadai, Tsukuba, 305-0074 Japan
            phone: 81-298-36-9189, fax: 81-298-36-9199
            e-mail: abe@rtc.riken.jp
            PRIMERS
            Sequencing : T7
            LIBRARY
            Vector     : pBACe3.6
            R.Site 1   : EcoRI
            R.Site 2   : EcoRI.
FEATURES             Location/Qualifiers
     source          1. .755
                     /organism="Mus musculus molossinus"
                     /mol_type="genomic DNA"
                     /sub_species="molossinus"
                     /db_xref="taxon:57486"
                     /clone="MSMg01-350N23.T7"
                     /sex="male"
                     /tissue_type="mixture of kidney and spleen"
                     /clone_lib="MSMg01 Mouse Male BAC Library"
ORIGIN

  Query Match             2.1%;  Score 21;  DB 14;  Length 755;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        346 ATCTTAAGGGAACAGAAAGAA 366
              |||||||||||||||||||||
Db        102 ATCTTAAGGGAACAGAAAGAA 122


RESULT 57
CC698019/c
LOCUS       CC698019                762 bp    DNA     linear   GSS 19-JUN-2003
DEFINITION  OGWBY19TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0532D13,
            genomic survey sequence.
ACCESSION   CC698019
VERSION     CC698019.1  GI:32102795
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
            Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
  TITLE     Consortium for Maize Genomics
  JOURNAL   Unpublished (2002)
COMMENT     Other_GSSs: OGWBY19TV
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TR
            Class: methylation filtered.
```

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FEATURES             Location/Qualifiers
     source          1. .762
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBMa0532D13"
                     /clone_lib="ZM_0.7_1.5_KB"
                     /note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
                     methylation filtered genomic DNA library"
ORIGIN

  Query Match             2.1%;  Score 21;  DB 12;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        308 TACTCCTGAAGAAGATGACAT 288


RESULT 58
CG122646
LOCUS       CG122646                 803 bp    DNA     linear   GSS 20-AUG-2003
DEFINITION  PUIMH25TB ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0615F02,
            genomic survey sequence.
ACCESSION   CG122646
VERSION     CG122646.1  GI:34006083
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 803)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
  TITLE     Maize Genomics Consortium
  JOURNAL   Unpublished (2003)
COMMENT     Other_GSSs: PUIMH25TD
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TR
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .803
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBTa0615F02"
                     /clone_lib="ZM_0.6_1.0_KB"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
                     CoT selected genomic DNA library"
ORIGIN

  Query Match             2.1%;  Score 21;  DB 12;  Length 803;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        252 TACTCCTGAAGAAGATGACAT 272


RESULT 59
CG134486/c
LOCUS       CG134486                 837 bp    DNA     linear   GSS 21-AUG-2003
DEFINITION  PUFSJ61TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0722K02,
            genomic survey sequence.
ACCESSION   CG134486
VERSION     CG134486.1  GI:34021933
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 837)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
  TITLE     Maize Genomics Consortium
  JOURNAL   Unpublished (2003)
COMMENT     Other_GSSs: PUFSJ61TB
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .837
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBTa0722K02"
                     /clone_lib="ZM_0.6_1.0_KB"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
                     CoT selected genomic DNA library"
ORIGIN

  Query Match             2.1%;  Score 21;  DB 12;  Length 837;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        441 AATCAGTACCGATTTGAAATT 461
              |||||||||||||||||||||
Db        401 AATCAGTACCGATTTGAAATT 381


RESULT 60
CC927699/c
LOCUS       CC927699                 853 bp    DNA     linear   GSS 11-AUG-2003
DEFINITION  ZMMBBc0532M21r ZMMBBc Zea mays genomic clone ZMMBBc0532M21 3',
            genomic survey sequence.
ACCESSION   CC927699
VERSION     CC927699.1  GI:33578797
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 853)
  AUTHORS   Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
            Rouzard,K., Fuks,G., Yu,Y., Wing,R. and Messing,J.
  TITLE     Sequencing of the maize genome at PGIR (2003b)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Bharti,A.K.
            Dr.Joachim Messing's lab
            The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
            University
            190 Frelinghuysen Road, Piscataway, NJ 08854, USA
            Tel: 732 445 3801
            Fax: 732 445 5735
            Email: bharti@waksman.rutgers.edu
            Seq primer: SP6
```

```
            Class: BAC ends
            High quality sequence start: 431.
FEATURES             Location/Qualifiers
     source          1. .853
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /cultivar="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBBc0532M21"
                     /lab_host="E. coli DH10B"
                     /clone_lib="ZMMBBc"
                     /note="Vector: pTARBAC1.3; Site_1: BamHI; Site_2: BamHI"
ORIGIN

  Query Match             2.1%;  Score 21;  DB 12;  Length 853;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        708 GGACCCACCCAAGAACCTGCA 728
              |||||||||||||||||||||
Db         86 GGACCCACCCAAGAACCTGCA 66


RESULT 61
BF241716/c
LOCUS       BF241716                 895 bp    mRNA    linear   EST 14-NOV-2000
DEFINITION  601879850F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108381 5',
            mRNA sequence.
ACCESSION   BF241716
VERSION     BF241716.1  GI:11155642
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 895)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: CLONETECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM991  row: d  column: 14
            High quality sequence stop: 588.
FEATURES             Location/Qualifiers
     source          1. .895
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4108381"
                     /tissue_type="from acute myelogenous leukemia"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_55"
                     /note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
                     Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI
                     (ggccattatggcc); Double-stranded cDNA was prepared from
                     cell line RNA.  5' and 3' adaptors were used in cloning as
                     follows: 5' adaptor sequence:  5'-CACGGCCATTATGGCC-3' and
                     3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).   Average insert size
                     1.65 kb (range 0.9-4.0 kb).  14/15 colonies contained
                     inserts by PCR. This library was enriched for full-length
                     clones and was constructed by Clontech  Laboratories (Palo
                     Alto, CA)."
ORIGIN

  Query Match             2.1%;  Score 21;  DB 7;  Length 895;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        593 GTGCCTGCCCGGCTGCCGAGG 613
              |||||||||||||||||||||
Db        813 GTGCCTGCCCGGCTGCCGAGG 793


RESULT 62
CG033595/c
LOCUS       CG033595                 983 bp    DNA     linear   GSS 19-AUG-2003
DEFINITION  PUKDR51TB ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0795J06,
            genomic survey sequence.
ACCESSION   CG033595
VERSION     CG033595.1  GI:33905751
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 983)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
  TITLE     Maize Genomics Consortium
  JOURNAL   Unpublished (2003)
COMMENT     Other_GSSs: PUKDR51TD
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TR
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .983
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBTa0795J06"
                     /clone_lib="ZM_0.6_1.0_KB"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
                     CoT selected genomic DNA library"
ORIGIN

  Query Match             2.1%;  Score 21;  DB 12;  Length 983;
  Best Local Similarity   100.0%;  Pred. No. 29;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        267 TACTCCTGAAGAAGATGACAT 247


RESULT 63
BZ782656
LOCUS       BZ782656                 987 bp    DNA     linear   GSS 17-MAR-2003
DEFINITION  PUFDX77TB ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa297M10,
            genomic survey sequence.
ACCESSION   BZ782656
VERSION     BZ782656.1  GI:28976253
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 987)
```

```
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
  TITLE     Maize Genomics Consortium
  JOURNAL   Unpublished (2003)
COMMENT     Other_GSSs: PUFDX77TD
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TR
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBTa297M10"
                     /clone_lib="ZM_0.6_1.0_KB"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
                     CoT selected genomic DNA library"
ORIGIN

  Query Match             2.1%;  Score 21;  DB 12;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 29;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        463 TACTCCTGAAGAAGATGACAT 483


RESULT 64
BZ782662/c
LOCUS       BZ782662                 999 bp    DNA     linear   GSS 17-MAR-2003
DEFINITION  PUFDX77TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa297M10,
            genomic survey sequence.
ACCESSION   BZ782662
VERSION     BZ782662.1  GI:28976259
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 999)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
  TITLE     Maize Genomics Consortium
  JOURNAL   Unpublished (2003)
COMMENT     Other_GSSs: PUFDX77TB
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .999
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBTa297M10"
                     /clone_lib="ZM_0.6_1.0_KB"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
                     CoT selected genomic DNA library"
ORIGIN

  Query Match             2.1%;  Score 21;  DB 12;  Length 999;
  Best Local Similarity   100.0%;  Pred. No. 29;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        686 TACTCCTGAAGAAGATGACAT 666


RESULT 65
CE034167
LOCUS       CE034167                 366 bp    DNA     linear   GSS 24-SEP-2003
DEFINITION  tigr-gss-dog-17000348379744 Dog Library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION   CE034167
VERSION     CE034167.1  GI:35059603
KEYWORDS    GSS.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 366)
  AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
            Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
            Venter,J.C.
  TITLE     The dog genome: survey sequencing and comparative analysis
  JOURNAL   Science 301 (5641), 1898-1903 (2003)
   PUBMED   14512627
COMMENT     Contact: Kirkness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirknes@tigr.org
            Class: shotgun.
FEATURES             Location/Qualifiers
     source          1. .366
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /strain="Standard Poodle"
                     /db_xref="taxon:9615"
                     /clone_lib="Dog Library"
                     /note="Site_1: BstXI; Libraries were prepared from
                     peripheral blood"
ORIGIN

  Query Match             2.0%;  Score 20;  DB 12;  Length 366;
  Best Local Similarity   100.0%;  Pred. No. 92;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        314 ACAAAAAGGAAGATGGAATT 333
              ||||||||||||||||||||
Db         58 ACAAAAAGGAAGATGGAATT 77


RESULT 66
DN901347
LOCUS       DN901347                 376 bp    mRNA    linear   EST 25-APR-2005
DEFINITION  naq18f07.y1 Zebrafish retina. Unnormalized (naq) Danio rerio cDNA
            clone naq18f07 5', mRNA sequence.
ACCESSION   DN901347
VERSION     DN901347.1  GI:62886110
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 376)
```

```
  AUTHORS   Wistow,G.
  TITLE     NEIBank analysis of Zebrafish retina
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Wistow G
            Section on Molecular Structure and Function
            National Eye Institute
            6/331, NIH, Bethesda, MD 20892-2740, USA
            Tel: 301 402 3452
            Fax: 301 496 0078
            Email: graeme@helix.nih.gov
            Plate: 18  row: f  column: 07
            Seq primer: Universal M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .376
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="naq18f07"
                     /tissue_type="Retina"
                     /dev_stage="Adult"
                     /lab_host="EMDH10B"
                     /clone_lib="Zebrafish retina. Unnormalized (naq)"
                     /note="Organ: Eye; Vector: pCMVSport6; RNA was extracted
                     from Zebrafish retina tissue. A directionally cloned cDNA
                     library in the pCMVSPORT6 vector (Invitrogen) was
                     constructed at Bioserve Biotechnology (Laurel MD)
                     essentially following the protocols of the SuperScript
                     Plasmid System, full details of which are contained in the
                     manufacturer's Instruction manual
                     (http://www.lifetech.com/). First strand synthesis was
                     carried out using a Not I primer-adapter
                     [5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)15-3']. cDNA was
                     cloned in Not I/Sal I sites. EST analysis was performed at
                     the NIH Intramural Sequencing Center (NISC). Analyzed data
                     available through http://neibank.nei.nih.gov."
ORIGIN

  Query Match             2.0%;  Score 20;  DB 9;  Length 376;
  Best Local Similarity   100.0%;  Pred. No. 92;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        842 AGAACAACAGAGAAAAGAAA 861
              ||||||||||||||||||||
Db         72 AGAACAACAGAGAAAAGAAA 91


RESULT 67
BH772784
LOCUS       BH772784                454 bp    DNA     linear   GSS 01-AUG-2002
DEFINITION  4CTF CTSSR-PCRlibrary Biomphalaria glabrata genomic clone 4-CTF,
            genomic survey sequence.
ACCESSION   BH772784
VERSION     BH772784.1  GI:22038714
KEYWORDS    GSS.
SOURCE      Biomphalaria glabrata
  ORGANISM  Biomphalaria glabrata
            Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata;
            Basommatophora; Lymnaeoidea; Planorbidae; Biomphalaria.
REFERENCE   1  (bases 1 to 454)
  AUTHORS   Caldeira,R.L., Carvalho,O.S., Lage,R.C.G., Cardoso,P.C.M. and
            Oliveira,G.C.
  TITLE     Sequence Characterization of Biomphalaria glabrata Simple Sequence
            Repeat Anchored Polymerase Chain Reaction Amplification Products
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Oliveira GC
            Laboratorio de Parasitologia Celular e Molecular
            Centro de Pesquisas Rene Rachou - FIOCRUZ
            Av. Augusto de Lima 1715, Barro Preto, Belo Horizonte, MG,
            30190-002, Brazil
            Tel: 55 31 32953566
            Fax: 55 31 32953115
            Email: oliveira@cpqrr.fiocruz.br
            PCR fragment amplified with CAA(CT)6.
            Seq primer: M13-Forward Universal
            Class: Random amplified microsatellites.
FEATURES             Location/Qualifiers
     source          1. .454
                     /organism="Biomphalaria glabrata"
                     /mol_type="genomic DNA"
                     /strain="Rene Rachou"
                     /db_xref="taxon:6526"
                     /clone="4-CTF"
                     /sex="hermaphrodite"
                     /dev_stage="Adult"
                     /clone_lib="CTSSR-PCRlibrary"
                     /note="The sequence was obtained by SSR-PCR amplification
                     using primer CAA(CT)6 for CT named clones or (CA)8RY for
                     CA named clones. The PCR products were cloned into the pCR
                     II vector (Invitrogen), selected on LB/amp plates and
                     sequenced in an ALF automated sequencer using the Thermo
                     Sequenase Kit (Amersham) using the universal reverse
                     primer."
ORIGIN

  Query Match             2.0%;  Score 20;  DB 11;  Length 454;
  Best Local Similarity   100.0%;  Pred. No. 94;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        848 ACAGAGAAAAGAAAGACAGA 867
              ||||||||||||||||||||
Db        404 ACAGAGAAAAGAAAGACAGA 423


RESULT 68
BM849607
LOCUS       BM849607                460 bp    mRNA    linear   EST 06-MAR-2002
DEFINITION  K-EST0129703 S21SNU520 Homo sapiens cDNA clone S21SNU520-38-F05 5',
            mRNA sequence.
ACCESSION   BM849607
VERSION     BM849607.1  GI:19206006
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 460)
  AUTHORS   Oh,J.H., Yang,J.O., Hahn,Y., Kim,M.R., Byun,S.S., Jeon,Y.J.,
            Kim,J.M., Song,K.S., Noh,S.M., Kim,S., Yoo,H.S., Kim,Y.S. and
            Kim,N.S.
  TITLE     Transcriptome analysis of human gastric cancer
  JOURNAL   Mamm. Genome 16 (12), 942-954 (2005)
   PUBMED   16341674
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 38  row: F  column: 05
            High quality sequence stop: 460.
FEATURES             Location/Qualifiers
     source          1. .460
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="S21SNU520-38-F05"
                     /sex="F"
                     /tissue_type="Stomach"
                     /cell_type="Floating aggregates"
                     /cell_line="SNU-520"
                     /lab_host="Top10F'"
                     /clone_lib="S21SNU520"
                     /note="Organ: Stomach; Vector: pTZ18RP1; Site_1: EcoRI;
                     Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
```

bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

```
  Query Match             2.0%;  Score 20;  DB 3;  Length 460;
  Best Local Similarity   100.0%;  Pred. No. 94;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        842 AGAACAACAGAGAAAAGAAA 861
              ||||||||||||||||||||
Db         65 AGAACAACAGAGAAAAGAAA 84
```

RESULT 69
DN504486/c

```
LOCUS       DN504486                467 bp    mRNA    linear   EST 10-MAR-2005
DEFINITION  HL010009000_F09_70_075 Equine lymphocyte cDNA Library Equus
            caballus cDNA clone HL010009000_F09_70_075, mRNA sequence.
ACCESSION   DN504486
VERSION     DN504486.1  GI:60714676
KEYWORDS    EST.
SOURCE      Equus caballus (horse)
  ORGANISM  Equus caballus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
REFERENCE   1  (bases 1 to 467)
  AUTHORS   Antczak,D.F.
  TITLE     Expressed sequence tags from a normalized equine lymphocyte cDNA
            library
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Antczak DF
            Baker Institute for Animal Health, College of Veterinary Medicine
            Cornell University
            Hungerford Hill Rd., Ithaca, NY 14853, USA
            Tel: 607.256.5633
            Fax: 607.256.5608
            Email: dfa1@cornell.edu
            High quality sequence stop: 467.
FEATURES             Location/Qualifiers
     source          1. .467
                     /organism="Equus caballus"
                     /mol_type="mRNA"
                     /strain="Thoroughbred & Standardbred breeds"
                     /db_xref="taxon:9796"
                     /clone="HL010009000_F09_70_075"
                     /tissue_type="Lymphocytes"
                     /dev_stage="Unstimulated [Tag-(polyA)TCGGA] & stimulated
                     in vitro with PWM [Tag-(polyA)TGCGA]"
                     /lab_host="DH12S E. coli cells (Invitrogen)"
                     /clone_lib="Equine lymphocyte cDNA Library"
                     /note="Vector: pGEM11Zf(+) (Promega); Site_1: EcoR1;
                     Site_2: Not1"
ORIGIN
```

```
  Query Match             2.0%;  Score 20;  DB 9;  Length 467;
  Best Local Similarity   100.0%;  Pred. No. 94;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        356 AACAGAAAGAATCCAAAAAT 375
              ||||||||||||||||||||
Db         79 AACAGAAAGAATCCAAAAAT 60
```

RESULT 70
BI983815

```
LOCUS       BI983815                479 bp    mRNA    linear   EST 24-OCT-2001
DEFINITION  fu08a02.x3 Campbell zebrafish ovary Danio rerio cDNA clone
            IMAGE:5304482 3', mRNA sequence.
ACCESSION   BI983815
VERSION     BI983815.1  GI:16374696
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 479)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
            Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library constructed by Library constructed by Invitrogen and
            donated by R. Campbell (Marine Biology Laboratory, Woods Hole, MA).
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: the I.M.A.G.E. Consortium/LLNL, send email to:
            info@image.llnl.gov
            Seq primer: T7 from Gibco
            High quality sequence stop: 417.
FEATURES             Location/Qualifiers
     source          1. .479
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:5304482"
                     /sex="female"
                     /dev_stage="4-5 months, 1 year and 2 years"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="Campbell zebrafish ovary"
                     /note="Organ: ovary(pooled); Vector: pCMV-SPORT6; Site_1:
                     NotI; Site_2: SalI; Whole ovaries collected from zebrafish
                     aged 4-5 months, 1 year and 2 years.  Oligo-dT primed,
                     directionally cloned.  Average insert size 2 kb.  Library
                     constructed by Invitrogen and donated by R. Campbell
                     (Marine Biology Laboratory, Woods Hole, MA)."
ORIGIN
```

```
  Query Match             2.0%;  Score 20;  DB 2;  Length 479;
  Best Local Similarity   100.0%;  Pred. No. 94;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        842 AGAACAACAGAGAAAAGAAA 861
              ||||||||||||||||||||
Db        188 AGAACAACAGAGAAAAGAAA 207
```

RESULT 71
BH772785/c

```
LOCUS       BH772785                486 bp    DNA     linear   GSS 01-AUG-2002
DEFINITION  4CTr CTSSR-PCRlibrary Biomphalaria glabrata genomic clone 4-CTr,
            genomic survey sequence.
ACCESSION   BH772785
VERSION     BH772785.1  GI:22038715
KEYWORDS    GSS.
SOURCE      Biomphalaria glabrata
```

```
  ORGANISM  Biomphalaria glabrata
            Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata;
            Basommatophora; Lymnaeoidea; Planorbidae; Biomphalaria.
REFERENCE   1  (bases 1 to 486)
  AUTHORS   Caldeira,R.L., Carvalho,O.S., Lage,R.C.G., Cardoso,P.C.M. and
            Oliveira,G.C.
  TITLE     Sequence Characterization of Biomphalaria glabrata Simple Sequence
            Repeat Anchored Polymerase Chain Reaction Amplification Products
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Oliveira GC
            Laboratorio de Parasitologia Celular e Molecular
            Centro de Pesquisas Rene Rachou - FIOCRUZ
            Av. Augusto de Lima 1715, Barro Preto, Belo Horizonte, MG,
            30190-002, Brazil
            Tel: 55 31 32953566
            Fax: 55 31 32953115
            Email: oliveira@cpqrr.fiocruz.br
            PCR fragment amplified with CAA(CT)6.
            Seq primer: M13-Forward Universal
            Class: Random amplified microsatellites.
FEATURES             Location/Qualifiers
     source          1. .486
                     /organism="Biomphalaria glabrata"
                     /mol_type="genomic DNA"
                     /strain="Rene Rachou"
                     /db_xref="taxon:6526"
                     /clone="4-CTr"
                     /sex="hermaphrodite"
                     /dev_stage="Adult"
                     /clone_lib="CTSSR-PCRlibrary"
                     /note="The sequence was obtained by SSR-PCR amplification
                     using primer CAA(CT)6 for CT named clones or (CA)8RY for
                     CA named clones. The PCR products were cloned into the pCR
                     II vector (Invitrogen), selected on LB/amp plates and
                     sequenced in an ALF automated sequencer using the Thermo
                     Sequenase Kit (Amersham) using the universal reverse
                     primer."
ORIGIN

  Query Match             2.0%;  Score 20;  DB 11;  Length 486;
  Best Local Similarity   100.0%;  Pred. No. 94;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        848 ACAGAGAAAAGAAAGACAGA 867
              ||||||||||||||||||||
Db        201 ACAGAGAAAAGAAAGACAGA 182


RESULT 72
AI292392
LOCUS       AI292392                488 bp    mRNA    linear   EST 01-DEC-1998
DEFINITION  NYZ036 Appel-Eisen zebrafish embryo 15-19 hr Danio rerio cDNA clone
            ZAE24 3', mRNA sequence.
ACCESSION   AI292392
VERSION     AI292392.1  GI:3941779
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 488)
  AUTHORS   Gates,M.A., Cardozo,T., Tobin,T., Egan,E., Sirotkin,H., Schier,A.F.
            and Talbot,W.S.
  TITLE     NYU zebrafish embryo EST project
  JOURNAL   Unpublished (1998)
COMMENT     Contact: William S. Talbot
            Skirball Institute, New York University School of Medicine
            540 First Avenue, New York, NY 10016, USA
            Fax: 212 263 7760
            Email: talbot@saturn.med.nyu.edu
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .488
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="ZAE24"
                     /sex="mixed"
                     /tissue_type="pooled 15-19 hr zebrafish embryos"
                     /clone_lib="Appel-Eisen zebrafish embryo 15-19 hr"
                     /note="Vector: pBluescript SK (-); Site_1: EcoRI; Site_2:
                     XhoI; Library was constructed by Bruce Appel and Judith
                     Eisen in Stratagene Uni-Zap XR lambda vector with Zap-cDNA
                     synthesis kit: EcoRI linkers were added to 5' ends and
                     XhoI linkers were added to 3' ends and resulting cDNAs
                     were ligated into Uni-Zap XR lambda vector. In vivo mass
                     excision was used to generate cDNAs in pBluescript SK."
ORIGIN

  Query Match             2.0%;  Score 20;  DB 1;  Length 488;
  Best Local Similarity   100.0%;  Pred. No. 95;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        842 AGAACAACAGAGAAAAGAAA 861
              ||||||||||||||||||||
Db        149 AGAACAACAGAGAAAAGAAA 168


RESULT 73
BI476340
LOCUS       BI476340                496 bp    mRNA    linear   EST 26-JUL-2002
DEFINITION  fq26h04.x3 zebrafish adult brain Danio rerio cDNA clone
            IMAGE:4832862 3', mRNA sequence.
ACCESSION   BI476340
VERSION     BI476340.1  GI:15309207
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 496)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
            Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library Preparation: John Ngai. cDNA Library Arrayed by:
            Matthew Clark. DNA Sequencing by: Washington University Genome
            Sequencing Center Clone distribution: Genome Systems, St. Louis,
            Missouri (web address: www.genomesystems.com) (email contact:
            info@genomesystems.com) and Research Genetics, Huntsville, Alabama
            (web address: www.resgen.com) (email contact: info@resgen.com) and
            RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
            www.rzpd.de)
            Seq primer: -40UP
            High quality sequence stop: 447.
FEATURES             Location/Qualifiers
     source          1. .496
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:4832862"
                     /sex="mixed male and female"
                     /tissue_type="brain"
                     /dev_stage="adult"
```

```
                     /lab_host="E. coli DH10B"
                     /clone_lib="zebrafish adult brain"
                     /note="Vector: pZIPLOX; Site_1: NotI; Site_2: SalI;
                     Original library was constructed in lambdaZIPLOX.  Mass
                     excision of the cDNA library was performed to yield
                     pZIPLOX plasmids. Insert check was done in original
                     library."
ORIGIN

  Query Match             2.0%;  Score 20;  DB 2;  Length 496;
  Best Local Similarity   100.0%;  Pred. No. 95;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        842 AGAACAACAGAGAAAAGAAA 861
              ||||||||||||||||||||
Db         84 AGAACAACAGAGAAAAGAAA 103


RESULT 74
BI981239
LOCUS       BI981239                504 bp    mRNA    linear   EST 26-JUL-2002
DEFINITION  fu41h06.x1 zebrafish adult brain Danio rerio cDNA clone
            IMAGE:5332091 3', mRNA sequence.
ACCESSION   BI981239
VERSION     BI981239.1  GI:16369655
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 504)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
            Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library Preparation: John Ngai. cDNA Library Arrayed by:
            Matthew Clark. DNA Sequencing by: Washington University Genome
            Sequencing Center Clone distribution: Genome Systems, St. Louis,
            Missouri (web address: www.genomesystems.com) (email contact:
            info@genomesystems.com) and Research Genetics, Huntsville, Alabama
            (web address: www.resgen.com) (email contact: info@resgen.com) and
            RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
            www.rzpd.de)
            Seq primer: -40UP
            High quality sequence stop: 444.
FEATURES             Location/Qualifiers
     source          1. .504
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:5332091"
                     /sex="mixed male and female"
                     /tissue_type="brain"
                     /dev_stage="adult"
                     /lab_host="E. coli DH10B"
                     /clone_lib="zebrafish adult brain"
                     /note="Vector: pZIPLOX; Site_1: NotI; Site_2: SalI;
                     Original library was constructed in lambdaZIPLOX.  Mass
                     excision of the cDNA library was performed to yield
                     pZIPLOX plasmids. Insert check was done in original
                     library."
ORIGIN

  Query Match             2.0%;  Score 20;  DB 2;  Length 504;
  Best Local Similarity   100.0%;  Pred. No. 95;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        842 AGAACAACAGAGAAAAGAAA 861
              ||||||||||||||||||||
Db         83 AGAACAACAGAGAAAAGAAA 102


RESULT 75
CB179502
LOCUS       CB179502                515 bp    mRNA    linear   EST 31-JAN-2003
DEFINITION  EST0595 Zea mays sperm cell cDNA library Zea mays cDNA clone
            Zmsp3098 5' similar to putative polyprotein, mRNA sequence.
ACCESSION   CB179502
VERSION     CB179502.1  GI:28187892
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 515)
  AUTHORS   Engel,M.L., Chaboud,A., Dumas,C. and McCormick,S.
  TITLE     Sperm cells of Zea mays have a complex complement of mRNAs
  JOURNAL   Plant J. 34 (5), 697-707 (2003)
   PUBMED   12787250
COMMENT     Contact: McCormick, S.
            Plant Gene Expression Center
            USDA/ARS
            800 Buchanan St. Albany, CA 94710, USA
            Tel: 510 559 5906
            Fax: 510 559 5678
            Email: sheilamc@nature.berkeley.edu.
FEATURES             Location/Qualifiers
     source          1. .515
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="A188"
                     /db_xref="taxon:4577"
                     /clone="Zmsp3098"
                     /cell_type="sperm"
                     /clone_lib="Zea mays sperm cell cDNA library"
                     /note="Vector: Clontech Triplex2; RNA was isolated from
                     fluorescent-activated cell sorted sperm cells. A cDNA
                     library was constructed by oligo dT priming using the
                     Clontech SMART cDNA synthesis kit. The cDNAs were
                     directionally cloned."
ORIGIN

  Query Match             2.0%;  Score 20;  DB 4;  Length 515;
  Best Local Similarity   100.0%;  Pred. No. 95;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        375 TAAGATCTTTCTAAAATGTG 394
              ||||||||||||||||||||
Db        182 TAAGATCTTTCTAAAATGTG 201


RESULT 76
BM270069
LOCUS       BM270069                520 bp    mRNA    linear   EST 08-JUL-2004
DEFINITION  sak24b12.y1 Gm-c1075 Glycine max cDNA clone SOYBEAN CLONE ID:
            Gm-c1075-3912 5' similar to TR:O22892 O22892 T2P4.22 PROTEIN. ;,
            mRNA sequence.
ACCESSION   BM270069
VERSION     BM270069.1  GI:17963327
KEYWORDS    EST.
SOURCE      Glycine max (soybean)
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
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            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 520)
  AUTHORS   Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
            Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
            Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
            Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
            Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
            McCann,R., Waterston,R. and Wilson,R.
  TITLE     Public Soybean EST Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            When it has been determined, an EST from the other end of this
            clone is listed in the 'Other ESTs on clone' field. This clone is
            available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
            57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
            Seq primer: -40RP from Gibco
            High quality sequence stop: 435.
FEATURES             Location/Qualifiers
     source          1. .520
                     /organism="Glycine max"
                     /mol_type="mRNA"
                     /cultivar="Jack"
                     /db_xref="taxon:3847"
                     /clone="SOYBEAN CLONE ID: Gm-c1075-3912"
                     /tissue_type="differentiating somatic embryos cultered on
                     MSM6AC"
                     /lab_host="DH10B"
                     /clone_lib="Gm-c1075"
                     /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
                     XhoI; The cDNA library was constructed from mRNA isolated
                     from differentiating  somatic embryos cultered on MSM6AC.
                     The library was prepared using the  Stratagene pBluescript
                     II SK(+) library construction kit. Complementary  DNA was
                     synthesized from mRNA using a primer consisting of a
                     poly(dT)  sequence with an XhoI restriction site. EcoRI
                     adaptors were ligated to the  blunt-ended cDNA fragments
                     followed by XhoI digestion. The cDNA fragments  were
                     directionally cloned into the EcoRI-XhoI restriction site
                     of the  pBluescript vector. The ligated cDNA fragments
                     were transformed into E.coli ElectroMax DH10B host cells.
                     Tissue culture and library construction were performed by
                     Franooise Thibaud-Nissen and Anu Khana (Lila Vodkin lab,
                     University of Illinois)."
ORIGIN

  Query Match             2.0%;  Score 20;  DB 2;  Length 520;
  Best Local Similarity   100.0%;  Pred. No. 95;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        841 AAGAACAACAGAGAAAAGAA 860
              ||||||||||||||||||||
Db         35 AAGAACAACAGAGAAAAGAA 54


RESULT 77
BQ777940
LOCUS       BQ777940                526 bp    mRNA    linear   EST 26-JUL-2002
DEFINITION  il39a02.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6032162 5',
            mRNA sequence.
ACCESSION   BQ777940
VERSION     BQ777940.1  GI:21986412
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 526)
  AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
            Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
            Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
            Williams,T., Jackson,Y. and Bowers,Y.
  TITLE     Endocrine Pancreas Consortium
  JOURNAL   Unpublished (2000)
COMMENT     Other_ESTs: il39a02.x1
            Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
            Washington University Genome Sequencing Center For information on
            obtaining a clone please contact: Dr. Hiroshi Inoue
            (hinoue@im.wustl.edu)
            Seq primer: -40RP from Gibco
            High quality sequence stop: 412.
FEATURES             Location/Qualifiers
     source          1. .526
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6032162"
                     /tissue_type="Purified pancreatic islet"
                     /lab_host="DH10B"
                     /clone_lib="HR85 islet"
                     /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
                     NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
                     Size-selected on agarose gel. Average insert size ~1kb. 5'
                     XhoI site was destroyed after directional cloning.
                     Amplified once. Contact information: Hiroshi Inoue, MD,
                     Metabolism Div. (Alan Permutt Lab), Washington University
                     School of Medicine, Box 8127, 660 South Euclid Ave., St.
                     Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
                     314-362-1916, Fax: 314-747-2692."
ORIGIN

  Query Match             2.0%;  Score 20;  DB 3;  Length 526;
  Best Local Similarity   100.0%;  Pred. No. 95;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        842 AGAACAACAGAGAAAAGAAA 861
              ||||||||||||||||||||
Db        109 AGAACAACAGAGAAAAGAAA 128


RESULT 78
CW070565/c
LOCUS       CW070565                528 bp    DNA     linear   GSS 28-OCT-2004
DEFINITION  104_321_10526839_5_30098 Sorghum methylation filtered library
            (LibID: 104) Sorghum bicolor genomic clone 10526839, genomic survey
            sequence.
ACCESSION   CW070565
VERSION     CW070565.1  GI:54747295
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 528)
  AUTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
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            Martienssen,R.A.
  TITLE     Sorghum genome sequencing by methylation filtration
  JOURNAL   PLoS Biol. 3 (1), e13 (2005)
   PUBMED   15660154
COMMENT     Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: 321  row: n  column: 05
            Seq primer: SKPrimer Reverse
            Class: methylation filtered
            High quality sequence stop: 528.
FEATURES             Location/Qualifiers
     source          1. .528
                     /organism="Sorghum bicolor"
                     /mol_type="genomic DNA"
                     /cultivar="ATx623"
                     /db_xref="taxon:4558"
                     /clone="10526839"
                     /clone_lib="Sorghum methylation filtered library (LibID:
                     104)"
                     /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                     prepared from purified nuclei was randomly sheared,
                     end-repaired, size fractionated to enrich for the 0.5 to 5
                     kb fraction, ligated into HincII-digested pBCSK(-) vector
                     and electroporated into E. coli cells. This is a
                     methylation filtered library."
ORIGIN

  Query Match             2.0%;  Score 20;  DB 13;  Length 528;
  Best Local Similarity   100.0%;  Pred. No. 95;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        305 TCCTGATACACAAAAAGGAA 324
              ||||||||||||||||||||
Db        388 TCCTGATACACAAAAAGGAA 369


RESULT 79
CK902268
LOCUS       CK902268                535 bp    mRNA    linear   EST 11-MAR-2004
DEFINITION  il39a02.x5 HR85 islet Homo sapiens cDNA clone IMAGE:6032162 3',
            mRNA sequence.
ACCESSION   CK902268
VERSION     CK902268.1  GI:45363799
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 535)
  AUTHORS   Melton,D., Meadows,A., Clifton,S., Hillier,L., Marra,M., Pape,D.,
            Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B.,
            Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M.,
            McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and
            Bowers,Y.
  TITLE     WashU-Harvard Pancreas EST Project
  JOURNAL   Unpublished (2000)
COMMENT     Other_ESTs: il39a02.y1
            Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            This read is a 3' RESEQUENCE of a previously sequenced pancreas
            clone
            Good hit to opposite strand read. . .wrong orientation BUT PASSED FOR
            MOUSE-PANCREAS VERIFICATION
            Seq primer: -40RP from Gibco
            High quality sequence stop: 535.
FEATURES             Location/Qualifiers
     source          1. .535
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6032162"
                     /tissue_type="Purified pancreatic islet"
                     /lab_host="DH10B"
                     /clone_lib="HR85 islet"
                     /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
                     NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
                     Size-selected on agarose gel. Average insert size ~1kb. 5'
                     XhoI site was destroyed after directional cloning.
                     Amplified once. Contact information: Hiroshi Inoue, MD,
                     Metabolism Div. (Alan Permutt Lab), Washington University
                     School of Medicine, Box 8127, 660 South Euclid Ave., St.
                     Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
                     314-362-1916, Fax: 314-747-2692."
ORIGIN

  Query Match             2.0%;  Score 20;  DB 5;  Length 535;
  Best Local Similarity   100.0%;  Pred. No. 95;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        842 AGAACAACAGAGAAAAGAAA 861
              ||||||||||||||||||||
Db        108 AGAACAACAGAGAAAAGAAA 127


RESULT 80
CO854235/c
LOCUS       CO854235                555 bp    mRNA    linear   EST 21-NOV-2004
DEFINITION  LM_SH5_004998 Locusta migratoria solitarious phase's head cDNA
            library Locusta migratoria cDNA, mRNA sequence.
ACCESSION   CO854235
VERSION     CO854235.1  GI:55914042
KEYWORDS    EST.
SOURCE      Locusta migratoria (migratory locust)
  ORGANISM  Locusta migratoria
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
            Acridoidea; Acrididae; Oedipodinae; Locusta.
REFERENCE   1  (bases 1 to 555)
  AUTHORS   Kang,L., Chen,X., Zhou,Y., Liu,B., Zheng,W., Li,R., Wang,J. and
            Yu,J.
  TITLE     The analysis of large-scale gene expression correlated to the phase
            changes of the migratory locust
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 101 (51), 17611-17615 (2004)
   PUBMED   15591108
COMMENT     Contact: Le Kang
            National Laboratory of Integrated Management of Insect Pests and
            Rodents
            Institute of zoology, Chinese Academy of Sciences
            25 Beisihuanxi Road, Haidian, Beijing, 100080, China
            Tel: 86-10-68597439
            Fax: 86-10-68597486
            Email: lkang@panda.ioz.ac.cn
            High quality sequence stop: 555.
FEATURES             Location/Qualifiers
     source          1. .555
                     /organism="Locusta migratoria"
                     /mol_type="mRNA"
                     /db_xref="taxon:7004"
                     /tissue_type="head"
                     /dev_stage="fifth-instar"
                     /clone_lib="Locusta migratoria solitarious phase's head
                     cDNA library"
ORIGIN

  Query Match             2.0%;  Score 20;  DB 8;  Length 555;
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  Best Local Similarity   100.0%;  Pred. No. 96;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        674 CCAGCAGCTTCTTCATCAGG 693
              ||||||||||||||||||||
Db        362 CCAGCAGCTTCTTCATCAGG 343


RESULT 81
BI785024
LOCUS       BI785024                556 bp    mRNA    linear   EST 21-JUL-2004
DEFINITION  saf96h10.y3 Gm-c1079 Glycine max cDNA clone GENOME SYSTEMS CLONE
            ID: Gm-c1079-1915 5' similar to TR:O22892 O22892 T2P4.22 PROTEIN.
            ;, mRNA sequence.
ACCESSION   BI785024
VERSION     BI785024.1  GI:15812749
KEYWORDS    EST.
SOURCE      Glycine max (soybean)
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 556)
  AUTHORS   Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
            Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
            Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
            Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
            Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
            McCann,R., Waterston,R. and Wilson,R.
  TITLE     Public Soybean EST Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            When it has been determined, an EST from the other end of this
            clone is listed in the 'Other ESTs on clone' field. This clone is
            available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
            57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
            Seq primer: -40RP from Gibco
            High quality sequence stop: 421.
FEATURES             Location/Qualifiers
     source          1. .556
                     /organism="Glycine max"
                     /mol_type="mRNA"
                     /cultivar="Bragg"
                     /db_xref="taxon:3847"
                     /clone="GENOME SYSTEMS CLONE ID: Gm-c1079-1915"
                     /tissue_type="Roots of 8 day old 'Bragg' seedlings"
                     /dev_stage="8 days old"
                     /lab_host="DH10B"
                     /clone_lib="Gm-c1079"
                     /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
                     XhoI; The mRNA was isolated from roots of 8 day old
                     'Bragg' seedlings that were mock-infected 72 hours prior
                     to harvest. Dr. Gary Stacey generously  donated the
                     tissue. The roots were flash-frozen in liquid nitrogen.
                     Stratagene's cDNA Synthesis Kit (catalog number 200401)
                     was used  to synthesize the cDNA. First-strand synthesis
                     was performed with  5-methyl dCTP, hence the ligated cDNA
                     was hemimethylated. A modification  of Stratagene's
                     first-strand synthesis primer was used. An 'anchor'
                     nucleotide (V=A, C, or G) was added to the 3' end of the
                     primer [GAGAGAGAGAGAGAGAGAACTAGTCTCGAG(T)18V] to anchor
                     the primer at the 5' end of the poly(A) tract. After
                     second-strand synthesis, the cDNA ends were filled in with
                     cloned Pfu DNA, ligated to EcoRI adapters and subsequently
                     phosphorylated. The cDNA was then precipitated and
                     redissolved in sterile, RNase-, DNase-free water. The XhoI
                     site within the first- strand synthesis primer was then
                     restricted by digestion with XhoI from Promega (40U/ul);
                     all XhoI sites in the cDNA would be protected by their
                     hemimethylated status. The cDNA constructs were
                     size-fractionated with  a 500bp cutoff, using Sephacryl
                     S-500 High Resolution (Pharmacia Biotech) in a 2-mm
                     diameter column and a bed volume of approximately 1ml. The
                     column eluent was precipitated, redissolved, and ligated
                     into Stratagene's pBluescript II XR Predigested vector
                     (pBluescript II SK(+) vector that has been digested with
                     EcoRI and XhoI, and phosphorylated by Stratagene). This
                     library was constucted in the laboratory of Dr. Paul Keim
                     and Dr. Virginia H. Coryell at Northern Arizona
                     University."
ORIGIN

  Query Match             2.0%;  Score 20;  DB 2;  Length 556;
  Best Local Similarity   100.0%;  Pred. No. 96;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        841 AAGAACAACAGAGAAAAGAA 860
              ||||||||||||||||||||
Db        160 AAGAACAACAGAGAAAAGAA 179


RESULT 82
AL956562
LOCUS       AL956562                563 bp    mRNA    linear   EST 04-DEC-2003
DEFINITION  AL956562 XGC-gastrula Xenopus tropicalis cDNA clone TGas105e12 5',
            mRNA sequence.
ACCESSION   AL956562
VERSION     AL956562.2  GI:38706017
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 563)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     On Nov 27, 2002 this sequence version replaced gi:25780157.
            Contact: Taylor R
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TGas105e12.p1kSP6
            Sequencing primer: SP6
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from stages 10-13
            gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with
            EcoRI at the 5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli XL1- blue.
FEATURES             Location/Qualifiers
     source          1. .563
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TGas105e12"
                     /dev_stage="gastrula (stages 10.5-12 mixed)"
                     /lab_host="Escherichia coli XL1-blue"
                     /clone_lib="XGC-gastrula"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from stages
                     10-13 gastrulae.  EcoRI-NotI cut cDNA was then ligated
                     into pCS107 with EcoRI at the 5' end and NotI at the 3'
                     end."
ORIGIN
```

```
  Query Match             2.0%;  Score 20;  DB 1;  Length 563;
  Best Local Similarity   100.0%;  Pred. No. 96;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        250 GATGCTGGCCAGTATACCTG 269
              ||||||||||||||||||||
Db        246 GATGCTGGCCAGTATACCTG 265


RESULT 83
BJ030774
LOCUS       BJ030774                564 bp    mRNA    linear   EST 26-SEP-2003
DEFINITION  BJ030774 NIBB Mochii normalized Xenopus neurula library Xenopus
            laevis cDNA clone XL005c01 5', mRNA sequence.
ACCESSION   BJ030774
VERSION     BJ030774.1  GI:17377868
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Xenopus.
REFERENCE   1  (bases 1 to 564)
  AUTHORS   Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
            Kohara,Y.
  TITLE     Expressed genes in X. laevis embryo
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp
            The information of this clone is available through the following
            URL.
            http://xenopus.nibb.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .564
                     /organism="Xenopus laevis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8355"
                     /clone="XL005c01"
                     /tissue_type="whole embryo"
                     /dev_stage="stage 15"
                     /clone_lib="NIBB Mochii normalized Xenopus neurula
                     library"
ORIGIN

  Query Match             2.0%;  Score 20;  DB 2;  Length 564;
  Best Local Similarity   100.0%;  Pred. No. 96;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        250 GATGCTGGCCAGTATACCTG 269
              ||||||||||||||||||||
Db        178 GATGCTGGCCAGTATACCTG 197


RESULT 84
AI666909
LOCUS       AI666909                570 bp    mRNA    linear   EST 08-JUN-1999
DEFINITION  fd16d08.x1 Sugano Kawakami zebrafish DRA Danio rerio cDNA clone
            IMAGE:2351727 3', mRNA sequence.
ACCESSION   AI666909
VERSION     AI666909.1  GI:4805265
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 570)
  AUTHORS   Sugano,S., Kawakami,K., Johnson,S., Li,F., Marra,M., Eddy,S.,
            Hillier,L., Clifton,S., Allen,M., Gibbons,M., Jost,S., Kucaba,T.,
            Martin,J., Pape,D., Steptoe,M., Underwood,K., Theising,B.,
            Ritter,E., Bowers,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1999
  JOURNAL   Unpublished (1999)
COMMENT     Contact: S.L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Library constructed by Dr. Sumio Sugano and D. Koichi Kawakami DNA
            Sequencing by: Washington University Genome Sequencing Center
            Seq primer: T7 ET from Amersham
            High quality sequence stop: 499.
FEATURES             Location/Qualifiers
     source          1. .570
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /strain="AB"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:2351727"
                     /sex="mixed (one male and one female, including
                     unfertilized eggs)"
                     /dev_stage="adult"
                     /lab_host="DH10B (phage resistant)"
                     /clone_lib="Sugano Kawakami zebrafish DRA"
                     /note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
                     Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
                     with an oligo(dT) primer  [ATGTGGCCTTTTTTTTTTTTTTTT];
                     double-stranded cDNA was ligated to a  DraIII adaptor
                     [TGTTGGCCTACTGG], digested and cloned into distinct DraIII
                     sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
                     CACCATGTG). XhoI should be used to isolate the cDNA
                     insert.  Size selection was performed to exclude fragments
                     <1.5kb.  Library constructed by Dr. Sumio Sugano
                     (University of Tokyo Institute of Medical Science) and
                     kindly donated by Dr. Koichi Kawakami.  Custom primers for
                     sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
                     primer CGACCTGCAGCTCGAGCACA.  "
ORIGIN

  Query Match             2.0%;  Score 20;  DB 1;  Length 570;
  Best Local Similarity   100.0%;  Pred. No. 96;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        842 AGAACAACAGAGAAAAGAAA 861
              ||||||||||||||||||||
Db         83 AGAACAACAGAGAAAAGAAA 102


RESULT 85
BJ032049
LOCUS       BJ032049                571 bp    mRNA    linear   EST 26-SEP-2003
DEFINITION  BJ032049 NIBB Mochii normalized Xenopus neurula library Xenopus
            laevis cDNA clone XL015h03 5', mRNA sequence.
ACCESSION   BJ032049
VERSION     BJ032049.1  GI:17375617
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Xenopus.
REFERENCE   1  (bases 1 to 571)
  AUTHORS   Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
            Kohara,Y.
  TITLE     Expressed genes in X. laevis embryo
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
```

```
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp
            The information of this clone is available through the following
            URL.
            http://xenopus.nibb.ac.jp.
FEATURES              Location/Qualifiers
     source           1. .571
                      /organism="Xenopus laevis"
                      /mol_type="mRNA"
                      /db_xref="taxon:8355"
                      /clone="XL015h03"
                      /tissue_type="whole embryo"
                      /dev_stage="stage 15"
                      /clone_lib="NIBB Mochii normalized Xenopus neurula
                      library"
ORIGIN

  Query Match             2.0%;  Score 20;  DB 2;  Length 571;
  Best Local Similarity   100.0%;  Pred. No. 96;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        250 GATGCTGGCCAGTATACCTG 269
              ||||||||||||||||||||
Db        140 GATGCTGGCCAGTATACCTG 159


RESULT 86
BJ627752
LOCUS       BJ627752                 578 bp    mRNA    linear   EST 01-OCT-2003
DEFINITION  BJ627752 NIBB Mochii normalized Xenopus early gastrula library
            Xenopus laevis cDNA clone XL219d21 5', mRNA sequence.
ACCESSION   BJ627752
VERSION     BJ627752.1  GI:37274652
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Xenopus.
REFERENCE   1  (bases 1 to 578)
  AUTHORS   Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
            Kohara,Y.
  TITLE     Expressed genes in X. laevis embryo
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp
            The information of this clone is available through the following
            URL.
            http://xenopus.nibb.ac.jp.
FEATURES              Location/Qualifiers
     source           1. .578
                      /organism="Xenopus laevis"
                      /mol_type="mRNA"
                      /db_xref="taxon:8355"
                      /clone="XL219d21"
                      /tissue_type="whole embryo"
                      /dev_stage="stage 10.5"
                      /clone_lib="NIBB Mochii normalized Xenopus early gastrula
                      library"
ORIGIN

  Query Match             2.0%;  Score 20;  DB 2;  Length 578;
  Best Local Similarity   100.0%;  Pred. No. 96;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        250 GATGCTGGCCAGTATACCTG 269
              ||||||||||||||||||||
Db        417 GATGCTGGCCAGTATACCTG 436


RESULT 87
CX600301/c
LOCUS       CX600301                 621 bp    mRNA    linear   EST 13-JAN-2005
DEFINITION  CT020026A20C01 Equine Articular Cartilage cDNA Library Equus
            caballus cDNA clone CT020026A20C01, mRNA sequence.
ACCESSION   CX600301
VERSION     CX600301.1  GI:57713619
KEYWORDS    EST.
SOURCE      Equus caballus (horse)
  ORGANISM  Equus caballus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
REFERENCE   1  (bases 1 to 621)
  AUTHORS   MacLeod,J.N.
  TITLE     Expressed sequence tags from a normalized equine articular
            cartilage cDNA library
  JOURNAL   Unpublished (2005)
COMMENT     Contact: MacLeod JN
            Department of Veterinary Science
            University of Kentucky
            Gluck Equine Research Center, Lexington, KY 40546-0099, USA
            Tel: 859.257.4757
            Fax: 859.257.8542
            Email: jnmacleod@uky.edu
            High quality sequence stop: 621.
FEATURES              Location/Qualifiers
     source           1. .621
                      /organism="Equus caballus"
                      /mol_type="mRNA"
                      /strain="Thoroughbred"
                      /db_xref="taxon:9796"
                      /clone="CT020026A20C01"
                      /sex="male"
                      /tissue_type="articular cartilage"
                      /dev_stage="1.5 year old"
                      /lab_host="DH12S E. Coli cells (Invitrogen)"
                      /clone_lib="Equine Articular Cartilage cDNA Library"
                      /note="Vector: pGEM11Zf(+) (Promega); Site_1: EcoR1;
                      Site_2: Not1"
ORIGIN

  Query Match             2.0%;  Score 20;  DB 9;  Length 621;
  Best Local Similarity   100.0%;  Pred. No. 97;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        356 AACAGAAAGAATCCAAAAAT 375
              ||||||||||||||||||||
Db        569 AACAGAAAGAATCCAAAAAT 550


RESULT 88
AL900775
LOCUS       AL900775                 633 bp    mRNA    linear   EST 04-DEC-2003
DEFINITION  AL900775 XGC-egg Xenopus tropicalis cDNA clone TEgg018m09 5', mRNA
            sequence.
ACCESSION   AL900775
VERSION     AL900775.2  GI:38699538
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 633)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     On Sep 16, 2002 this sequence version replaced gi:22953010.
            Contact: Taylor R
            Sanger Institute
```

```
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TEgg018m09.p1kSP6
            Sequencing primer: SP6
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from egg.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
            5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli XL1-blue.
FEATURES                Location/Qualifiers
     source             1. .633
                        /organism="Xenopus tropicalis"
                        /mol_type="mRNA"
                        /db_xref="taxon:8364"
                        /clone="TEgg018m09"
                        /dev_stage="egg"
                        /lab_host="Escherichia coli XL1-blue"
                        /clone_lib="XGC-egg"
                        /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                        was oligo dT primed from 5ug of poly A+ RNA from egg.
                        EcoRI-NotI cut cDNA was then ligated into pCS107 with
                        EcoRI at the 5' end and NotI at the 3' end"
ORIGIN

  Query Match              2.0%;  Score 20;  DB 1;  Length 633;
  Best Local Similarity   100.0%;  Pred. No. 97;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        250 GATGCTGGCCAGTATACCTG 269
              ||||||||||||||||||||
Db        183 GATGCTGGCCAGTATACCTG 202


RESULT 89
CE454520/c
LOCUS       CE454520                646 bp    DNA     linear   GSS 27-SEP-2003
DEFINITION  tigr-gss-dog-17000319465791 Dog Library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION   CE454520
VERSION     CE454520.1  GI:36748105
KEYWORDS    GSS.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 646)
  AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
            Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
            Venter,J.C.
  TITLE     The dog genome: survey sequencing and comparative analysis
  JOURNAL   Science 301 (5641), 1898-1903 (2003)
   PUBMED   14512627
COMMENT     Contact: Kirkness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirknes@tigr.org
            Class: shotgun.
FEATURES                Location/Qualifiers
     source             1. .646
                        /organism="Canis familiaris"
                        /mol_type="genomic DNA"
                        /strain="Standard Poodle"
                        /db_xref="taxon:9615"
                        /clone_lib="Dog Library"
                        /note="Site_1: BstXI; Libraries were prepared from
                        peripheral blood"
ORIGIN

  Query Match              2.0%;  Score 20;  DB 12;  Length 646;
  Best Local Similarity   100.0%;  Pred. No. 97;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        307 CTGATACACAAAAAGGAAGA 326
              ||||||||||||||||||||
Db        140 CTGATACACAAAAAGGAAGA 121


RESULT 90
CZ709509
LOCUS       CZ709509                649 bp    DNA     linear   GSS 25-JUL-2005
DEFINITION  OC__Ba0030E21.r OC__Ba Oryza coarctata genomic clone OC__Ba0030E21
            3', genomic survey sequence.
ACCESSION   CZ709509
VERSION     CZ709509.1  GI:71114283
KEYWORDS    GSS.
SOURCE      Oryza coarctata (Porteresia coarctata)
  ORGANISM  Oryza coarctata
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 649)
  AUTHORS   Kim,H., Collura,K., Wissotski,M., Byrne,M., Stum,D., Smart,D.,
            Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and
            Wing,R.
  TITLE     OMAP (Oryza Map Alignment Project)- Arizona Genomics Institute
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Rod A. Wing
            Arizona Genomics Institute
            University of Arizona
            Forbes Building Room 303, Tucson, AZ 85721-0036, USA
            Tel: 520 626 9595
            Fax: 520 621 1259
            Email: rwing@genome.arizona.edu
            PCR PRimers
            FORWARD: TAA TAC GAC TCA CTA TAG GG
            BACKWARD: CAC TCA TTA GGC ACC CCA
            Plate: 0030  row: E  column: 21
            Seq primer: CAC TCA TTA GGC ACC CCA
            Class: BAC ends.
FEATURES                Location/Qualifiers
     source             1. .649
                        /organism="Oryza coarctata"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:77588"
                        /clone="OC__Ba0030E21"
                        /tissue_type="leaves"
                        /dev_stage="mature"
                        /lab_host="DH10B"
                        /clone_lib="OC__Ba"
                        /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
ORIGIN

  Query Match              2.0%;  Score 20;  DB 13;  Length 649;
  Best Local Similarity   100.0%;  Pred. No. 97;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        310 ATACACAAAAAGGAAGATGG 329
              ||||||||||||||||||||
Db         27 ATACACAAAAAGGAAGATGG 46


RESULT 91
BM096034
LOCUS       BM096034                654 bp    mRNA    linear   EST 20-NOV-2001
DEFINITION  fv29g12.x1 Sugano SJD adult male Danio rerio cDNA clone
            IMAGE:5410006 3', mRNA sequence.
ACCESSION   BM096034
VERSION     BM096034.1  GI:17025000
KEYWORDS    EST.
```

```
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 654)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
            Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution information can be found through the I.M.A.G.E.
            Consortium/LLNL, send email to: info@image.llnl.gov
            High quality sequence stop: 525.
FEATURES             Location/Qualifiers
     source          1. .654
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:5410006"
                     /sex="male"
                     /tissue_type="whole body"
                     /dev_stage="adult"
                     /lab_host="DH10B (phage resistant)"
                     /clone_lib="Sugano SJD adult male"
                     /note="Vector: pME18S-FL3; Site_1: DraIII (CACCATGTG);
                     Site_2: DraIII (CACTGTGTG); 1st strand cDNA was primed
                     with an oligo(dT) primer  [ATGTGGCCTTTTTTTTTTTTTTTT];
                     double-stranded cDNA was ligated to a  DraIII adaptor
                     [TGTTGGCCTACTGG], digested and cloned into distinct DraIII
                     sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
                     CACCATGTG). XhoI should be used to isolate the cDNA
                     insert. Size selection was performed to exclude fragments
                     <1.5kb. Library constructed and donated by Dr. Sumio
                     Sugano (University of Tokyo Institute of Medical Science).
                     Custom primers for sequencing: 5' end primer
                     CTTCTGCTCTAAAAGCTGCG and 3' end primer
                     CGACCTGCAGCTCGAGCACA. "
ORIGIN

  Query Match             2.0%;  Score 20;  DB 2;  Length 654;
  Best Local Similarity   100.0%;  Pred. No. 98;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        842 AGAACAACAGAGAAAAGAAA 861
              ||||||||||||||||||||
Db         95 AGAACAACAGAGAAAAGAAA 114


RESULT 92
BJ042592
LOCUS       BJ042592                667 bp    mRNA    linear   EST 29-SEP-2003
DEFINITION  BJ042592 NIBB Mochii normalized Xenopus neurula library Xenopus
            laevis cDNA clone XL032c23 5', mRNA sequence.
ACCESSION   BJ042592
VERSION     BJ042592.1  GI:17392768
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Xenopus.
REFERENCE   1  (bases 1 to 667)
  AUTHORS   Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
            Kohara,Y.
  TITLE     Expressed genes in X. laevis embryo
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp
            The information of this clone is available through the following
            URL.
            http://xenopus.nibb.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .667
                     /organism="Xenopus laevis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8355"
                     /clone="XL032c23"
                     /tissue_type="whole embryo"
                     /dev_stage="stage 15"
                     /clone_lib="NIBB Mochii normalized Xenopus neurula
                     library"
ORIGIN

  Query Match             2.0%;  Score 20;  DB 2;  Length 667;
  Best Local Similarity   100.0%;  Pred. No. 98;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        250 GATGCTGGCCAGTATACCTG 269
              ||||||||||||||||||||
Db        281 GATGCTGGCCAGTATACCTG 300


RESULT 93
CT167835
LOCUS       CT167835                667 bp    DNA     linear   GSS 02-NOV-2005
DEFINITION  Sus scrofa genomic clone CH242-122N13, genomic survey sequence.
ACCESSION   CT167835
VERSION     CT167835.1  GI:79683824
KEYWORDS    GSS.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 667)
  AUTHORS   Humphray,S.J., Plumb,R.W. and Durham,J.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Unpublished
COMMENT     This sequence was generated from the SP6 end of BAC 122N13. 122N13
            is part of the CHORI-242 BAC Library created by P. de Jong. Further
            details: http://www.sanger.ac.uk/Projects/S_scrofa/.
FEATURES             Location/Qualifiers
     source          1. .667
                     /organism="Sus scrofa"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9823"
                     /clone="CH242-122N13"
                     /tissue_type="White blood cells"
                     /note="vector pTARBAC1.3_BamHI
                     sex female"
ORIGIN

  Query Match             2.0%;  Score 20;  DB 14;  Length 667;
  Best Local Similarity   100.0%;  Pred. No. 98;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        842 AGAACAACAGAGAAAAGAAA 861
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```
                    ||||||||||||||||||||
Db        164 AGAACAACAGAGAAAAGAAA 183


RESULT 94
CC008436/c
LOCUS       CC008436                681 bp    DNA     linear   GSS 31-MAR-2003
DEFINITION  PUDHR12TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa213B24,
            genomic survey sequence.
ACCESSION   CC008436
VERSION     CC008436.1  GI:29387056
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 681)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
  TITLE     Maize Genomics Consortium
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .681
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBTa213B24"
                     /clone_lib="ZM_0.6_1.0_KB"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
                     CoT selected genomic DNA library"
ORIGIN

  Query Match             2.0%;  Score 20;  DB 12;  Length 681;
  Best Local Similarity   100.0%;  Pred. No. 98;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        375 TAAGATCTTTCTAAAATGTG 394
              ||||||||||||||||||||
Db        677 TAAGATCTTTCTAAAATGTG 658


RESULT 95
AZ424475/c
LOCUS       AZ424475                690 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0204A12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0204A12 F, genomic survey sequence.
ACCESSION   AZ424475
VERSION     AZ424475.1  GI:10548488
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 690)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0204  row: A  column: 12
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 690.
FEATURES             Location/Qualifiers
     source          1. .690
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0204A12"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             2.0%;  Score 20;  DB 11;  Length 690;
  Best Local Similarity   100.0%;  Pred. No. 98;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        551 ACAGGGATTATAAGAAGTAC 570
              ||||||||||||||||||||
Db        250 ACAGGGATTATAAGAAGTAC 231


RESULT 96
BZ240832/c
LOCUS       BZ240832                696 bp    DNA     linear   GSS 12-OCT-2002
DEFINITION  CH230-272O10.TJB CHORI-230 Segment 2 Rattus norvegicus genomic
            clone CH230-272O10, genomic survey sequence.
ACCESSION   BZ240832
VERSION     BZ240832.1  GI:23901096
KEYWORDS    GSS.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 696)
  AUTHORS   Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
            Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D.,
            Riggs,F., de Jong,P. and Fraser,C.M.
  TITLE     Rat BAC End Sequences from Library CHORI-230 MboI segment
  JOURNAL   Unpublished (1999)
COMMENT     Other_GSSs: CH230-272O10.TV
```

```
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the rat BAC library CHORI-230
            (http://www.chori.org/bacpac/rat230.htm). For BAC library
            availability, please contact Pieter de Jong (pdejong@mail.cho.org).
            Clones may be purchased from BACPAC Resources
            (http://www.chori.org/bacpac/or ering_information.htm). BAC end
            page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
            Plate: 272  row: O  column: 10
            Seq primer: SP6
            Class: BAC ends.
FEATURES              Location/Qualifiers
     source           1. .696
                      /organism="Rattus norvegicus"
                      /mol_type="genomic DNA"
                      /strain="BN/SsNHsd/MCW"
                      /db_xref="taxon:10116"
                      /clone="CH230-272O10"
                      /sex="Female"
                      /cell_type="Brain"
                      /clone_lib="CHORI-230 Segment 2"
                      /note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
                      CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
                      Pieter de Jong"
ORIGIN

  Query Match              2.0%;  Score 20;  DB 11;  Length 696;
  Best Local Similarity   100.0%;  Pred. No. 98;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        155 CTCCTGAAGAAGATGACATC 174
              ||||||||||||||||||||
Db        105 CTCCTGAAGAAGATGACATC 86


RESULT 97
BG740695
LOCUS       BG740695                 698 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602631544F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4776634 5',
            mRNA sequence.
ACCESSION   BG740695
VERSION     BG740695.1  GI:14051348
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 698)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
            Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10629  row: h  column: 11
            High quality sequence stop: 694.
FEATURES              Location/Qualifiers
     source           1. .698
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:4776634"
                      /lab_host="DH10B (T1 phage-resistant)"
                      /clone_lib="NCI_CGAP_Skn3"
                      /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                      Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                      Average insert size 1.5kb.  Library constructed by Life
                      Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match              2.0%;  Score 20;  DB 2;  Length 698;
  Best Local Similarity   100.0%;  Pred. No. 98;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        842 AGAACAACAGAGAAAAGAAA 861
              ||||||||||||||||||||
Db        281 AGAACAACAGAGAAAAGAAA 300


RESULT 98
DT267303/c
LOCUS       DT267303                 701 bp    mRNA    linear   EST 18-AUG-2005
DEFINITION  JGI_CAAV1671.rev CAAV Pimephales promelas testis 7-8 month adults,
            males and females pooled (H) Pimephales promelas cDNA clone
            CAAV1671 3', mRNA sequence.
ACCESSION   DT267303
VERSION     DT267303.1  GI:73569252
KEYWORDS    EST.
SOURCE      Pimephales promelas
  ORGANISM  Pimephales promelas
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Pimephales.
REFERENCE   1  (bases 1 to 701)
  AUTHORS   Richardson,P., Lucas,S., Rokhsar,D., Detter,J.C., Ng,D.C.,
            Brokstein,P. and Lindquist,E.A.
  TITLE     DOE Joint Genome Institute Pimephales promelas EST project
  JOURNAL   Unpublished (2005)
COMMENT     Other_ESTs: JGI_CAAV1671.fwd
            Contact: Lindquist,E.A., Richardson,P.
            DOE Joint Genome Institute
            2800 Mitchell Drive, Walnut Creek, CA 94598, USA
            Tel: 925 296 5600
            Fax: 925 296 5710
            Email: cdna@jgi-psf.org
            cDNA Library Preparation: DOE Joint Genome Institute:
            http://www.jgi.doe.gov
            DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
            Naming Conventions: EST name is generated by the concatenation of
            the JGI Clone Id and the direction of sequencing. The suffix '.rev'
            indicates a reverse sequencing read of the insert. It does not
            necessarily reflect the orientation of the insert.
            Small Insert: Based upon one or more sequencing reads of this clone
            where vector sequence was present at both ends, this clone has been
            determined to contain a cDNA insert on the order of 600-1000 bases.
            Plate: CAAV 0017  row: n  column: 9
            High quality sequence stop: 701.
FEATURES              Location/Qualifiers
     source           1. .701
                      /organism="Pimephales promelas"
                      /mol_type="mRNA"
                      /db_xref="taxon:90988"
                      /clone="CAAV1671"
                      /tissue_type="testis"
                      /clone_lib="CAAV Pimephales promelas testis 7-8 month
                      adults, males and females pooled (H)"
                      /note="Vector: pCMVsport6; The library was made from dT
                      primed cDNA and cloned into Invitrogen vector pCMVsport6.
                      Poly A RNA were primed with an oligo dT primer (5'-
                      GACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTT -3') ligated
                      to a SalI adapter (5'- TCGACCCACGCGTCCG and 5'-
                      CGGACGCGTGGG) and digested with NotI. cDNA was size
                      selected using 1.1% agarose gel electrophoresis (L
                      ~0.5-1.2k, M ~1.2-2.5k, H ~>2.5k) then ligated into NotI
```

and SalI digested pCMVsport6 vector. The work was done at DOE Joint Genome Institute."
ORIGIN

Query Match 2.0%; Score 20; DB 10; Length 701;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 684 CTTCATCAGGGACATCATCA 703
||||||||||||||||||||
Db 660 CTTCATCAGGGACATCATCA 641

RESULT 99
DT267304
LOCUS DT267304 701 bp mRNA linear EST 18-AUG-2005
DEFINITION JGI_CAAV1671.fwd CAAV Pimephales promelas testis 7-8 month adults, males and females pooled (H) Pimephales promelas cDNA clone CAAV1671 5', mRNA sequence.
ACCESSION DT267304
VERSION DT267304.1 GI:73569253
KEYWORDS EST.
SOURCE Pimephales promelas
ORGANISM Pimephales promelas
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Pimephales.
REFERENCE 1 (bases 1 to 701)
AUTHORS Richardson,P., Lucas,S., Rokhsar,D., Detter,J.C., Ng,D.C., Brokstein,P. and Lindquist,E.A.
TITLE DOE Joint Genome Institute Pimephales promelas EST project
JOURNAL Unpublished (2005)
COMMENT Other_ESTs: JGI_CAAV1671.rev
Contact: Lindquist,E.A., Richardson,P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org
cDNA Library Preparation: DOE Joint Genome Institute: http://www.jgi.doe.gov
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Naming Conventions: EST name is generated by the concatenation of the JGI Clone Id and the direction of sequencing. The suffix '.fwd' indicates a forward sequencing read of the insert. It does not necessarily reflect the orientation of the insert.
Small Insert: Based upon one or more sequencing reads of this clone where vector sequence was present at both ends, this clone has been determined to contain a cDNA insert on the order of 600-1000 bases.
Plate: CAAV 0017 row: n column: 9
High quality sequence stop: 701.
FEATURES Location/Qualifiers
source 1. .701
/organism="Pimephales promelas"
/mol_type="mRNA"
/db_xref="taxon:90988"
/clone="CAAV1671"
/tissue_type="testis"
/clone_lib="CAAV Pimephales promelas testis 7-8 month adults, males and females pooled (H)"
/note="Vector: pCMVsport6; The library was made from dT primed cDNA and cloned into Invitrogen vector pCMVsport6. Poly A RNA were primed with an oligo dT primer (5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTT -3') ligated to a SalI adapter (5'- TCGACCCACGCGTCCG and 5'-CGGACGCGTGGG) and digested with NotI. cDNA was size selected using 1.1% agarose gel electrophoresis (L ~0.5-1.2k, M ~1.2-2.5k, H ~>2.5k) then ligated into NotI and SalI digested pCMVsport6 vector. The work was done at DOE Joint Genome Institute."
ORIGIN

Query Match 2.0%; Score 20; DB 10; Length 701;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 684 CTTCATCAGGGACATCATCA 703
||||||||||||||||||||
Db 42 CTTCATCAGGGACATCATCA 61

RESULT 100
DT283860/c
LOCUS DT283860 719 bp mRNA linear EST 18-AUG-2005
DEFINITION JGI_CAAV11218.rev CAAV Pimephales promelas testis 7-8 month adults, males and females pooled (H) Pimephales promelas cDNA clone CAAV11218 3', mRNA sequence.
ACCESSION DT283860
VERSION DT283860.1 GI:73585809
KEYWORDS EST.
SOURCE Pimephales promelas
ORGANISM Pimephales promelas
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Pimephales.
REFERENCE 1 (bases 1 to 719)
AUTHORS Richardson,P., Lucas,S., Rokhsar,D., Detter,J.C., Ng,D.C., Brokstein,P. and Lindquist,E.A.
TITLE DOE Joint Genome Institute Pimephales promelas EST project
JOURNAL Unpublished (2005)
COMMENT Other_ESTs: JGI_CAAV11218.fwd
Contact: Lindquist,E.A., Richardson,P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org
cDNA Library Preparation: DOE Joint Genome Institute: http://www.jgi.doe.gov
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Naming Conventions: EST name is generated by the concatenation of the JGI Clone Id and the direction of sequencing. The suffix '.rev' indicates a reverse sequencing read of the insert. It does not necessarily reflect the orientation of the insert.
Poly-A: Based upon the presence of a run of 14 or more T residues at the beginning of the sequence, this clone was polyadenylated. The resulting Poly-T sequence has been removed.
Plate: CAAV 0117 row: c column: 21
High quality sequence stop: 643
POLYA=Yes.
FEATURES Location/Qualifiers
source 1. .719
/organism="Pimephales promelas"
/mol_type="mRNA"
/db_xref="taxon:90988"
/clone="CAAV11218"
/tissue_type="testis"
/clone_lib="CAAV Pimephales promelas testis 7-8 month adults, males and females pooled (H)"
/note="Vector: pCMVsport6; The library was made from dT primed cDNA and cloned into Invitrogen vector pCMVsport6. Poly A RNA were primed with an oligo dT primer (5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTT -3') ligated to a SalI adapter (5'- TCGACCCACGCGTCCG and 5'-CGGACGCGTGGG) and digested with NotI. cDNA was size selected using 1.1% agarose gel electrophoresis (L ~0.5-1.2k, M ~1.2-2.5k, H ~>2.5k) then ligated into NotI and SalI digested pCMVsport6 vector. The work was done at DOE Joint Genome Institute."
ORIGIN

Query Match 2.0%; Score 20; DB 10; Length 719;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2006, 22:44:33 ; Search time 223.93 Seconds
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8230.433 Million cell updates/sec

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Perfect score: 985
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1403666 seqs, 935554401 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
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;   NAME/KEY: CDS
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US-09-917-265A-55

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Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
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Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 2
US-09-917-265A-57/c
; Sequence 57, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-57

  Query Match             100.0%;  Score 985;  DB 3;  Length 985;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86
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Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGCA 1


RESULT 3
US-09-917-265A-29
; Sequence 29, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
US-09-917-265A-29

  Query Match             100.0%;  Score 985;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 4
US-09-917-265A-31/c
; Sequence 31, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-31

  Query Match             100.0%;  Score 985;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808
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Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGCA 3
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RESULT 5
US-09-011-143-5
; Sequence 5, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2193 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-5

  Query Match             94.2%;  Score 928;  DB 3;  Length 2193;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  928;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy         58 CTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCT 117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCT 180

Qy        118 GATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACC 177
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Db        181 GATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACC 240

Qy        178 TGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTC 237
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Db        241 TGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTC 300

Qy        238 AAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCAT 297
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Db        301 AAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCAT 360

Qy        298 TCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAA 357
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Db        361 TCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAA 420

Qy        358 CAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGT 417
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Db        421 CAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGT 480

Qy        418 TTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGC 477
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGC 540

Qy        478 AGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAG 537
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAG 600

Qy        538 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 597
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 660
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Qy        598 TGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTC 657
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTC 720

Qy        658 AAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCC 717
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCC 780

Qy        718 AAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATAC 777
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATAC 840

Qy        778 CCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAG 837
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAG 900

Qy        838 GGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTC 897
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Db        901 GGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTC 960

Qy        898 GTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCC 957
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCC 1020

Qy        958 TGGAGCAACTGGGCATCCGTGTCCTGCA 985
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Db       1021 TGGAGCAACTGGGCATCCGTGTCCTGCA 1048
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RESULT 6
US-09-302-495-5
; Sequence 5, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2193 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-302-495-5

  Query Match           94.2%;  Score 928;  DB 3;  Length 2193;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  928;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         58 CTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCT 117
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Db        121 CTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCT 180

Qy        118 GATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACC 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACC 240

Qy        178 TGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTC 237
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Db        241 TGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTC 300

Qy        238 AAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCAT 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCAT 360

Qy        298 TCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAA 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAA 420

Qy        358 CAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGT 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGT 480

Qy        418 TTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGC 477
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Db        481 TTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGC 540

Qy        478 AGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAG 537
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        538 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 597
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 660

Qy        598 TGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTC 657
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTC 720

Qy        658 AAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCC 717
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Db        721 AAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCC 780

Qy        718 AAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATAC 777
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATAC 840

Qy        778 CCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAG 837
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAG 900

Qy        838 GGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTC 897
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Db        901 GGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTC 960

Qy        898 GTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCC 957
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Db        961 GTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCC 1020
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Qy        958 TGGAGCAACTGGGCATCCGTGTCCTGCA 985
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Db       1021 TGGAGCAACTGGGCATCCGTGTCCTGCA 1048


RESULT 7
US-10-079-616-5
; Sequence 5, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2193 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-079-616-5

  Query Match             94.2%;  Score 928;  DB 3;  Length 2193;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  928;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         58 CTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCT 117
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Db        121 CTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCT 180

Qy        118 GATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACC 177
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Db        181 GATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACC 240

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTC 300

Qy        238 AAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCAT 297
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Db        301 AAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCAT 360

Qy        298 TCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAA 357
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Db        361 TCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAA 420

Qy        358 CAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGT 417
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Db        421 CAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGT 480

Qy        418 TTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGC 477
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Db        481 TTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGC 540

Qy        478 AGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAG 537
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Db        541 AGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAG 600

Qy        538 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 597
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Db        601 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 660

Qy        598 TGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTC 657
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Db        661 TGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTC 720

Qy        658 AAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCC 717
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Db        721 AAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCC 780

Qy        718 AAGAACCTGCAACTGAAGCCATTAAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATAC 777
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Db        781 AAGAACCTGCAACTGAAGCCATTAAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATAC 840

Qy        778 CCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAG 837
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAG 900

Qy        838 GGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTC 897
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Qy        898 GTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCC 957
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Db        961 GTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCC 1020

Qy        958 TGGAGCAACTGGGCATCCGTGTCCTGCA 985
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Db       1021 TGGAGCAACTGGGCATCCGTGTCCTGCA 1048


RESULT 8
US-09-011-143-6
; Sequence 6, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
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;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/011,143
;       FILING DATE:  04-FEB-1998
;       CLASSIFICATION:  536
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/JP97/01824
;       FILING DATE:  29-MAY-1997
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 165249/1996
;       FILING DATE:  04-JUN-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  BROWDY, Roger L.
;       REGISTRATION NUMBER:  25,618
;       REFERENCE/DOCKET NUMBER:  IMAMURA=1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-628-5197
;       TELEFAX:  202-737-3528
;   INFORMATION FOR SEQ ID NO:  6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  921 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-09-011-143-6

  Query Match             93.3%;  Score 919;  DB 3;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  919;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
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Db          61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
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Db         121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

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Db         181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
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Db         241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy         367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
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Db         301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy         427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
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Db         361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy         487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
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Db         421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy         547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy         607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
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Db         541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy         667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
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Db         601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

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Db         661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy         787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
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Db         721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy         847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy         907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
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Db         841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy         967 TGGGCATCCGTGTCCTGCA 985
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Db         901 TGGGCATCCGTGTCCTGCA 919


RESULT 9
US-09-302-495-6
; Sequence 6, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/302,495
;            FILING DATE: 30-Apr-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 6:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 921 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
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;            TOPOLOGY: linear
;         MOLECULE TYPE: cDNA
;         SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-302-495-6

  Query Match             93.3%;  Score 919;  DB 3;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  919;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
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Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
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Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCA 985
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Db        901 TGGGCATCCGTGTCCTGCA 919
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RESULT 10
US-10-079-616-6
; Sequence 6, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-079-616-6

  Query Match             93.3%;  Score 919;  DB 3;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  919;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
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Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
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Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
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Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
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Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
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Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
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Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
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Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
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Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
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Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
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Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
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Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCA 985
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Db        901 TGGGCATCCGTGTCCTGCA 919
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RESULT 11
US-09-917-265A-38
; Sequence 38, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1599)
US-09-917-265A-38

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  Query Match             91.7%;  Score 903;  DB 3;  Length 1599;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  953;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db         32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91

Qy         92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151
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Db         92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151

Qy        152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211
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Db        152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211

Qy        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271

Qy        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331
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Db        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331

Qy        332 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 391

Qy        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451

Qy        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTG 511
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTG 511

Qy        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571

Qy        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631

Qy        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691

Qy        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751

Qy        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811

Qy        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 871
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 871

Qy        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931

Qy        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCA 985
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RESULT 12
US-09-917-265A-40/c
; Sequence 40, Application US/09917265A

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; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-40

  Query Match             91.7%;  Score 903;  DB 3;  Length 1599;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  953;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91
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Qy         92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151
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Db       1508 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 1449

Qy        152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211
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Db       1448 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 1389

Qy        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271
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Db       1388 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 1329

Qy        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1328 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 1269

Qy        332 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1268 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 1209

Qy        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1208 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 1149

Qy        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTG 511
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       1148 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTG 1089

Qy        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1088 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 1029

Qy        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1028 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 969

Qy        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        968 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 909

Qy        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        908 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 849

Qy        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 789

Qy        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 871
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        788 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 729

Qy        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 669

Qy        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCA 985
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCA 615


RESULT 13
US-09-011-143-7
; Sequence 7, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  921 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-7

  Query Match             88.1%;  Score 868;  DB 3;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
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Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
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Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
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Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
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Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCA 985
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Db        901 TGGGCATCCGTGTCCTGCA 919


RESULT 14
US-09-302-495-7
; Sequence 7, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 7:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-302-495-7

  Query Match            88.1%;  Score 868;  DB 3;  Length 921;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
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Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
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Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
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Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
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Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
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Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

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Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCA 985
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Db        901 TGGGCATCCGTGTCCTGCA 919


RESULT 15
US-10-079-616-7
; Sequence 7, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 7:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-079-616-7

  Query Match             88.1%;  Score 868;  DB 3;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
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Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
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Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
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Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
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Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
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Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
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Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
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Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
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Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
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Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
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Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
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Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCA 985
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Db        901 TGGGCATCCGTGTCCTGCA 919


RESULT 16
US-09-917-265A-26
; Sequence 26, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(921)
US-09-917-265A-26

  Query Match             88.1%;  Score 868;  DB 3;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCA 985
              ||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCA 919


RESULT 17
US-09-917-265A-28/c
; Sequence 28, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-28

  Query Match             88.1%;  Score 868;  DB 3;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682
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Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        967 TGGGCATCCGTGTCCTGCA 985
              ||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCA 3
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RESULT 18
US-09-917-265A-43
; Sequence 43, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)

US-09-917-265A-43

Query Match 88.1%; Score 868; DB 3; Length 1533;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 918; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCA 985
              ||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCA 919
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RESULT 19
US-09-917-265A-45/c

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; Sequence 45, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-45

  Query Match             88.1%;  Score 868;  DB 3;  Length 1533;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy         367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy         427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy         487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
               |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy         547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy         607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy         667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy         727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy         787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy         847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy         907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy         967 TGGGCATCCGTGTCCTGCA 985
               ||||||||||||||||||||
Db         633 TGGGCATCCGTGTCCTGCA 615


RESULT 20
US-09-917-265A-52
; Sequence 52, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(921)
US-09-917-265A-52

  Query Match              6.7%;  Score 66;  DB 3;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy         597 CTGCCC 602
               ||||||
Db         531 CTGCCC 536


RESULT 21
US-09-917-265A-54/c
; Sequence 54, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
;   LENGTH: 921
;   TYPE: DNA
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;   ORGANISM: Canis familiaris
US-09-917-265A-54

  Query Match             6.7%;  Score 66;  DB 3;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy        597 CTGCCC 602
              ||||||
Db        391 CTGCCC 386


RESULT 22
US-09-917-265A-58
; Sequence 58, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
US-09-917-265A-58

  Query Match             6.7%;  Score 66;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 23
US-09-917-265A-60/c
; Sequence 60, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-60

  Query Match             6.7%;  Score 66;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy        597 CTGCCC 602
              ||||||
Db        391 CTGCCC 386


RESULT 24
US-09-079-984A-1
; Sequence 1, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,984A
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  990 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 987
;      IDENTIFICATION METHOD:  Similarity
US-09-079-984A-1

  Query Match             6.7%;  Score 66;  DB 3;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
```

```
Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 25
US-09-079-984A-11
; Sequence 11, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,984A
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  990 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 987
;      IDENTIFICATION METHOD:  Similarity
US-09-079-984A-11

  Query Match             6.7%;  Score 66;  DB 3;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 26
US-09-390-729-1
; Sequence 1, Application US/09390729
; Patent No. 6562334
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/390,729
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/079,984
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  990 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 987
;      IDENTIFICATION METHOD:  Similarity
US-09-390-729-1

  Query Match             6.7%;  Score 66;  DB 3;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 27
US-09-390-729-11
; Sequence 11, Application US/09390729
; Patent No. 6562334
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
```

```
;       STREET:  1600 Market Street, 39th Floor
;       CITY:  Philadelphia
;       STATE:  PA
;       COUNTRY:  USA
;       ZIP:  19103
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy Disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  WordPerfect 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/390,729
;       FILING DATE:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  09/079,984
;       FILING DATE:  15-MAY-1998
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Austin R. Miller
;       REGISTRATION NUMBER:  16,602
;       REFERENCE/DOCKET NUMBER:  1051-98
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (215) 563-1810
;       TELEFAX:  (215) 568-6946
;   INFORMATION FOR SEQ ID NO:  11:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  990 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA to mRNA
;     ORIGINAL SOURCE:
;       ORGANISM:  Canis familiaris
;     FEATURE:
;       NAME/KEY:  Canine IL12
;       LOCATION:  1 to 987
;       IDENTIFICATION METHOD:  Similarity
US-09-390-729-11

  Query Match             6.7%;  Score 66;  DB 3;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 28
US-09-917-265A-66
; Sequence 66, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-09-917-265A-66

  Query Match             6.7%;  Score 66;  DB 3;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy        597 CTGCCC 602
              ||||||
Db        531 CTGCCC 536


RESULT 29
US-09-917-265A-68/c
; Sequence 68, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-68

  Query Match             6.7%;  Score 66;  DB 3;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy        597 CTGCCC 602
              ||||||
Db       1003 CTGCCC 998


RESULT 30
US-09-917-265A-61
; Sequence 61, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
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;   LOCATION: (1)..(1599)
US-09-917-265A-61

  Query Match             6.7%;  Score 66;  DB 3;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 31
US-09-917-265A-63/c
; Sequence 63, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-63

  Query Match             6.7%;  Score 66;  DB 3;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy        597 CTGCCC 602
              ||||||
Db       1003 CTGCCC 998


RESULT 32
US-09-917-265A-107
; Sequence 107, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 107
;   LENGTH: 2267
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (154)..(1140)
US-09-917-265A-107

  Query Match             6.7%;  Score 66;  DB 3;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 749

Qy        597 CTGCCC 602
              ||||||
Db        750 CTGCCC 755


RESULT 33
US-09-917-265A-109/c
; Sequence 109, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 109
;   LENGTH: 2267
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-109

  Query Match             6.7%;  Score 66;  DB 3;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1578 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1519

Qy        597 CTGCCC 602
              ||||||
Db       1518 CTGCCC 1513


RESULT 34
US-08-186-529-1
; Sequence 1, Application US/08186529
; Patent No. 5573764
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
```

```
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,529
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McDaniels, Patricia A.
;      REGISTRATION NUMBER:  33,194
;      REFERENCE/DOCKET NUMBER:  GI 5225
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8401
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  987 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Lymphoblast
;      CELL LINE:  RPMI 8866
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..987
US-08-186-529-1

  Query Match             4.5%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 35
US-08-640-386A-1
; Sequence 1, Application US/08640386A
; Patent No. 5756085
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/640,386A
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;      REFERENCE/DOCKET NUMBER:  GI 5225A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8224
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  987 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Lymphoblast
;      CELL LINE:  RPMI 8866
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..987
US-08-640-386A-1

  Query Match             4.5%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 36
US-08-848-760B-24
; Sequence 24, Application US/08848760B
; Patent No. 6248721
;   GENERAL INFORMATION:
;        APPLICANT: Chang, Lung-Ji
;        TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
;        NUMBER OF SEQUENCES: 33
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
;             STREET: 2421 N.W. 41st Street, Suite A-1
;             CITY: Gainesville
;             STATE: Florida
;             COUNTRY: United States of America
;             ZIP: 32606
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/848,760B
;             FILING DATE: 25-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/838,702
;             FILING DATE: 09-APR-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: PACE, DORAN R.
;             REGISTRATION NUMBER: 38,261
;             REFERENCE/DOCKET NUMBER: CNG-100C1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (352) 375-8100
;             TELEFAX: (352) 372-5800
;   INFORMATION FOR SEQ ID NO: 24:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 987 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: other nucleic acid
;             DESCRIPTION: /desc = "DNA"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-08-848-760B-24

  Query Match             4.5%;  Score 44;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704
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RESULT 37
US-09-826-025-24
; Sequence 24, Application US/09826025
; Patent No. 6730512
;  GENERAL INFORMATION:
;       APPLICANT: Chang, Lung-Ji
;       TITLE OF INVENTION: Combination Immunogene Therapy
;       NUMBER OF SEQUENCES: 25
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Medlen & Carroll, LLP
;            STREET: 220 Montgomery Street, Suite 2200
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: United States of America
;            ZIP: 94104
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/826,025
;            FILING DATE: 04-Apr-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/838,702
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Ingolia, Diane E.
;            REGISTRATION NUMBER: 40,027
;            REFERENCE/DOCKET NUMBER: CHANG-02687
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 705-8410
;            TELEFAX: (415) 397-8338
;  INFORMATION FOR SEQ ID NO: 24:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 987 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: other nucleic acid
;            DESCRIPTION: /desc = "DNA"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-826-025-24

  Query Match             4.5%;  Score 44;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 38
US-08-184-009-194
; Sequence 194, Application US/08184009
; Patent No. 5833975
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/184,009
;      FILING DATE:  19-JAN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  194:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1018 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-184-009-194

  Query Match             4.5%;  Score 44;  DB 2;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 39
US-08-458-356-194
; Sequence 194, Application US/08458356
; Patent No. 5942235
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,356
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  194:
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;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1018 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-458-356-194

  Query Match             4.5%;  Score 44;  DB 2;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 40
US-08-460-736-194
; Sequence 194, Application US/08460736
; Patent No. 6265189
;  GENERAL INFORMATION:
;     APPLICANT:  Paoletti, Enzo
;     APPLICANT:  Tartaglia, James
;     APPLICANT:  Cox, William I.
;     TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;     NUMBER OF SEQUENCES:  217
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Curtis, Morris & Safford
;       STREET:  530 Fifth Avenue
;       CITY:  New York
;       STATE:  NY
;       COUNTRY:  USA
;       ZIP:  10036
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/460,736
;       FILING DATE:  02-JUN-1995
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/184,009
;       FILING DATE:  19-JAN-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Frommer, William S.
;       REGISTRATION NUMBER:  25,506
;       REFERENCE/DOCKET NUMBER:  454310-2530
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 840-3333
;       TELEFAX:  (212) 840-0712
;       TELEX:  425066CURTMS
;   INFORMATION FOR SEQ ID NO:  194:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1018 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-460-736-194

  Query Match             4.5%;  Score 44;  DB 3;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 41
US-09-535-370-194
; Sequence 194, Application US/09535370
; Patent No. 6537594
;   GENERAL INFORMATION:
;       APPLICANT: Paoletti, Enzo
;                  Tartaglia, James
;                  Cox, William I.
;       TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
;       NUMBER OF SEQUENCES: 217
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Curtis, Morris & Safford
;            STREET: 530 Fifth Avenue
;            CITY: New York
;            STATE: NY
;            COUNTRY: USA
;            ZIP: 10036
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/535,370
;            FILING DATE: 24-Mar-2000
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/460,736
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Frommer, William S.
;            REGISTRATION NUMBER: 25,506
;            REFERENCE/DOCKET NUMBER: 454310-2530
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 840-3333
;            TELEFAX: (212) 840-0712
;            TELEX: 425066CURTMS
;   INFORMATION FOR SEQ ID NO: 194:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1018 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-09-535-370-194

  Query Match             4.5%;  Score 44;  DB 3;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 42
US-09-663-667-194
; Sequence 194, Application US/09663667
; Patent No. 6780407
;   GENERAL INFORMATION:
;       APPLICANT: Paoletti, Enzo
;                  Tartaglia, James
;                  Cox, William I.
;       TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
;       NUMBER OF SEQUENCES: 217
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Curtis, Morris & Safford
;            STREET: 530 Fifth Avenue
;            CITY: New York
;            STATE: NY
;            COUNTRY: USA
;            ZIP: 10036
;       COMPUTER READABLE FORM:
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;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/663,667
;             FILING DATE: 15-Sep-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/184,009
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Frommer, William S.
;             REGISTRATION NUMBER: 25,506
;             REFERENCE/DOCKET NUMBER: 454310-2530
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 840-3333
;             TELEFAX: (212) 840-0712
;             TELEX: 425066CURTMS
;   INFORMATION FOR SEQ ID NO: 194:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1018 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-09-663-667-194

  Query Match             4.5%;  Score 44;  DB 3;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 43
US-09-634-368-4
; Sequence 4, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 1389
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: human
;   OTHER INFORMATION: p40-IL-2 fusion protein coding sequence
US-09-634-368-4

  Query Match             4.5%;  Score 44;  DB 3;  Length 1389;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 44
US-08-751-767A-3
; Sequence 3, Application US/08751767A
; Patent No. 5994104
; GENERAL INFORMATION:
;   APPLICANT:  ANDERSON, ROBERT J.
;   APPLICANT:  GRANT, HUGH
;   APPLICANT:  MACDONALD, IAN D.
;   TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;   NUMBER OF SEQUENCES:  80
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  NIXON & VANDERHYE P.C.
;     STREET:  1100 NORTH GLEBE ROAD
;     CITY:  ARLINGTON
;     STATE:  VA
;     COUNTRY:  USA
;     ZIP:  22201
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/751,767A
;     FILING DATE:  08-NOV-1996
;     CLASSIFICATION:  536
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  SADOFF, B.J.
;     REGISTRATION NUMBER:  36,663
;     REFERENCE/DOCKET NUMBER:  117-221
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  7038164091
;     TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  3:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  1399 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  double
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  cDNA
;   FEATURE:
;     NAME/KEY:  CDS
;     LOCATION:  43..1026
US-08-751-767A-3

  Query Match             4.5%;  Score 44;  DB 2;  Length 1399;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        703 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 746


RESULT 45
US-08-751-767A-11
; Sequence 11, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
```

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;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/751,767A
;       FILING DATE:  08-NOV-1996
;       CLASSIFICATION:  536
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  SADOFF, B.J.
;       REGISTRATION NUMBER:  36,663
;       REFERENCE/DOCKET NUMBER:  117-221
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  7038164091
;       TELEFAX:  7038164100
;   INFORMATION FOR SEQ ID NO:  11:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1560 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..1557
US-08-751-767A-11

  Query Match             4.5%;  Score 44;  DB 2;  Length 1560;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641


RESULT 46
US-08-751-767A-9
; Sequence 9, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1623 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1620
US-08-751-767A-9

  Query Match             4.5%;  Score 44;  DB 2;  Length 1623;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 47
US-09-310-842-4
; Sequence 4, Application US/09310842A
; Patent No. 6451593
; GENERAL INFORMATION:
;  APPLICANT: Wittig, Prof. Burghardt
;  APPLICANT: Junghans, Claas
;  TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
;  TITLE OF INVENTION: Therapy
;  FILE REFERENCE: XI 597/99
;  CURRENT APPLICATION NUMBER: US/09/310,842A
;  CURRENT FILING DATE: 1999-05-12
;  EARLIER APPLICATION NUMBER: DE 196 48 625.4
;  EARLIER FILING DATE: 1996-11-13
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 1870
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (1)..(1870)
;   OTHER INFORMATION: Interleukin-12 (IL-12, p40-subunit); Oligo DNA Dumbbell
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1)..(2)
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to
;   OTHER INFORMATION: 2  can be modified with amino or caroxy features
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1869)..(1870)
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1869
;   OTHER INFORMATION: to 1870  can be modified with amino or caroxy features
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Strandness: both;  nucleic
;   OTHER INFORMATION: acid (linear),  hypothetical: No. 6451593 anti-sense: No
US-09-310-842-4

  Query Match             4.5%;  Score 44;  DB 3;  Length 1870;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db       1293 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 1336


RESULT 48
US-09-949-016-5452
; Sequence 5452, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
```

```
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5452
;   LENGTH: 2307
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-5452

  Query Match             4.5%;  Score 44;  DB 3;  Length 2307;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        663 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 706


RESULT 49
US-09-851-062-3
; Sequence 3, Application US/09851062
; Patent No. 6448081
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0247
;  CURRENT APPLICATION NUMBER: US/09/851,062
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 3
;   LENGTH: 2318
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (14)...(1000)
US-09-851-062-3

  Query Match             4.5%;  Score 44;  DB 3;  Length 2318;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        674 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 717


RESULT 50
US-09-949-016-315
; Sequence 315, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 315
;   LENGTH: 2318
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-315

  Query Match             4.5%;  Score 44;  DB 3;  Length 2318;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        674 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 717


RESULT 51
US-08-265-087-1
; Sequence 1, Application US/08265087
; Patent No. 5571515
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/265,087
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2362 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  33..1016
US-08-265-087-1

  Query Match             4.5%;  Score 44;  DB 2;  Length 2362;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        693 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 736


RESULT 52
US-08-621-493-1
```

```
; Sequence 1, Application US/08621493
; Patent No. 5723127
; GENERAL INFORMATION:
;   APPLICANT:  Scott, Phillip
;   APPLICANT:  Trinchieri, Giorgio
;   TITLE OF INVENTION:  Compositions and Methods for Use of
;   TITLE OF INVENTION:  IL-12 as an Adjuvant
;   NUMBER OF SEQUENCES:  4
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Howson and Howson
;     STREET:  Spring House Corporate Center, PO Box 457
;     CITY:  Spring House
;     STATE:  Pennsylvania
;     COUNTRY:  USA
;     ZIP:  19477
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/621,493
;     FILING DATE:  25-MAR-1996
;     CLASSIFICATION:  424
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/265,087
;     FILING DATE:  17-JUN-1994
;     APPLICATION NUMBER:  US 08/229,282
;     FILING DATE:  18-APR-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Bak, Mary E.
;     REGISTRATION NUMBER:  31,215
;     REFERENCE/DOCKET NUMBER:  WST51AUSA
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  215-540-9206
;     TELEFAX:  215-540-5818
; INFORMATION FOR SEQ ID NO:  1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  2362 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  double
;     TOPOLOGY:  unknown
;   MOLECULE TYPE:  cDNA
;   FEATURE:
;     NAME/KEY:  CDS
;     LOCATION:  33..1016
US-08-621-493-1

  Query Match             4.5%;  Score 44;  DB 2;  Length 2362;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        693 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 736


RESULT 53
US-08-965-688-1
; Sequence 1, Application US/08965688
; Patent No. 5976539
; GENERAL INFORMATION:
;   APPLICANT:  Scott, Phillip
;   APPLICANT:  Trinchieri, Giorgio
;   TITLE OF INVENTION:  Compositions and Methods for Use of
;   TITLE OF INVENTION:  IL-12 as an Adjuvant
;   NUMBER OF SEQUENCES:  4
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Howson and Howson
;     STREET:  Spring House Corporate Center, PO Box 457
;     CITY:  Spring House
;     STATE:  Pennsylvania
;     COUNTRY:  USA
;     ZIP:  19477
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/965,688
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/621,493
;     FILING DATE:  25-MAR-1996
;     APPLICATION NUMBER:  08/265,087
;     FILING DATE:  17-JUN-1994
;     APPLICATION NUMBER:  US 08/229,282
;     FILING DATE:  18-APR-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Bak, Mary E.
;     REGISTRATION NUMBER:  31,215
;     REFERENCE/DOCKET NUMBER:  WST51AUSA
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  215-540-9206
;     TELEFAX:  215-540-5818
; INFORMATION FOR SEQ ID NO:  1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  2362 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  double
;     TOPOLOGY:  unknown
;   MOLECULE TYPE:  cDNA
;   FEATURE:
;     NAME/KEY:  CDS
;     LOCATION:  33..1016
US-08-965-688-1

  Query Match             4.5%;  Score 44;  DB 2;  Length 2362;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        693 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 736


RESULT 54
US-09-260-173-1
; Sequence 1, Application US/09260173
; Patent No. 6168923
;   GENERAL INFORMATION:
;       APPLICANT: Scott, Phillip
;                  Trinchieri, Giorgio
;       TITLE OF INVENTION: Compositions and Methods for Use of
;                           IL-12 as an Adjuvant
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Howson and Howson
;            STREET: Spring House Corporate Center, PO Box 457
;            CITY: Spring House
;            STATE: Pennsylvania
;            COUNTRY: USA
;            ZIP: 19477
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/260,173
;            FILING DATE: 01-Mar-1999
;            CLASSIFICATION: <Unknown>
;                            17-JUN-1994
;                            18-APR-1994
```

```
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/965,688
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: 08/265,087
;             FILING DATE: 17-JUN-1994
;             APPLICATION NUMBER: US 08/229,282
;             FILING DATE: 18-APR-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Bak, Mary E.
;             REGISTRATION NUMBER: 31,215
;             REFERENCE/DOCKET NUMBER: WST51AUSA
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 215-540-9206
;             TELEFAX: 215-540-5818
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2362 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: unknown
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  33..1016
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-260-173-1

  Query Match             4.5%;  Score 44;  DB 3;  Length 2362;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        693 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 736


RESULT 55
US-09-924-703-3
; Sequence 3, Application US/09924703
; Patent No. 6555658
; GENERAL INFORMATION:
;  APPLICANT: TRINCHIERI, GIORGIO
;  APPLICANT:  PERUSSIA, BICE
;  APPLICANT:  CLARK, STEVEN C.
;  APPLICANT:  WONG, GORDON G.
;  APPLICANT:  HEWICK, RODNEY
;  APPLICANT:  KOBAYASHI, MICHIKO
;  TITLE OF INVENTION: ANTIBODIES TO NATURAL KILLER STIMULATORY FACTOR
;  FILE REFERENCE: 01142.0142.0100
;  CURRENT APPLICATION NUMBER: US/09/924,703
;  CURRENT FILING DATE:  2001-08-09
;  PRIOR APPLICATION NUMBER: 09/325,958
;  PRIOR FILING DATE: 1999-06-04
;  PRIOR APPLICATION NUMBER: 08/858,000
;  PRIOR FILING DATE: 1997-05-16
;  PRIOR APPLICATION NUMBER: 08/403,013
;  PRIOR FILING DATE: 1995-03-13
;  PRIOR APPLICATION NUMBER: 07/584,941
;  PRIOR FILING DATE: 1990-09-18
;  PRIOR APPLICATION NUMBER: 07/307,817
;  PRIOR FILING DATE: 1989-02-07
;  PRIOR APPLICATION NUMBER: 07/269,945
;  PRIOR FILING DATE: 1988-11-10
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 2362
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
;   OTHER INFORMATION: sequence of the 40 kD subunit of NKSF
;   NAME/KEY: CDS
;   LOCATION: (33)..(1016)
US-09-924-703-3

  Query Match             4.5%;  Score 44;  DB 3;  Length 2362;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        693 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 736


RESULT 56
US-08-751-767A-7
; Sequence 7, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6139 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3222..4841
US-08-751-767A-7

  Query Match             4.5%;  Score 44;  DB 2;  Length 6139;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db       3882 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 3925


RESULT 57
US-09-949-016-12057
; Sequence 12057, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
```

```
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12057
;   LENGTH: 16002
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-12057

  Query Match             4.0%;  Score 39;  DB 3;  Length 16002;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-09;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        400 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 438
              |||||||||||||||||||||||||||||||||||||||
Db       6309 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 6347


RESULT 58
US-09-949-016-17194
; Sequence 17194, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17194
;   LENGTH: 16003
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-17194

  Query Match             4.0%;  Score 39;  DB 3;  Length 16003;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-09;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        400 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 438
              |||||||||||||||||||||||||||||||||||||||
Db       6309 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 6347


RESULT 59
US-09-949-016-24253/c
; Sequence 24253, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24253
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-24253

  Query Match             3.8%;  Score 37;  DB 3;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-08;
  Matches   37;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCA 700
              |||||||||||||||||||||||||||||||||||||
Db         87 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCA 51


RESULT 60
US-09-949-016-190686/c
; Sequence 190686, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 190686
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-190686

  Query Match             3.8%;  Score 37;  DB 3;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-08;
  Matches   37;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCA 700
              |||||||||||||||||||||||||||||||||||||
Db         87 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCA 51


RESULT 61
US-09-823-549-77
; Sequence 77, Application US/09823549
; Patent No. 6664442
; GENERAL INFORMATION:
;  APPLICANT: McConlogue, Lisa  C
;  APPLICANT:  Games, Kate D.
;  APPLICANT:  Yednock, Theodore A.
;  APPLICANT:  Hua, Tan
;  APPLICANT:  Messersmith, Elizabeth
;  APPLICANT:  Bard, Frederique
;  TITLE OF INVENTION: SCREENING MARKERS AND METHODS FOR NEURODEGENERATIVE DISORDERS
;  FILE REFERENCE: 015270-009110US
;  CURRENT APPLICATION NUMBER: US/09/823,549
;  CURRENT FILING DATE:  2001-03-30
;  PRIOR APPLICATION NUMBER: US 60/193,847
;  PRIOR FILING DATE: 2000-03-30
```

```
;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
;   LENGTH: 73
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: IL-12 p40, #1 marker
US-09-823-549-77

  Query Match             3.0%;  Score 30;  DB 3;  Length 73;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-05;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||
Db          8 CAGCTTCTTCATCAGGGACATCATCAAACC 37


RESULT 62
US-08-385-335A-13
; Sequence 13, Application US/08385335A
; Patent No. 5891680
;  GENERAL INFORMATION:
;    APPLICANT:  Lieschke, Graham J.
;    APPLICANT:  Mulligan, Richard C.
;    TITLE OF INVENTION:  Bioactive Fusion Proteins
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/385,335A
;      FILING DATE:  08-FEB-1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  WHI95-01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-861-6240
;      TELEFAX:  617-861-9540
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1061 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-08-385-335A-13

  Query Match             3.0%;  Score 30;  DB 2;  Length 1061;
  Best Local Similarity   100.0%;  Pred. No. 5.9e-05;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||
Db        715 CAGCTTCTTCATCAGGGACATCATCAAACC 744


RESULT 63
US-09-634-368-3
; Sequence 3, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1409
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p40-GM-CSF fusion protein coding sequence
US-09-634-368-3

  Query Match             3.0%;  Score 30;  DB 3;  Length 1409;
  Best Local Similarity   100.0%;  Pred. No. 6e-05;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||
Db        689 CAGCTTCTTCATCAGGGACATCATCAAACC 718


RESULT 64
US-09-634-368-2
; Sequence 2, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 1472
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p40-IL-2 fusion protein coding sequence
US-09-634-368-2

  Query Match             3.0%;  Score 30;  DB 3;  Length 1472;
  Best Local Similarity   100.0%;  Pred. No. 6e-05;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||
Db        689 CAGCTTCTTCATCAGGGACATCATCAAACC 718


RESULT 65
US-09-634-368-12
; Sequence 12, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
```

```
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 1569
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p35-linker-p40 fusion protein coding sequence
US-09-634-368-12

  Query Match             3.0%;  Score 30;  DB 3;  Length 1569;
  Best Local Similarity   100.0%;  Pred. No. 6e-05;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||
Db       1230 CAGCTTCTTCATCAGGGACATCATCAAACC 1259


RESULT 66
US-09-634-368-11
; Sequence 11, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 2013
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p35-linker-p40-IL-2 fusion protein coding sequence
US-09-634-368-11

  Query Match             3.0%;  Score 30;  DB 3;  Length 2013;
  Best Local Similarity   100.0%;  Pred. No. 6.1e-05;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||
Db       1230 CAGCTTCTTCATCAGGGACATCATCAAACC 1259


RESULT 67
US-09-634-368-13
; Sequence 13, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 13
;   LENGTH: 2709
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: Fc-p35-linker-p40-IL-2 fusion protein coding
;   OTHER INFORMATION: sequence
US-09-634-368-13

  Query Match             3.0%;  Score 30;  DB 3;  Length 2709;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-05;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||
Db       1926 CAGCTTCTTCATCAGGGACATCATCAAACC 1955


RESULT 68
US-08-659-206A-4
; Sequence 4, Application US/08659206A
; Patent No. 5922685
;  GENERAL INFORMATION:
;    APPLICANT:  Rakhmilevich, Alexander
;    TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/659,206A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  110229.91144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6295 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "plasmid pWRG3196"
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(955..1260, 1334..1675)
;      OTHER INFORMATION:  /product= "p35 gene product"
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2377..3384
;      OTHER INFORMATION:  /product= "p40 gene product"
US-08-659-206A-4

  Query Match             3.0%;  Score 30;  DB 2;  Length 6295;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-05;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||
Db       3045 CAGCTTCTTCATCAGGGACATCATCAAACC 3074
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RESULT 69
US-08-659-206A-1
; Sequence 1, Application US/08659206A
; Patent No. 5922685
;  GENERAL INFORMATION:
;    APPLICANT:  Rakhmilevich, Alexander
;    TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/659,206A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  110229.91144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7287 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Plasmid DNA"
;    IMMEDIATE SOURCE:
;      CLONE:  pWRG3169
;    FEATURE:
;      NAME/KEY:  promoter
;      LOCATION:  1..628
;    FEATURE:
;      NAME/KEY:  iDNA
;      LOCATION:  629..810
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(953..1258, 1332..1673)
;      OTHER INFORMATION:  /product= "p35 gene product"
;    FEATURE:
;      NAME/KEY:  polyA_site
;      LOCATION:  1797..2024
;    FEATURE:
;      NAME/KEY:  promoter
;      LOCATION:  2110..2737
;    FEATURE:
;      NAME/KEY:  iDNA
;      LOCATION:  2738..2919
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2983..3990
;      OTHER INFORMATION:  /product= "p40 gene product"
;    FEATURE:
;      NAME/KEY:  polyA_site
;      LOCATION:  4075..4306
US-08-659-206A-1

  Query Match             3.0%;  Score 30;  DB 2;  Length 7287;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-05;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||
Db       3651 CAGCTTCTTCATCAGGGACATCATCAAACC 3680


RESULT 70
US-09-917-265A-85
; Sequence 85, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 85
;   LENGTH: 28
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-917-265A-85

  Query Match             2.8%;  Score 28;  DB 3;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00054;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCT 28
              ||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCT 28


RESULT 71
US-09-917-265A-87
; Sequence 87, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 87
;   LENGTH: 37
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-917-265A-87

  Query Match             2.8%;  Score 28;  DB 3;  Length 37;
  Best Local Similarity   100.0%;  Pred. No. 0.00055;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCT 28
              ||||||||||||||||||||||||||||
Db         10 ATGCATCCTCAGCAGTTGGTCATCGCCT 37


RESULT 72
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```
US-09-917-265A-86/c
; Sequence 86, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 86
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-917-265A-86

  Query Match             2.5%;  Score 25;  DB 3;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 0.018;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGCA 1


RESULT 73
US-09-079-984A-13
; Sequence 13, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,984A
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  39 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other DNA; synthetic DNA
US-09-079-984A-13

  Query Match             2.4%;  Score 24;  DB 3;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 0.061;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATC 24
              ||||||||||||||||||||||||
Db         10 ATGCATCCTCAGCAGTTGGTCATC 33


RESULT 74
US-09-390-729-13
; Sequence 13, Application US/09390729
; Patent No. 6562334
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/390,729
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/079,984
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  39 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other DNA; synthetic DNA
US-09-390-729-13

  Query Match             2.4%;  Score 24;  DB 3;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 0.061;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATC 24
              ||||||||||||||||||||||||
Db         10 ATGCATCCTCAGCAGTTGGTCATC 33


RESULT 75
US-09-445-724B-13
; Sequence 13, Application US/09445724B
; Patent No. 6600020
; GENERAL INFORMATION:
;  APPLICANT: OKANO, FUMIYOSHI
;  TITLE OF INVENTION: CANINE INTERLEUKIN 18, CANINE INTERLEUKIN 1 CONVERTING
```

```
;  TITLE OF INVENTION:  ENZYME, DNA SEQUENCES ENCODING THESE, INTERLEUKIN 18
;  TITLE OF INVENTION:  PRODUCTION METHOD AND CANINE IMMUNE DISEASE REMEDY
;  FILE REFERENCE: 2109-15
;  CURRENT APPLICATION NUMBER: US/09/445,724B
;  CURRENT FILING DATE:  1999-12-13
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
;   LENGTH: 540
;   TYPE: DNA
;   ORGANISM: Caninus sp.
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(537)
US-09-445-724B-13

  Query Match             2.4%;  Score 24;  DB 3;  Length 540;
  Best Local Similarity   100.0%;  Pred. No. 0.067;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATC 24
              ||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATC 24


RESULT 76
US-09-949-016-24250/c
; Sequence 24250, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24250
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-24250

  Query Match             2.3%;  Score 23;  DB 3;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 0.22;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        127 GGAGAAATGGTGGTCCTCACCTG 149
              |||||||||||||||||||||||
Db         69 GGAGAAATGGTGGTCCTCACCTG 47


RESULT 77
US-09-949-016-24251/c
; Sequence 24251, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24251
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-24251

  Query Match             2.3%;  Score 23;  DB 3;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 0.22;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        127 GGAGAAATGGTGGTCCTCACCTG 149
              |||||||||||||||||||||||
Db         88 GGAGAAATGGTGGTCCTCACCTG 66


RESULT 78
US-09-949-016-190683/c
; Sequence 190683, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 190683
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-190683

  Query Match             2.3%;  Score 23;  DB 3;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 0.22;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        127 GGAGAAATGGTGGTCCTCACCTG 149
              |||||||||||||||||||||||
Db         69 GGAGAAATGGTGGTCCTCACCTG 47


RESULT 79
US-09-949-016-190684/c
; Sequence 190684, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
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```
; SEQ ID NO 190684
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-190684

  Query Match             2.3%;  Score 23;  DB 3;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 0.22;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        127 GGAGAAATGGTGGTCCTCACCTG 149
              |||||||||||||||||||||||
Db         88 GGAGAAATGGTGGTCCTCACCTG 66


RESULT 80
US-08-781-891-79/c
; Sequence 79, Application US/08781891
; Patent No. 6090620
;  GENERAL INFORMATION:
;    APPLICANT:  Fu, Ying-Hui
;    APPLICANT:  Yu, Chang-En
;    APPLICANT:  Oshima, Junko
;    APPLICANT:  Mulligan, John T.
;    APPLICANT:  Schellenberg, Gerald D.
;    TITLE OF INVENTION:  GENE AND GENE PRODUCTS RELATED TO
;    TITLE OF INVENTION:  WERNER'S SYNDROME
;    NUMBER OF SEQUENCES:  209
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/781,891
;      FILING DATE:  27-DEC-1996
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 6090620tenburg Ph.D., Carol
;      REGISTRATION NUMBER:  39,317
;      REFERENCE/DOCKET NUMBER:  240052.419
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  79:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  87350 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-781-891-79

  Query Match             2.2%;  Score 22;  DB 3;  Length 87350;
  Best Local Similarity   100.0%;  Pred. No. 0.85;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        843 GAACAACAGAGAAAAGAAAGAC 864
              ||||||||||||||||||||||
Db      80388 GAACAACAGAGAAAAGAAAGAC 80367


RESULT 81
US-09-618-166-79/c
; Sequence 79, Application US/09618166
; Patent No. 6583112
;   GENERAL INFORMATION:
;       APPLICANT: Fu, Ying-Hui
;                  Yu, Chang-En
;                  Oshima, Junko
;                  Mulligan, John T.
;                  Schellenberg, Gerald D.
;       TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
;                           WERNER'S SYNDROME
;       NUMBER OF SEQUENCES: 209
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Seed Intellectual Property Law Group
;            STREET: 701 Fifth Avenue, Suite 6300
;            CITY: Seattle
;            STATE: Washington
;            COUNTRY: USA
;            ZIP: 98104-7092
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/618,166
;            FILING DATE: 17-Jul-2000
;            CLASSIFICATION: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: McMasters, David D.
;            REGISTRATION NUMBER: 33,963
;            REFERENCE/DOCKET NUMBER: 240052.419C1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (206) 622-4900
;            TELEFAX: (206) 682-6031
;   INFORMATION FOR SEQ ID NO: 79:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 87350 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-09-618-166-79

  Query Match             2.2%;  Score 22;  DB 3;  Length 87350;
  Best Local Similarity   100.0%;  Pred. No. 0.85;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        843 GAACAACAGAGAAAAGAAAGAC 864
              ||||||||||||||||||||||
Db      80388 GAACAACAGAGAAAAGAAAGAC 80367


RESULT 82
US-09-791-211-3/c
; Sequence 3, Application US/09791211
; Patent No. 6448080
; GENERAL INFORMATION:
;  APPLICANT:  Donna T. Ward
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION:  ANTISENSE MODULATION OF WRN EXPRESSION
;  FILE REFERENCE:  RTS-0205
;  CURRENT APPLICATION NUMBER: US/09/791,211
;  CURRENT FILING DATE:  2001-02-23
;  NUMBER OF SEQ ID NOS:  90
; SEQ ID NO 3
;   LENGTH: 87543
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 7421
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 7427
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
```

; LOCATION: 11609
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 12605
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 12742
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 29370
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 29422
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 29979
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 29980
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 29981
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 30136
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 30140
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 31205
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 31206
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 31592
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 33095
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 33160
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 34066
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 34072
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 36816
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 39020
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 42164
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 42459
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 46808
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 46823
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 46826
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 47291
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 52786
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 52787
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 53384
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 54684
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 59215
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 59235
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 59242
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 63290
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 66614
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 68660
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 68697
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 68718
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 68733
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 68739
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 69785
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 79134
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 79198
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 86336
; OTHER INFORMATION: unknown
; OTHER INFORMATION:
US-09-791-211-3

Query Match 2.2%; Score 22; DB 3; Length 87543;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        843 GAACAACAGAGAAAAGAAAGAC 864
              ||||||||||||||||||||||
Db      80581 GAACAACAGAGAAAAGAAAGAC 80560
```

RESULT 83
US-09-011-143-14
; Sequence 14, Application US/09011143
; Patent No. 6472509
; GENERAL INFORMATION:
; APPLICANT: IMAMURA, Takayuki

```
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  44 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-14

  Query Match             2.1%;  Score 21;  DB 3;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 2.1;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        547 GACAACAGGGATTATAAGAAG 567
              |||||||||||||||||||||
Db         24 GACAACAGGGATTATAAGAAG 44


RESULT 84
US-09-302-495-14
; Sequence 14, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 14:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 44 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-302-495-14

  Query Match             2.1%;  Score 21;  DB 3;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 2.1;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        547 GACAACAGGGATTATAAGAAG 567
              |||||||||||||||||||||
Db         24 GACAACAGGGATTATAAGAAG 44


RESULT 85
US-10-079-616-14
; Sequence 14, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
```

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;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 14:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 44 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-079-616-14

  Query Match             2.1%;  Score 21;  DB 3;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 2.1;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        547 GACAACAGGGATTATAAGAAG 567
              |||||||||||||||||||||
Db         24 GACAACAGGGATTATAAGAAG 44


RESULT 86
US-09-851-062-17/c
; Sequence 17, Application US/09851062
; Patent No. 6448081
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0247
;  CURRENT APPLICATION NUMBER: US/09/851,062
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 17
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-062-17

  Query Match             2.0%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        223 CTGACCATCCAAGTCAAAGA 242
              ||||||||||||||||||||
Db         20 CTGACCATCCAAGTCAAAGA 1


RESULT 87
US-09-851-062-22/c
; Sequence 22, Application US/09851062
; Patent No. 6448081
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0247
;  CURRENT APPLICATION NUMBER: US/09/851,062
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 22
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-062-22

  Query Match             2.0%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        320 AGGAAGATGGAATTTGGTCC 339
              ||||||||||||||||||||
Db         20 AGGAAGATGGAATTTGGTCC 1


RESULT 88
US-09-851-062-23/c
; Sequence 23, Application US/09851062
; Patent No. 6448081
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0247
;  CURRENT APPLICATION NUMBER: US/09/851,062
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 23
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-062-23

  Query Match             2.0%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        326 ATGGAATTTGGTCCACTGAT 345
              ||||||||||||||||||||
Db         20 ATGGAATTTGGTCCACTGAT 1


RESULT 89
US-09-851-062-26/c
; Sequence 26, Application US/09851062
; Patent No. 6448081
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0247
;  CURRENT APPLICATION NUMBER: US/09/851,062
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 26
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-062-26

  Query Match             2.0%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        418 TTCACCTGCTGGTGGCTGAC 437
              ||||||||||||||||||||
Db         20 TTCACCTGCTGGTGGCTGAC 1


RESULT 90
```

```
US-09-851-062-34/c
; Sequence 34, Application US/09851062
; Patent No. 6448081
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0247
;  CURRENT APPLICATION NUMBER: US/09/851,062
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 34
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-062-34

  Query Match             2.0%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACA 697
              ||||||||||||||||||||
Db         20 CAGCTTCTTCATCAGGGACA 1


RESULT 91
US-09-851-062-35/c
; Sequence 35, Application US/09851062
; Patent No. 6448081
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0247
;  CURRENT APPLICATION NUMBER: US/09/851,062
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 35
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-062-35

  Query Match             2.0%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        683 TCTTCATCAGGGACATCATC 702
              ||||||||||||||||||||
Db         20 TCTTCATCAGGGACATCATC 1


RESULT 92
US-09-851-062-36/c
; Sequence 36, Application US/09851062
; Patent No. 6448081
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0247
;  CURRENT APPLICATION NUMBER: US/09/851,062
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 36
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-062-36

  Query Match             2.0%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        688 ATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||
Db         20 ATCAGGGACATCATCAAACC 1


RESULT 93
US-09-917-265A-88/c
; Sequence 88, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 88
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-917-265A-88

  Query Match             2.0%;  Score 20;  DB 3;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 6.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        966 CTGGGCATCCGTGTCCTGCA 985
              ||||||||||||||||||||
Db         25 CTGGGCATCCGTGTCCTGCA 6


RESULT 94
US-09-011-143-13/c
; Sequence 13, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
```

```
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-13

  Query Match             2.0%;  Score 20;  DB 3;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 6.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        526 TCAGCAGAGAAGGTCAGAGT 545
              ||||||||||||||||||||
Db         32 TCAGCAGAGAAGGTCAGAGT 13


RESULT 95
US-09-302-495-13/c
; Sequence 13, Application US/09302495
; Patent No. 6518045
;  GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/302,495
;            FILING DATE: 30-Apr-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 13:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 32 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-302-495-13

  Query Match             2.0%;  Score 20;  DB 3;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 6.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        526 TCAGCAGAGAAGGTCAGAGT 545
              ||||||||||||||||||||
Db         32 TCAGCAGAGAAGGTCAGAGT 13


RESULT 96
US-10-079-616-13/c
; Sequence 13, Application US/10079616
; Patent No. 6566097
;  GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 13:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 32 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-079-616-13

  Query Match             2.0%;  Score 20;  DB 3;  Length 32;
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Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        526 TCAGCAGAGAAGGTCAGAGT 545
              ||||||||||||||||||||
Db         32 TCAGCAGAGAAGGTCAGAGT 13
```

RESULT 97
US-09-949-016-11844
; Sequence 11844, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11844
; LENGTH: 119981
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11844

Query Match 2.0%; Score 20; DB 3; Length 119981;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        371 AAAATAAGATCTTTCTAAAA 390
              ||||||||||||||||||||
Db      89012 AAAATAAGATCTTTCTAAAA 89031
```

RESULT 98
US-09-949-016-13606
; Sequence 13606, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13606
; LENGTH: 119982
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13606

Query Match 2.0%; Score 20; DB 3; Length 119982;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        371 AAAATAAGATCTTTCTAAAA 390
              ||||||||||||||||||||
Db      89012 AAAATAAGATCTTTCTAAAA 89031
```

RESULT 99
US-09-949-016-15787
; Sequence 15787, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15787
; LENGTH: 120727
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(120727)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15787

Query Match 2.0%; Score 20; DB 3; Length 120727;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        485 CCTCTGACCCCCAAGGGGTG 504
              ||||||||||||||||||||
Db      80796 CCTCTGACCCCCAAGGGGTG 80815
```

RESULT 100
US-09-949-016-15788
; Sequence 15788, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15788
; LENGTH: 120727
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(120727)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15788

Query Match 2.0%; Score 20; DB 3; Length 120727;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        485 CCTCTGACCCCCAAGGGGTG 504
              ||||||||||||||||||||
Db      80796 CCTCTGACCCCCAAGGGGTG 80815
```

Search completed: June 9, 2006, 23:48:32
Job time : 226.93 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2006, 23:31:05 ; Search time 1655.75 Seconds
(without alignments)
7309.894 Million cell updates/sec

Title: US-10-821-670A-55
Perfect score: 985
Sequence: 1 atgcatcctcagcagttggt.....ctgggcatccgtgtcctgca 985

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 18892170 seqs, 6143817638 residues

Word size : 1

Total number of hits satisfying chosen parameters: 37781012

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

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2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
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;   ORGANISM: Felis catus
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;   NAME/KEY: CDS
;   LOCATION: (1)..(984)
;   OTHER INFORMATION:
US-09-917-265-55

  Query Match             100.0%;  Score 985;  DB 3;  Length 985;
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Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 2
US-09-917-265-57/c
; Sequence 57, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-57

  Query Match           100.0%;  Score 985;  DB 3;  Length 985;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGCA 1


RESULT 3
US-10-821-670-55
; Sequence 55, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(984)
US-10-821-670-55

  Query Match             100.0%;  Score 985;  DB 9;  Length 985;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 4
US-10-821-670-57/c
; Sequence 57, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-57

  Query Match             100.0%;  Score 985;  DB 9;  Length 985;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866
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Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
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Db         25 AGCAACTGGGCATCCGTGTCCTGCA 1
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RESULT 5
US-09-917-265-29
; Sequence 29, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
;   OTHER INFORMATION:
US-09-917-265-29

  Query Match            100.0%;  Score 985;  DB 3;  Length 987;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
```

```
Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 6
US-09-917-265-31/c
; Sequence 31, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-31

  Query Match             100.0%;  Score 985;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGCA 3


RESULT 7
US-10-821-670-29
; Sequence 29, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
US-10-821-670-29

  Query Match             100.0%;  Score 985;  DB 9;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
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Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 8
US-10-821-670-31/c
; Sequence 31, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-31

  Query Match             100.0%;  Score 985;  DB 9;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88
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Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGCA 3


RESULT 9
US-10-079-616-5
; Sequence 5, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2193 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-079-616-5

  Query Match             94.2%;  Score 928;  DB 6;  Length 2193;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  928;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         58 CTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCT 117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCT 180

Qy        118 GATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACC 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACC 240

Qy        178 TGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTC 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTC 300

Qy        238 AAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCAT 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCAT 360

Qy        298 TCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAA 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAA 420

Qy        358 CAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGT 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGT 480

Qy        418 TTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGC 477
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGC 540

Qy        478 AGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAG 537
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAG 600

Qy        538 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 597
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 660

Qy        598 TGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTC 657
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTC 720

Qy        658 AAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCC 717
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCC 780

Qy        718 AAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATAC 777
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATAC 840

Qy        778 CCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAG 837
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAG 900

Qy        838 GGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTC 897
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTC 960

Qy        898 GTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCC 957
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCC 1020

Qy        958 TGGAGCAACTGGGCATCCGTGTCCTGCA 985
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Db       1021 TGGAGCAACTGGGCATCCGTGTCCTGCA 1048


RESULT 10
US-10-079-616-6
; Sequence 6, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
```

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;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-079-616-6

  Query Match             93.3%;  Score 919;  DB 6;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  919;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy         367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy         427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy         487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy         547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy         607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy         667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy         727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy         787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy         847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy         907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy         967 TGGGCATCCGTGTCCTGCA 985
               ||||||||||||||||||
Db         901 TGGGCATCCGTGTCCTGCA 919


RESULT 11
US-09-917-265-38
; Sequence 38, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
US-09-917-265-38

  Query Match             91.7%;  Score 903;  DB 3;  Length 1599;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  953;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91

Qy          92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151

Qy         152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211
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Qy        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271

Qy        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331

Qy        332 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 391

Qy        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451

Qy        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTG 511
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTG 511

Qy        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571

Qy        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631

Qy        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691

Qy        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751

Qy        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811

Qy        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 871
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 871

Qy        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931

Qy        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCA 985
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCA 985
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RESULT 12
US-09-917-265-40/c
; Sequence 40, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265-40

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  Query Match             91.7%;  Score 903;  DB 3;  Length 1599;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  953;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1568 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 1509

Qy         92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1508 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 1449

Qy        152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1448 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 1389

Qy        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1388 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 1329

Qy        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1328 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 1269

Qy        332 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1268 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 1209

Qy        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1208 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 1149

Qy        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTG 511
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       1148 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTG 1089

Qy        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1088 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 1029

Qy        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1028 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 969

Qy        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        968 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 909

Qy        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        908 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 849

Qy        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 789

Qy        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 871
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        788 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 729

Qy        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 669

Qy        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCA 985
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCA 615
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RESULT 13
US-10-821-670-38
; Sequence 38, Application US/10821670

```
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-10-821-670-38

  Query Match             91.7%;  Score 903;  DB 9;  Length 1599;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  953;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91

Qy         92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151

Qy        152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211

Qy        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271

Qy        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331

Qy        332 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAAATAAGATCTTTCTAAAAT 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 391

Qy        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451

Qy        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTG 511
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTG 511

Qy        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571

Qy        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631

Qy        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691

Qy        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751

Qy        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811

Qy        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 871
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 871

Qy        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931

Qy        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 14
US-10-821-670-40/c
; Sequence 40, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-40

  Query Match             91.7%;  Score 903;  DB 9;  Length 1599;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  953;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1568 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 1509

Qy         92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1508 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 1449

Qy        152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1448 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 1389

Qy        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1388 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 1329

Qy        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1328 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 1269

Qy        332 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1268 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 1209

Qy        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1208 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 1149

Qy        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTG 511
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       1148 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTG 1089

Qy        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1088 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 1029

Qy        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1028 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 969

Qy        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        968 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 909

Qy        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        908 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 849

Qy        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 789

Qy        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 871
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        788 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 729

Qy        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 669

Qy        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCA 985
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCA 615


RESULT 15
US-10-041-672C-1
; Sequence 1, Application US/10041672C
; Publication No. US20030157059A1
; GENERAL INFORMATION:
;  APPLICANT: Mologen Forschungs-, Entwicklungs- und Vetriebs GmbH
;  APPLICANT:  Universitat Zurich
;  TITLE OF INVENTION: FELINE INTERLEUKIN-12 AS IMMUNOSTIMULANT
;  FILE REFERENCE: NHL-NP-36
;  CURRENT APPLICATION NUMBER: US/10/041,672C
;  CURRENT FILING DATE:  2002-01-08
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 990
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: feline IL-12 p40
US-10-041-672C-1

  Query Match             89.7%;  Score 884;  DB 7;  Length 990;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  934;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAG 935
              |||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAG 935


RESULT 16
US-10-041-672C-10
; Sequence 10, Application US/10041672C
; Publication No. US20030157059A1
; GENERAL INFORMATION:
;  APPLICANT: Mologen Forschungs-, Entwicklungs- und Vetriebs GmbH
;  APPLICANT:  Universitat Zurich
;  TITLE OF INVENTION: FELINE INTERLEUKIN-12 AS IMMUNOSTIMULANT
;  FILE REFERENCE: NHL-NP-36
;  CURRENT APPLICATION NUMBER: US/10/041,672C
;  CURRENT FILING DATE:  2002-01-08
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 4522
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pMol-fil12p40
US-10-041-672C-10
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  Query Match             89.7%;  Score 884;  DB 7;  Length 4522;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  934;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAG 935
              |||||||||||||||||||||||||||||||||||
Db       3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAG 3981


RESULT 17
US-09-917-265-26
; Sequence 26, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THER
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(921)
;   OTHER INFORMATION:
US-09-917-265-26

  Query Match             88.1%;  Score 868;  DB 3;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
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Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCA 985
              ||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCA 919


RESULT 18
US-09-917-265-28/c
; Sequence 28, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-28

  Query Match             88.1%;  Score 868;  DB 3;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||

Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
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Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        967 TGGGCATCCGTGTCCTGCA 985
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Db         21 TGGGCATCCGTGTCCTGCA 3


RESULT 19
US-10-079-616-7
; Sequence 7, Application US/10079616
; Publication No. US20020107366A1
;  GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
```

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;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 7:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 921 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-079-616-7

  Query Match           88.1%;  Score 868;  DB 6;  Length 921;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCA 985
              ||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCA 919


RESULT 20
US-10-821-670-26
; Sequence 26, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(921)
US-10-821-670-26

  Query Match           88.1%;  Score 868;  DB 9;  Length 921;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
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Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
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Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
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Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
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Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCA 985
              ||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCA 919


RESULT 21
US-10-821-670-28/c
; Sequence 28, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-28

  Query Match             88.1%;  Score 868;  DB 9;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
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Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
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Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
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Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
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Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        967 TGGGCATCCGTGTCCTGCA 985
              ||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCA 3


RESULT 22
US-09-917-265-43
; Sequence 43, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
;   OTHER INFORMATION:
US-09-917-265-43
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  Query Match             88.1%;  Score 868;  DB 3;  Length 1533;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCA 985
              ||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCA 919


RESULT 23
US-09-917-265-45/c
; Sequence 45, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-45

  Query Match             88.1%;  Score 868;  DB 3;  Length 1533;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        367 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754
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Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        967 TGGGCATCCGTGTCCTGCA 985
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Db        633 TGGGCATCCGTGTCCTGCA 615


RESULT 24
US-10-821-670-43
; Sequence 43, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-10-821-670-43

  Query Match             88.1%;  Score 868;  DB 9;  Length 1533;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCA 985
              ||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCA 919


RESULT 25
US-10-821-670-45/c
; Sequence 45, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-45

  Query Match             88.1%;  Score 868;  DB 9;  Length 1533;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354
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Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        967 TGGGCATCCGTGTCCTGCA 985
              ||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCA 615
```

```
RESULT 26
US-09-917-265-52
; Sequence 52, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(921)
;   OTHER INFORMATION:
US-09-917-265-52

  Query Match             6.7%;  Score 66;  DB 3;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy        597 CTGCCC 602
              ||||||
Db        531 CTGCCC 536


RESULT 27
US-09-917-265-54/c
; Sequence 54, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THER
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-54

  Query Match             6.7%;  Score 66;  DB 3;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy        597 CTGCCC 602
              ||||||
Db        391 CTGCCC 386


RESULT 28
US-10-821-670-52
; Sequence 52, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
```

```
;   NAME/KEY: CDS
;   LOCATION: (1)..(921)
US-10-821-670-52

  Query Match             6.7%;  Score 66;  DB 9;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy        597 CTGCCC 602
              ||||||
Db        531 CTGCCC 536


RESULT 29
US-10-821-670-54/c
; Sequence 54, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-54

  Query Match             6.7%;  Score 66;  DB 9;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy        597 CTGCCC 602
              ||||||
Db        391 CTGCCC 386


RESULT 30
US-09-917-265-58
; Sequence 58, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
;   OTHER INFORMATION:
US-09-917-265-58

  Query Match             6.7%;  Score 66;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 31
US-09-917-265-60/c
; Sequence 60, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERI
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-60

  Query Match             6.7%;  Score 66;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy        597 CTGCCC 602
              ||||||
Db        391 CTGCCC 386


RESULT 32
US-10-821-670-58
; Sequence 58, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
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;   LOCATION: (1)..(987)
US-10-821-670-58

  Query Match             6.7%;  Score 66;  DB 9;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 33
US-10-821-670-60/c
; Sequence 60, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-60

  Query Match             6.7%;  Score 66;  DB 9;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy        597 CTGCCC 602
              ||||||
Db        391 CTGCCC 386


RESULT 34
US-09-917-265-66
; Sequence 66, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
;   OTHER INFORMATION:
US-09-917-265-66

  Query Match             6.7%;  Score 66;  DB 3;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy        597 CTGCCC 602
              ||||||
Db        531 CTGCCC 536


RESULT 35
US-09-917-265-68/c
; Sequence 68, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THER
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-68

  Query Match             6.7%;  Score 66;  DB 3;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy        597 CTGCCC 602
              ||||||
Db       1003 CTGCCC 998


RESULT 36
US-10-821-670-66
; Sequence 66, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
```

```
US-10-821-670-66

  Query Match             6.7%;  Score 66;  DB 9;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy        597 CTGCCC 602
              ||||||
Db        531 CTGCCC 536


RESULT 37
US-10-821-670-68/c
; Sequence 68, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-68

  Query Match             6.7%;  Score 66;  DB 9;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy        597 CTGCCC 602
              ||||||
Db       1003 CTGCCC 998


RESULT 38
US-09-917-265-61
; Sequence 61, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
US-09-917-265-61

  Query Match             6.7%;  Score 66;  DB 3;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 39
US-09-917-265-63/c
; Sequence 63, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THER
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-63

  Query Match             6.7%;  Score 66;  DB 3;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy        597 CTGCCC 602
              ||||||
Db       1003 CTGCCC 998


RESULT 40
US-10-821-670-61
; Sequence 61, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-10-821-670-61
```

```
  Query Match             6.7%;  Score 66;  DB 9;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 41
US-10-821-670-63/c
; Sequence 63, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-63

  Query Match             6.7%;  Score 66;  DB 9;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy        597 CTGCCC 602
              ||||||
Db       1003 CTGCCC 998


RESULT 42
US-09-917-265-107
; Sequence 107, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 107
;   LENGTH: 2267
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (154)..(1140)
;   OTHER INFORMATION:
US-09-917-265-107

  Query Match             6.7%;  Score 66;  DB 3;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 749

Qy        597 CTGCCC 602
              ||||||
Db        750 CTGCCC 755


RESULT 43
US-09-917-265-109/c
; Sequence 109, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERI
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 109
;   LENGTH: 2267
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-109

  Query Match             6.7%;  Score 66;  DB 3;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1578 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1519

Qy        597 CTGCCC 602
              ||||||
Db       1518 CTGCCC 1513


RESULT 44
US-10-821-670-107
; Sequence 107, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 107
;   LENGTH: 2267
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (154)..(1140)
US-10-821-670-107
```

```
  Query Match             6.7%;  Score 66;  DB 9;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 749

Qy        597 CTGCCC 602
              ||||||
Db        750 CTGCCC 755


RESULT 45
US-10-821-670-109/c
; Sequence 109, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 109
;   LENGTH: 2267
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-109

  Query Match             6.7%;  Score 66;  DB 9;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1578 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1519

Qy         597 CTGCCC 602
               ||||||
Db        1518 CTGCCC 1513


RESULT 46
US-11-136-527-4408
; Sequence 4408, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William M
;  TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
;  FILE REFERENCE: 031896-041000 (AM101086)
;  CURRENT APPLICATION NUMBER: US/11/136,527
;  CURRENT FILING DATE:  2005-05-25
;  PRIOR APPLICATION NUMBER: US 60/574,294
;  PRIOR FILING DATE: 2005-05-26
;  NUMBER OF SEQ ID NOS: 362830
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4408
;   LENGTH: 600
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-11-136-527-4408

  Query Match             5.2%;  Score 51;  DB 16;  Length 600;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-16;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCA 728
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCA 311


RESULT 47
US-11-136-527-312
; Sequence 312, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William M
;  TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
;  FILE REFERENCE: 031896-041000 (AM101086)
;  CURRENT APPLICATION NUMBER: US/11/136,527
;  CURRENT FILING DATE:  2005-05-25
;  PRIOR APPLICATION NUMBER: US 60/574,294
;  PRIOR FILING DATE: 2005-05-26
;  NUMBER OF SEQ ID NOS: 362830
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 312
;   LENGTH: 1024
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-11-136-527-312

  Query Match             5.2%;  Score 51;  DB 16;  Length 1024;
  Best Local Similarity   100.0%;  Pred. No. 5.9e-16;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCA 728
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 CAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCA 735


RESULT 48
US-09-754-014-2
; Sequence 2, Application US/09754014
; Patent No. US20020119940A1
;   GENERAL INFORMATION:
;        APPLICANT: Jeff No. US20020119940A1dstrom
;                   Bruce Freimark
;                   Deepa Deshpande
;        TITLE OF INVENTION: GENE EXPRESSION AND DELIVERY SYTEMS
;                            AND USES
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                     Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 90071-2066
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                          storage
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: IBM P.C. DOS 5.0
;             SOFTWARE: FastSEQ for Windows 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/754,014
;             FILING DATE: 03-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/948,958
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Berkman, Charles S.
;             REGISTRATION NUMBER: 38,077
;             REFERENCE/DOCKET NUMBER: 226/284
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
```

```
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 987 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-754-014-2

  Query Match             4.5%;  Score 44;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 49
US-09-836-866-2
; Sequence 2, Application US/09836866
; Patent No. US20020123473A1
;   GENERAL INFORMATION:
;        APPLICANT: No. US20020123473A1dstrom, Jeff
;                   Freimark, Bruce
;                   Deshpande, Deepa
;        TITLE OF INVENTION: IL-12 GENE EXPRESSION AND
;                            DELIVERY SYTEMS AND USES
;        NUMBER OF SEQUENCES: 8
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                     Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 90071-2066
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                          storage
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: IBM P.C. DOS 5.0
;             SOFTWARE: FastSEQ for Windows 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/836,866
;             FILING DATE: 16-Apr-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/949,160
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Warburg, Richard J.
;             REGISTRATION NUMBER: 32,327
;             REFERENCE/DOCKET NUMBER: 226/285
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 987 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-836-866-2

  Query Match             4.5%;  Score 44;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 50
US-09-826-025-24
; Sequence 24, Application US/09826025
; Patent No. US20020162123A1
;   GENERAL INFORMATION:
;        APPLICANT: Chang, Lung-Ji
;        TITLE OF INVENTION: Combination Immunogene Therapy
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Medlen & Carroll, LLP
;             STREET: 220 Montgomery Street, Suite 2200
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: United States of America
;             ZIP: 94104
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/826,025
;             FILING DATE: 04-Apr-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/838,702
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ingolia, Diane E.
;             REGISTRATION NUMBER: 40,027
;             REFERENCE/DOCKET NUMBER: CHANG-02687
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 705-8410
;             TELEFAX: (415) 397-8338
;   INFORMATION FOR SEQ ID NO: 24:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 987 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: other nucleic acid
;             DESCRIPTION: /desc = "DNA"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-826-025-24

  Query Match             4.5%;  Score 44;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 51
US-10-785-577-24
; Sequence 24, Application US/10785577
; Publication No. US20040237129A1
;   GENERAL INFORMATION:
;        APPLICANT: Chang, Lung-Ji
;        TITLE OF INVENTION: Combination Immunogene Therapy
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Medlen & Carroll, LLP
;             STREET: 220 Montgomery Street, Suite 2200
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: United States of America
```

```
;             ZIP: 94104
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/785,577
;             FILING DATE: 23-Feb-2004
;             CLASSIFICATION: 424
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/838,702
;             FILING DATE: 9-Apr-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ingolia, Diane E.
;             REGISTRATION NUMBER: 40,027
;             REFERENCE/DOCKET NUMBER: CHANG-02687
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 705-8410
;             TELEFAX: (415) 397-8338
;   INFORMATION FOR SEQ ID NO: 24:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 987 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: other nucleic acid
;             DESCRIPTION: /desc = "DNA"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-785-577-24

  Query Match             4.5%;  Score 44;  DB 9;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 52
US-10-373-456-18
; Sequence 18, Application US/10373456
; Publication No. US20040009146A1
; GENERAL INFORMATION:
;  APPLICANT: Podhajcer, Osvaldo
;  TITLE OF INVENTION: Anti-Tumor Vaccine and Method
;  FILE REFERENCE: 1423P-US/101141-14
;  CURRENT APPLICATION NUMBER: US/10/373,456
;  CURRENT FILING DATE:  2003-02-25
;  PRIOR APPLICATION NUMBER: US 60/359,836
;  PRIOR FILING DATE: 2002-02-26
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 1005
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-373-456-18

  Query Match             4.5%;  Score 44;  DB 7;  Length 1005;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        669 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 712


RESULT 53
US-10-221-975A-1
; Sequence 1, Application US/10221975A
; Publication No. US20040023332A1
; GENERAL INFORMATION:
;  APPLICANT: Pohang University of Science and Technology
;  APPLICANT:  Progen Co., Ltd.
;  APPLICANT:  Sung, Young Chul
;  APPLICANT:  Lee, Sung Hee
;  APPLICANT:  Ha, Sang Jun
;  APPLICANT:  Song, Man Ki
;  APPLICANT:  Chang, Jun
;  TITLE OF INVENTION: Genes of IL-12p40 Subunit Mutated for Improving the Activity of
;  TITLE OF INVENTION:  IL-12 and Use Thereof for DNA Vaccine Adjuvant
;  FILE REFERENCE: 59520-00005
;  CURRENT APPLICATION NUMBER: US/10/221,975A
;  CURRENT FILING DATE:  2003-04-02
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 1007
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-221-975A-1

  Query Match             4.5%;  Score 44;  DB 8;  Length 1007;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        667 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 710


RESULT 54
US-10-373-456-20
; Sequence 20, Application US/10373456
; Publication No. US20040009146A1
; GENERAL INFORMATION:
;  APPLICANT: Podhajcer, Osvaldo
;  TITLE OF INVENTION: Anti-Tumor Vaccine and Method
;  FILE REFERENCE: 1423P-US/101141-14
;  CURRENT APPLICATION NUMBER: US/10/373,456
;  CURRENT FILING DATE:  2003-02-25
;  PRIOR APPLICATION NUMBER: US 60/359,836
;  PRIOR FILING DATE: 2002-02-26
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 1017
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-373-456-20

  Query Match             4.5%;  Score 44;  DB 7;  Length 1017;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        673 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 716


RESULT 55
US-10-267-384-194
; Sequence 194, Application US/10267384
; Publication No. US20030198623A1
;   GENERAL INFORMATION:
;        APPLICANT: Paoletti, Enzo
;                   Tartaglia, James
;                   Cox, William I.
;        TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
;        NUMBER OF SEQUENCES: 217
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Curtis, Morris & Safford
;             STREET: 530 Fifth Avenue
;             CITY: New York
```

```
;              STATE: NY
;              COUNTRY: USA
;              ZIP: 10036
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.25
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/10/267,384
;              FILING DATE: 09-Oct-2002
;              CLASSIFICATION: 435
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Frommer, William S.
;              REGISTRATION NUMBER: 25,506
;              REFERENCE/DOCKET NUMBER: 454310-2530
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (212) 840-3333
;              TELEFAX: (212) 840-0712
;              TELEX: 425066CURTMS
;    INFORMATION FOR SEQ ID NO: 194:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 1018 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;         MOLECULE TYPE: cDNA
;         SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-10-267-384-194

  Query Match             4.5%;  Score 44;  DB 7;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 56
US-10-603-064-4
; Sequence 4, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
;  APPLICANT: Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION: Multiple Cytokine Protein Complexes
;  FILE REFERENCE: LEX-010
;  CURRENT APPLICATION NUMBER: US/10/603,064
;  CURRENT FILING DATE:  2003-06-24
;  PRIOR APPLICATION NUMBER: US/09/634,368
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: 60/147,924
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 1389
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: human
;   OTHER INFORMATION: p40-IL-2 fusion protein coding sequence
US-10-603-064-4

  Query Match             4.5%;  Score 44;  DB 8;  Length 1389;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 57
US-10-349-507-2
; Sequence 2, Application US/10349507
; Publication No. US20030199002A1
; GENERAL INFORMATION:
;  APPLICANT: Hekimi , Siegfried
;  APPLICANT:  Jiang , Ning
;  APPLICANT:  Benard, Claire
;  APPLICANT:  Kebir , Hania
;  APPLICANT:  McCright, Brenton
;  APPLICANT:  Lakowski , Bernard
;  TITLE OF INVENTION: CLK-2 NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
;  FILE REFERENCE: 11202-006-999
;  CURRENT APPLICATION NUMBER: US/10/349,507
;  CURRENT FILING DATE:  2003-01-22
;  PRIOR APPLICATION NUMBER: 10/312,187
;  PRIOR FILING DATE: 2002-12-20
;  PRIOR APPLICATION NUMBER: PCT/CA01/00913
;  PRIOR FILING DATE: 2001-06-20
;  PRIOR APPLICATION NUMBER: 60/213,174
;  PRIOR FILING DATE: 2000-06-22
;  PRIOR APPLICATION NUMBER: 60/254,932
;  PRIOR FILING DATE: 2000-12-13
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 1397
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (41)...(1024)
US-10-349-507-2

  Query Match             4.5%;  Score 44;  DB 7;  Length 1397;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        701 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 744


RESULT 58
US-10-267-565-2
; Sequence 2, Application US/10267565
; Publication No. US20030204059A1
; GENERAL INFORMATION:
;  APPLICANT: Gately, Maurice
;  APPLICANT:  Gubler, Ulrich
;  APPLICANT:  Hulmes, Jeffery
;  APPLICANT:  Podlaski, Frank
;  APPLICANT:  Stern, Alvin
;  TITLE OF INVENTION: PURIFICATION AND CHARACTERIZATION OF CYTOTOXIC
;  TITLE OF INVENTION:  LYMPHOCYTE MATURATION FACTOR AND MONOCLONAL
;  TITLE OF INVENTION:  ANTIBODIES THERETO
;  FILE REFERENCE: 11126-005
;  CURRENT APPLICATION NUMBER: US/10/267,565
;  CURRENT FILING DATE:  2003-01-23
;  PRIOR APPLICATION NUMBER: 09/401,839
;  PRIOR FILING DATE: 1999-09-22
;  PRIOR APPLICATION NUMBER: 08/459,151
;  PRIOR FILING DATE: 1995-06-02
;  PRIOR APPLICATION NUMBER: 08/205,011
;  PRIOR FILING DATE: 1994-03-02
;  PRIOR APPLICATION NUMBER: 07/857,023
;  PRIOR FILING DATE: 1992-03-24
;  PRIOR APPLICATION NUMBER: 07/572,284
;  PRIOR FILING DATE: 1990-08-27
;  PRIOR APPLICATION NUMBER: 07/520,935
;  PRIOR FILING DATE: 1990-05-09
;  PRIOR APPLICATION NUMBER: 07/455,708
```

```
;  PRIOR FILING DATE: 1989-12-22
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 1397
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (41)...(1024)
US-10-267-565-2

  Query Match             4.5%;  Score 44;  DB 7;  Length 1397;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        701 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 744


RESULT 59
US-10-929-182-22
; Sequence 22, Application US/10929182
; Publication No. US20050064483A1
; GENERAL INFORMATION:
;  APPLICANT: Zang, Jingwu
;  APPLICANT:  Hong, Jian
;  TITLE OF INVENTION: Gene Expression Profiling Technology for Treatment Evaluation of
;  TITLE OF INVENTION:  Multiple Sclerosis
;  FILE REFERENCE: HO-P02859US1
;  CURRENT APPLICATION NUMBER: US/10/929,182
;  CURRENT FILING DATE:  2004-08-30
;  PRIOR APPLICATION NUMBER: US 60/498,731
;  PRIOR FILING DATE: 2003-08-28
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
;   LENGTH: 1399
;   TYPE: DNA
;   ORGANISM: HUMAN
US-10-929-182-22

  Query Match             4.5%;  Score 44;  DB 10;  Length 1399;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        703 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 746


RESULT 60
US-10-742-405-7
; Sequence 7, Application US/10742405
; Publication No. US20040213761A1
; GENERAL INFORMATION:
;  APPLICANT: Bowman, Edward P.
;  APPLICANT:  Chan, Jason R.
;  APPLICANT:  Moore, Kevin
;  APPLICANT:  Nguyen, Nhung
;  APPLICANT:  Churakova, Tatyana
;  APPLICANT:  Chen, Shi-Juan
;  APPLICANT:  Cua, Daniel J.
;  TITLE OF INVENTION: Uses of mammalian cytokine; related reagents
;  FILE REFERENCE: DX01578K
;  CURRENT APPLICATION NUMBER: US/10/742,405
;  CURRENT FILING DATE:  2003-12-18
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
;   LENGTH: 1580
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (7)..(1569)
US-10-742-405-7

  Query Match             4.5%;  Score 44;  DB 9;  Length 1580;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        673 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 716


RESULT 61
US-10-373-456-2
; Sequence 2, Application US/10373456
; Publication No. US20040009146A1
; GENERAL INFORMATION:
;  APPLICANT: Podhajcer, Osvaldo
;  TITLE OF INVENTION: Anti-Tumor Vaccine and Method
;  FILE REFERENCE: 1423P-US/101141-14
;  CURRENT APPLICATION NUMBER: US/10/373,456
;  CURRENT FILING DATE:  2003-02-25
;  PRIOR APPLICATION NUMBER: US 60/359,836
;  PRIOR FILING DATE: 2002-02-26
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 1828
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: p40-linker-p35 fragment cloned into MVL-hIL12lig vector (Fig. 11
US-10-373-456-2

  Query Match             4.5%;  Score 44;  DB 7;  Length 1828;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        673 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 716


RESULT 62
US-10-228-811-4
; Sequence 4, Application US/10228811
; Publication No. US20030054392A1
; GENERAL INFORMATION:
;  APPLICANT: Wittig, Prof. Burghardt
;  APPLICANT:  Junghans, Claas
;  TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
;  TITLE OF INVENTION:  Therapy
;  FILE REFERENCE: XI 597/99
;  CURRENT APPLICATION NUMBER: US/10/228,811
;  CURRENT FILING DATE:  2002-08-27
;  PRIOR APPLICATION NUMBER: DE 196 48 625.4
;  PRIOR FILING DATE: 1996-11-13
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 1870
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (1)..(1870)
;   OTHER INFORMATION: Interleukin-12 (IL-12, p40-subunit); Oligo DNA Dumbbell
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1)..(2)
```

```
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to
;   OTHER INFORMATION: 2  can be modified with amino or caroxy features
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1869)..(1870)
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1869
;   OTHER INFORMATION: to 1870  can be modified with amino or caroxy features
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Strandness: both;  nucleic
;   OTHER INFORMATION: acid (linear),  hypothetical: No. US20030054392A1 anti-sense: No
US-10-228-811-4

  Query Match             4.5%;  Score 44;  DB 6;  Length 1870;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db       1293 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 1336


RESULT 63
US-10-172-399-7
; Sequence 7, Application US/10172399
; Publication No. US20030045495A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Chuan-Yuan
;  APPLICANT:  Dewhirst, Mark
;  APPLICANT:  Huang, Qian
;  TITLE OF INVENTION: A METHOD FOR SELECTIVE EXPRESSION OF THERAPEUTIC GENES BY HYPERTH
;  FILE REFERENCE: 180-129
;  CURRENT APPLICATION NUMBER: US/10/172,399
;  CURRENT FILING DATE:  2002-06-14
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
;   LENGTH: 2318
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (14)..(1000)
US-10-172-399-7

  Query Match             4.5%;  Score 44;  DB 6;  Length 2318;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        674 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 717


RESULT 64
US-10-476-961-3
; Sequence 3, Application US/10476961
; Publication No. US20040241843A1
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Isis Pharmaceuticals, Inc.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTSP-0393
;  CURRENT APPLICATION NUMBER: US/10/476,961
;  CURRENT FILING DATE:  2003-11-05
;  PRIOR APPLICATION NUMBER: 2001-05-07
;  PRIOR FILING DATE: 09/851,062
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 3
;   LENGTH: 2318
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (14)...(1000)
US-10-476-961-3

  Query Match             4.5%;  Score 44;  DB 9;  Length 2318;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        674 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 717


RESULT 65
US-10-429-802-44
; Sequence 44, Application US/10429802
; Publication No. US20030228285A1
; GENERAL INFORMATION:
;  APPLICANT: HUNG, MIEN-CHIE
;  APPLICANT:  WONG, KA YIN
;  APPLICANT:  ZOU, YIYU
;  TITLE OF INVENTION: BIPARTITE T-CELL FACTOR (TCF)-RESPONSIVE PROMOTER
;  FILE REFERENCE: UTSC:752US
;  CURRENT APPLICATION NUMBER: US/10/429,802
;  CURRENT FILING DATE:  2003-05-05
;  PRIOR APPLICATION NUMBER: 60/377,672
;  PRIOR FILING DATE: 2002-05-03
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
;   LENGTH: 2347
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-429-802-44

  Query Match             4.5%;  Score 44;  DB 7;  Length 2347;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        703 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 746


RESULT 66
US-10-430-503-35
; Sequence 35, Application US/10430503
; Publication No. US20040005684A1
; GENERAL INFORMATION:
;  APPLICANT: HUNG, MIEN-CHIE
;  APPLICANT:  LAN, KENG-LI
;  APPLICANT:  OU-YANG, FU
;  APPLICANT:  LIU, JAW-CHING
;  APPLICANT:  LAN, KENG-HSIN
;  TITLE OF INVENTION: TARGETING PROTEINS TO DELIVER THERAPEUTIC OR DIAGNOSTIC
;  TITLE OF INVENTION:  REAGENTS
;  FILE REFERENCE: UTSC:797US
;  CURRENT APPLICATION NUMBER: US/10/430,503
;  CURRENT FILING DATE:  2003-05-06
;  PRIOR APPLICATION NUMBER: 60/383,063
;  PRIOR FILING DATE: 2002-05-06
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
;   LENGTH: 2347
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-430-503-35

  Query Match             4.5%;  Score 44;  DB 7;  Length 2347;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        703 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 746


RESULT 67
US-09-924-703-3
; Sequence 3, Application US/09924703
; Patent No. US20020137898A1
; GENERAL INFORMATION:
;  APPLICANT: TRINCHIERI, GIORGIO
;  APPLICANT:  PERUSSIA, BICE
;  APPLICANT:  CLARK, STEVEN C.
;  APPLICANT:  WONG, GORDON G.
;  APPLICANT:  HEWICK, RODNEY
;  APPLICANT:  KOBAYASHI, MICHIKO
;  TITLE OF INVENTION: ANTIBODIES TO NATURAL KILLER STIMULATORY FACTOR
;  FILE REFERENCE: 01142.0142.0100
;  CURRENT APPLICATION NUMBER: US/09/924,703
;  CURRENT FILING DATE:  2001-08-09
;  PRIOR APPLICATION NUMBER: 09/325,958
;  PRIOR FILING DATE: 1999-06-04
;  PRIOR APPLICATION NUMBER: 08/858,000
;  PRIOR FILING DATE: 1997-05-16
;  PRIOR APPLICATION NUMBER: 08/403,013
;  PRIOR FILING DATE: 1995-03-13
;  PRIOR APPLICATION NUMBER: 07/584,941
;  PRIOR FILING DATE: 1990-09-18
;  PRIOR APPLICATION NUMBER: 07/307,817
;  PRIOR FILING DATE: 1989-02-07
;  PRIOR APPLICATION NUMBER: 07/269,945
;  PRIOR FILING DATE: 1988-11-10
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 2362
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
;   OTHER INFORMATION: sequence of the 40 kD subunit of NKSF
;   NAME/KEY: CDS
;   LOCATION: (33)..(1016)
US-09-924-703-3

  Query Match             4.5%;  Score 44;  DB 3;  Length 2362;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        693 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 736


RESULT 68
US-10-358-395-3
; Sequence 3, Application US/10358395
; Publication No. US20040044186A1
; GENERAL INFORMATION:
;  APPLICANT: TRINCHIERI, GIORGIO
;  APPLICANT:  PERUSSIA, BICE
;  APPLICANT:  CLARK, STEVEN C.
;  APPLICANT:  WONG, GORDON G.
;  APPLICANT:  HEWICK, RODNEY
;  APPLICANT:  KOBAYASHI, MICHIKO
;  TITLE OF INVENTION: ANTIBODIES TO NATURAL KILLER STIMULATORY FACTOR
;  FILE REFERENCE: 01142.0142.0100
;  CURRENT APPLICATION NUMBER: US/10/358,395
;  CURRENT FILING DATE:  2003-02-05
;  PRIOR APPLICATION NUMBER: US/09/924,703
;  PRIOR FILING DATE: 2001-08-09
;  PRIOR APPLICATION NUMBER: 09/325,958
;  PRIOR FILING DATE: 1999-06-04
;  PRIOR APPLICATION NUMBER: 08/858,000
;  PRIOR FILING DATE: 1997-05-16
;  PRIOR APPLICATION NUMBER: 08/403,013
;  PRIOR FILING DATE: 1995-03-13
;  PRIOR APPLICATION NUMBER: 07/584,941
;  PRIOR FILING DATE: 1990-09-18
;  PRIOR APPLICATION NUMBER: 07/307,817
;  PRIOR FILING DATE: 1989-02-07
;  PRIOR APPLICATION NUMBER: 07/269,945
;  PRIOR FILING DATE: 1988-11-10
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 2362
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
;   OTHER INFORMATION: sequence of the 40 kD subunit of NKSF
;   NAME/KEY: CDS
;   LOCATION: (33)..(1016)
US-10-358-395-3

  Query Match             4.5%;  Score 44;  DB 8;  Length 2362;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        693 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 736


RESULT 69
US-10-373-456-1
; Sequence 1, Application US/10373456
; Publication No. US20040009146A1
; GENERAL INFORMATION:
;  APPLICANT: Podhajcer, Osvaldo
;  TITLE OF INVENTION: Anti-Tumor Vaccine and Method
;  FILE REFERENCE: 1423P-US/101141-14
;  CURRENT APPLICATION NUMBER: US/10/373,456
;  CURRENT FILING DATE:  2003-02-25
;  PRIOR APPLICATION NUMBER: US 60/359,836
;  PRIOR FILING DATE: 2002-02-26
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 2466
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: p35-IRES-p40 fragment cloned into MVL-hIL-12 and MVL-hIL-12-hIL-
;   OTHER INFORMATION: 0 vectors (Fig 11)
US-10-373-456-1

  Query Match             4.5%;  Score 44;  DB 7;  Length 2466;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db       2130 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 2173


RESULT 70
US-10-136-837-1
; Sequence 1, Application US/10136837
; Publication No. US20030181405A1
; GENERAL INFORMATION:
;  APPLICANT: NORDSTROM, Jeffrey L
;  APPLICANT:  PERICLE, Federica
;  APPLICANT:  ROLLAND, Alain
```

```
;  APPLICANT:  RALSTON, Robert
;  TITLE OF INVENTION: Interferon Alpha Plasmids and Delivery Systems, and Methods of Ma
;  TITLE OF INVENTION:  Using the Same
;  FILE REFERENCE: 273/082 (GM15-1USC1)
;  CURRENT APPLICATION NUMBER: US/10/136,837
;  CURRENT FILING DATE:  2002-04-29
;  PRIOR APPLICATION NUMBER: US 09/268,135
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 5686
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Human IL-12 Plasmid pIN1143
US-10-136-837-1

  Query Match             4.5%;  Score 44;  DB 7;  Length 5686;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db       3879 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 3922


RESULT 71
US-09-828-825-1
; Sequence 1, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 8578
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: enhancer
;   LOCATION: (1)..(659)
;   OTHER INFORMATION: CMV IE
;   NAME/KEY: promoter
;   LOCATION: (669)..(750)
;   OTHER INFORMATION: CMV  IE
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA Promoter
;   NAME/KEY: mRNA
;   LOCATION: (1090)..(1984)
;   OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
;   NAME/KEY: RBS
;   LOCATION: (2013)..(2593)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: mRNA
;   LOCATION: (2627)..(4263)
;   OTHER INFORMATION: Human IL12.0 (2640-4223 coding sequence, flexible
;   OTHER INFORMATION: linker at 3624-3629)
;   NAME/KEY: promoter
;   LOCATION: (4352)..(4431)
;   OTHER INFORMATION: T3 RNA polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4362)..(4583)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4678)..(5133)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5197)..(6564)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (6975)..(7835)
;   OTHER INFORMATION: Ampicillin resistance
;   OTHER INFORMATION: Description of Artificial Sequence: Plasmid
;   NAME/KEY: CDS
;   LOCATION: (2640)..(4223)
;   OTHER INFORMATION: IL 12.0 coding sequence - 2 amino acid linker at
;   OTHER INFORMATION: 3624
US-09-828-825-1

  Query Match             4.5%;  Score 44;  DB 3;  Length 8578;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db       3300 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 3343


RESULT 72
US-09-828-825-3
; Sequence 3, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 8578
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
;   NAME/KEY: enhancer
;   LOCATION: (1)..(659)
;   OTHER INFORMATION: CMV IE Enhancer
;   NAME/KEY: promoter
;   LOCATION: (669)..(750)
;   OTHER INFORMATION: CMV IE Promoter
;   NAME/KEY: misc_feature
;   LOCATION: (890)..(1002)
;   OTHER INFORMATION: InTervening Sequence
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(1984)
;   OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
;   NAME/KEY: RBS
;   LOCATION: (2013)..(2593)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (2627)..(4263)
;   OTHER INFORMATION: Human IL12.0 sequence (2640-4217 is coding
;   OTHER INFORMATION: sequence)
;   NAME/KEY: promoter
;   LOCATION: (4346)..(4425)
;   OTHER INFORMATION: T3 RNA polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4356)..(4577)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
```

```
;   NAME/KEY: rep_origin
;   LOCATION: (4672)..(5127)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5191)..(6558)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (6969)..(7829)
;   OTHER INFORMATION: Ampicillin resistance
;   NAME/KEY: CDS
;   LOCATION: (2640)..(4217)
;   OTHER INFORMATION: IL12.0 coding sequence - no linker
US-09-828-825-3

  Query Match             4.5%;  Score 44;  DB 3;  Length 8578;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db       3300 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 3343


RESULT 73
US-09-828-825-7
; Sequence 7, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 8608
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: misc_feature
;   LOCATION: (890)..(1002)
;   OTHER INFORMATION: Intervening sequence
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(1984)
;   OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
;   NAME/KEY: RBS
;   LOCATION: (2013)..(2593)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (2627)..(4263)
;   OTHER INFORMATION: Human IL12.2 sequence (2460-4253 is coding
;   OTHER INFORMATION: sequence, 13 amino acid flexible linker at
;   OTHER INFORMATION: 3606-3676)
;   NAME/KEY: CDS
;   LOCATION: (2640)..(4253)
;   OTHER INFORMATION: IL12.2 coding sequence (13 amino acid linker)
;   NAME/KEY: promoter
;   LOCATION: (4362)..(4383)
;   OTHER INFORMATION: T3 RNA Polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4393)..(4614)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4709)..(5164)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5228)..(6595)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (7006)..(7866)
;   OTHER INFORMATION: Ampicillin resistance
US-09-828-825-7

  Query Match             4.5%;  Score 44;  DB 3;  Length 8608;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db       3300 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 3343


RESULT 74
US-09-828-825-5
; Sequence 5, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 8623
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: misc_feature
;   LOCATION: (890)..(1002)
;   OTHER INFORMATION: Intervening sequence
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(1984)
;   OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
;   NAME/KEY: RBS
;   LOCATION: (2013)..(2593)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (2627)..(4278)
;   OTHER INFORMATION: Human IL12.3 - 2640-4268 is coding sequence,
;   OTHER INFORMATION: flexible linker from 3606-3690
;   NAME/KEY: CDS
;   LOCATION: (2640)..(4268)
;   OTHER INFORMATION: IL 12.3 coding sequence - has 28 amino acid linker
;   OTHER INFORMATION: sequence
;   NAME/KEY: promoter
;   LOCATION: (4398)..(4407)
;   OTHER INFORMATION: T3 RNA polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4408)..(4629)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4724)..(5179)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
```

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;   LOCATION: (5243)..(6610)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (7021)..(7881)
;   OTHER INFORMATION: Ampicillin resistance
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-828-825-5

  Query Match             4.5%;  Score 44;  DB 3;  Length 8623;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db       3300 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 3343


RESULT 75
US-09-828-825-15
; Sequence 15, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 8629
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(2726)
;   OTHER INFORMATION: Human IL12.2 (coding sequence is 1103-2716, 10
;   OTHER INFORMATION: amino acid linker at 2087-2116)
;   NAME/KEY: CDS
;   LOCATION: (1103)..(2716)
;   OTHER INFORMATION: Human IL12.2 (10 amino acid linker)
;   NAME/KEY: RBS
;   LOCATION: (2752)..(3332)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (3369)..(4263)
;   OTHER INFORMATION: Human B7.1 sequence
;   NAME/KEY: promoter
;   LOCATION: (4383)..(4404)
;   OTHER INFORMATION: T3 RNA Polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4414)..(4635)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4730)..(5185)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5249)..(6616)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (7027)..(7887)
;   OTHER INFORMATION: Ampicillin resistance gene
US-09-828-825-15

  Query Match             4.5%;  Score 44;  DB 3;  Length 8629;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db       1763 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 1806


RESULT 76
US-09-828-825-9
; Sequence 9, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 8638
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: misc_feature
;   LOCATION: (890)..(1002)
;   OTHER INFORMATION: Intervening sequence
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(1984)
;   OTHER INFORMATION: Human B7.1 (1090-1954 is coding sequence)
;   NAME/KEY: RBS
;   LOCATION: (2013)..(2593)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (2627)..(4293)
;   OTHER INFORMATION: Human IL12.4 (coding sequence is 2640-4283, 33
;   OTHER INFORMATION: amino acid linker at 3606-3706)
;   NAME/KEY: CDS
;   LOCATION: (2640)..(4283)
;   OTHER INFORMATION: IL12.4 coding sequence (33 amino acid linker)
;   NAME/KEY: promoter
;   LOCATION: (4392)..(4413)
;   OTHER INFORMATION: T3 RNA Polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4423)..(4644)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4739)..(5194)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5258)..(6625)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (7036)..(7896)
;   OTHER INFORMATION: Ampicillin resistance
US-09-828-825-9

  Query Match             4.5%;  Score 44;  DB 3;  Length 8638;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db       3300 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 3343


RESULT 77
US-09-828-825-13
; Sequence 13, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
;   LENGTH: 8644
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(2731)
;   OTHER INFORMATION: Human IL12.3 (1103-2731 is coding sequence, 15
;   OTHER INFORMATION: amino acid linker at 2087-2131)
;   NAME/KEY: CDS
;   LOCATION: (1103)..(2731)
;   OTHER INFORMATION: IL12.3 (15 amino acid linker)
;   NAME/KEY: RBS
;   LOCATION: (2767)..(3347)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (3384)..(4278)
;   OTHER INFORMATION: Human B7.1 sequence
;   NAME/KEY: promoter
;   LOCATION: (4398)..(4419)
;   OTHER INFORMATION: T3 RNA polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4429)..(4650)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4745)..(5200)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5264)..(5681)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (7042)..(7902)
;   OTHER INFORMATION: Ampicillin resistance gene
US-09-828-825-13

  Query Match             4.5%;  Score 44;  DB 3;  Length 8644;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db       1763 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 1806


RESULT 78
US-09-828-825-11
; Sequence 11, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 8659
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(2756)
;   OTHER INFORMATION: Human IL12.4 (coding sequence 1103-2746, 19 amino
;   OTHER INFORMATION: acid linker at 2087-2146)
;   NAME/KEY: CDS
;   LOCATION: (1103)..(2746)
;   OTHER INFORMATION: Human IL12.4 (19 amino acid linker)
;   NAME/KEY: RBS
;   LOCATION: (2782)..(3362)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (3399)..(4293)
;   OTHER INFORMATION: Human B7.1 sequence
;   NAME/KEY: promoter
;   LOCATION: (4413)..(4434)
;   OTHER INFORMATION: T3 RNA polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4444)..(4665)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4760)..(5215)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5279)..(6646)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (7057)..(7917)
;   OTHER INFORMATION: Ampicillin resistance gene
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-828-825-11

  Query Match             4.5%;  Score 44;  DB 3;  Length 8659;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db       1763 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 1806


RESULT 79
US-10-511-237-3
; Sequence 3, Application US/10511237
; Publication No. US20050233457A1
; GENERAL INFORMATION:
;  APPLICANT: Block, Andreas
;  TITLE OF INVENTION: Recombinant Viral Vectors for the Tetracycline-regulated Express
;  TITLE OF INVENTION:  Genes
```

```
;  FILE REFERENCE: 66741-043
;  CURRENT APPLICATION NUMBER: US/10/511,237
;  CURRENT FILING DATE:  2004-10-12
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 11453
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Adenoviral expression plasmid pShuttle.3r.hscIL-12 for regulated
;   OTHER INFORMATION: expression of human IL-12 following virus generation using AdEasy
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (327)..(713)
;   OTHER INFORMATION: VP16
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (714)..(1352)
;   OTHER INFORMATION: TetR
;   FEATURE:
;   NAME/KEY: Intron
;   LOCATION: (1353)..(1912)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: promoter
;   LOCATION: (1864)..(1902)
;   OTHER INFORMATION: TK-min
;   FEATURE:
;   NAME/KEY: protein_bind
;   LOCATION: (1913)..(2212)
;   OTHER INFORMATION: TetO7
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2213)..(2709)
;   OTHER INFORMATION: CMV-min + Intron
;   FEATURE:
;   NAME/KEY: promoter
;   LOCATION: (2226)..(2264)
;   OTHER INFORMATION: CMV-min
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (2710)..(4308)
;   OTHER INFORMATION: Human singe-chain IL-12
;   FEATURE:
;   NAME/KEY: mutation
;   LOCATION: (4020)..(4023)
;   OTHER INFORMATION: T/C, A/T, G/C, T/G
US-10-511-237-3

  Query Match             4.5%;  Score 44;  DB 10;  Length 11453;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db       3370 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 3413


RESULT 80
US-10-511-237-1
; Sequence 1, Application US/10511237
; Publication No. US20050233457A1
; GENERAL INFORMATION:
;  APPLICANT: Block, Andreas
;  TITLE OF INVENTION: Recombinant Viral Vectors for the Tetracycline-regulated Expressi
;  TITLE OF INVENTION:  Genes
;  FILE REFERENCE: 66741-043
;  CURRENT APPLICATION NUMBER: US/10/511,237
;  CURRENT FILING DATE:  2004-10-12
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 11569
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Adenoviral expression plasmid pAd.3r.hscIL-12 for regulated expr
;   OTHER INFORMATION: human IL-12
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (327)..(713)
;   OTHER INFORMATION: VP16
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (714)..(1352)
;   OTHER INFORMATION: TetR
;   FEATURE:
;   NAME/KEY: Intron
;   LOCATION: (1353)..(1912)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: promoter
;   LOCATION: (1864)..(1902)
;   OTHER INFORMATION: TK-min
;   FEATURE:
;   NAME/KEY: protein_bind
;   LOCATION: (1913)..(2212)
;   OTHER INFORMATION: TetO7
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2213)..(2709)
;   OTHER INFORMATION: CMV-min + Intron
;   FEATURE:
;   NAME/KEY: promoter
;   LOCATION: (2226)..(2264)
;   OTHER INFORMATION: CMV-min
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (2710)..(4308)
;   OTHER INFORMATION: Human single-chain IL-12
;   FEATURE:
;   NAME/KEY: mutation
;   LOCATION: (4020)..(4023)
;   OTHER INFORMATION: T/C, A/T, G/C, T/G
US-10-511-237-1

  Query Match             4.5%;  Score 44;  DB 10;  Length 11569;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db       3370 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 3413


RESULT 81
US-10-528-644A-53
; Sequence 53, Application US/10528644A
; Publication No. US20050287117A1
; GENERAL INFORMATION:
;  APPLICANT: SUNG, Young Chul
;  APPLICANT:  YOUN, Jin-Won
;  APPLICANT:  YANG, Se-Hwan
;  APPLICANT:  PARK, Su-Hwan
;  APPLICANT:  LEE, Chang Geun
;  TITLE OF INVENTION: A VACCINE ENHANCING THE PROTECTIVE IMMUNITY TO
;  TITLE OF INVENTION:  HEPATITIS C VIRUS USING PLASMID DNA AND RECOMBINANT ADENOVIRUS
;  FILE REFERENCE: 428.1049
;  CURRENT APPLICATION NUMBER: US/10/528,644A
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: PCT/KR03/01951
;  PRIOR FILING DATE: 2003-11-19
;  PRIOR APPLICATION NUMBER: KR 2002-0058712
;  PRIOR FILING DATE: 2002-09-27
;  PRIOR APPLICATION NUMBER: KR 2002-68496
```

```
;  PRIOR FILING DATE: 2002-11-06
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: KopatentIn 1.71
; SEQ ID NO 53
;    LENGTH: 2390
;    TYPE: DNA
;    ORGANISM: Homo sapiens (hIL-12m)
US-10-528-644A-53

  Query Match             4.0%;  Score 39;  DB 10;  Length 2390;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-09;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        400 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 438
              |||||||||||||||||||||||||||||||||||||||
Db       1803 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 1841


RESULT 82
US-10-240-376A-130
; Sequence 130, Application US/10240376A
; Publication No. US20040161747A1
; GENERAL INFORMATION:
;  APPLICANT: Morahan, Grant
;  TITLE OF INVENTION: A METHOD FOR SCREENING FOR AUTOIMMUNE
;  TITLE OF INVENTION:  DISEASE BY IDENTIFYING POLYMORPHISMS IN IL-12 p40
;  FILE REFERENCE: DAVI186.001APC
;  CURRENT APPLICATION NUMBER: US/10/240,376A
;  CURRENT FILING DATE:  2002-09-27
;  PRIOR APPLICATION NUMBER: PCT/AU01/00340
;  PRIOR FILING DATE: 2001-03-27
;  PRIOR APPLICATION NUMBER: PQ 6466
;  PRIOR FILING DATE: 2000-03-27
;  PRIOR APPLICATION NUMBER: US 60/204,366
;  PRIOR FILING DATE: 2000-05-15
;  NUMBER OF SEQ ID NOS: 140
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 130
;    LENGTH: 18340
;    TYPE: DNA
;    ORGANISM: mammalian
US-10-240-376A-130

  Query Match             4.0%;  Score 39;  DB 8;  Length 18340;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-09;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        400 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 438
              |||||||||||||||||||||||||||||||||||||||
Db      10439 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 10477


RESULT 83
US-10-029-386-16833/c
; Sequence 16833, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
;  TITLE OF INVENTION:  EXPRESSION ANALYSIS TWO
;  FILE REFERENCE: AEOMICA-X-2
;  CURRENT APPLICATION NUMBER: US/10/029,386
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 34288
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 16833
;    LENGTH: 270
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    OTHER INFORMATION: MAP TO CHR5.1
;    OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.84
;    OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.72
;    OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.93
;    OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.79
;    OTHER INFORMATION: NT HIT: AY008847.1, EVALUE 0.00e+00
;    OTHER INFORMATION: EST_HUMAN HIT: BF204907.1, EVALUE 9.20e-02
;    OTHER INFORMATION: SWISSPROT HIT: P29460, EVALUE 4.00e-41
US-10-029-386-16833

  Query Match             3.6%;  Score 35;  DB 7;  Length 270;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-07;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        313 CACAAAAAGGAAGATGGAATTTGGTCCACTGATAT 347
              |||||||||||||||||||||||||||||||||||
Db         41 CACAAAAAGGAAGATGGAATTTGGTCCACTGATAT 7


RESULT 84
US-10-029-386-3133/c
; Sequence 3133, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
;  TITLE OF INVENTION:  EXPRESSION ANALYSIS TWO
;  FILE REFERENCE: AEOMICA-X-2
;  CURRENT APPLICATION NUMBER: US/10/029,386
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 34288
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 3133
;    LENGTH: 556
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    OTHER INFORMATION: MAP TO CHR5.1
;    OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.84
;    OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.72
;    OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.93
;    OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.79
;    OTHER INFORMATION: NT HIT: AY008847.1, EVALUE 0.00e+00
;    OTHER INFORMATION: SWISSPROT HIT: P29460, EVALUE 5.00e-43
;    OTHER INFORMATION: EST_HUMAN HIT: BG389008.1, EVALUE 2.00e-01
US-10-029-386-3133

  Query Match             3.6%;  Score 35;  DB 7;  Length 556;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        313 CACAAAAAGGAAGATGGAATTTGGTCCACTGATAT 347
              |||||||||||||||||||||||||||||||||||
Db        236 CACAAAAAGGAAGATGGAATTTGGTCCACTGATAT 202


RESULT 85
US-09-823-549-77
; Sequence 77, Application US/09823549
; Publication No. US20020147998A1
; GENERAL INFORMATION:
;  APPLICANT: McConlogue, Lisa  C
;  APPLICANT:  Games, Kate D.
;  APPLICANT:  Yednock, Theodore A.
;  APPLICANT:  Hua, Tan
;  APPLICANT:  Messersmith, Elizabeth
;  APPLICANT:  Bard, Frederique
;  TITLE OF INVENTION: SCREENING MARKERS AND METHODS FOR NEURODEGENERATIVE DISORDERS
;  FILE REFERENCE: 015270-009110US
;  CURRENT APPLICATION NUMBER: US/09/823,549
;  CURRENT FILING DATE:  2001-03-30
;  PRIOR APPLICATION NUMBER: US 60/193,847
```

; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
; LENGTH: 73
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-12 p40, #1 marker
US-09-823-549-77

Query Match 3.0%; Score 30; DB 3; Length 73;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
||||||||||||||||||||||||||||||
Db 8 CAGCTTCTTCATCAGGGACATCATCAAACC 37

RESULT 86
US-10-685-992-77
; Sequence 77, Application US/10685992
; Publication No. US20040213739A1
; GENERAL INFORMATION:
; APPLICANT: McConlogue, Lisa C
; APPLICANT: Games, Kate D.
; APPLICANT: Yednock, Theodore A.
; APPLICANT: Hua, Tan
; APPLICANT: Messersmith, Elizabeth
; APPLICANT: Bard, Frederique
; TITLE OF INVENTION: SCREENING MARKERS AND METHODS FOR NEURODEGENERATIVE DISORDERS
; FILE REFERENCE: 015270-009110US
; CURRENT APPLICATION NUMBER: US/10/685,992
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: US/09/823,549
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/193,847
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
; LENGTH: 73
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-12 p40, #1 marker
US-10-685-992-77

Query Match 3.0%; Score 30; DB 9; Length 73;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
||||||||||||||||||||||||||||||
Db 8 CAGCTTCTTCATCAGGGACATCATCAAACC 37

RESULT 87
US-10-603-064-3
; Sequence 3, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin Ming
; TITLE OF INVENTION: Multiple Cytokine Protein Complexes
; FILE REFERENCE: LEX-010
; CURRENT APPLICATION NUMBER: US/10/603,064
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: US/09/634,368
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 60/147,924
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1409
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: murine
; OTHER INFORMATION: p40-GM-CSF fusion protein coding sequence
US-10-603-064-3

Query Match 3.0%; Score 30; DB 8; Length 1409;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
||||||||||||||||||||||||||||||
Db 689 CAGCTTCTTCATCAGGGACATCATCAAACC 718

RESULT 88
US-10-603-064-2
; Sequence 2, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin Ming
; TITLE OF INVENTION: Multiple Cytokine Protein Complexes
; FILE REFERENCE: LEX-010
; CURRENT APPLICATION NUMBER: US/10/603,064
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: US/09/634,368
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 60/147,924
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1472
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: murine
; OTHER INFORMATION: p40-IL-2 fusion protein coding sequence
US-10-603-064-2

Query Match 3.0%; Score 30; DB 8; Length 1472;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
||||||||||||||||||||||||||||||
Db 689 CAGCTTCTTCATCAGGGACATCATCAAACC 718

RESULT 89
US-10-603-064-12
; Sequence 12, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin Ming
; TITLE OF INVENTION: Multiple Cytokine Protein Complexes
; FILE REFERENCE: LEX-010
; CURRENT APPLICATION NUMBER: US/10/603,064
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: US/09/634,368
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 60/147,924
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12

```
;   LENGTH: 1569
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p35-linker-p40 fusion protein coding sequence
US-10-603-064-12

  Query Match             3.0%;  Score 30;  DB 8;  Length 1569;
  Best Local Similarity   100.0%;  Pred. No. 0.0001;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||
Db       1230 CAGCTTCTTCATCAGGGACATCATCAAACC 1259


RESULT 90
US-10-742-405-5
; Sequence 5, Application US/10742405
; Publication No. US20040213761A1
; GENERAL INFORMATION:
;  APPLICANT: Bowman, Edward P.
;  APPLICANT:  Chan, Jason R.
;  APPLICANT:  Moore, Kevin
;  APPLICANT:  Nguyen, Nhung
;  APPLICANT:  Churakova, Tatyana
;  APPLICANT:  Chen, Shi-Juan
;  APPLICANT:  Cua, Daniel J.
;  TITLE OF INVENTION: Uses of mammalian cytokine; related reagents
;  FILE REFERENCE: DX01578K
;  CURRENT APPLICATION NUMBER: US/10/742,405
;  CURRENT FILING DATE:  2003-12-18
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 1610
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (7)..(1599)
US-10-742-405-5

  Query Match             3.0%;  Score 30;  DB 9;  Length 1610;
  Best Local Similarity   100.0%;  Pred. No. 0.0001;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||
Db        681 CAGCTTCTTCATCAGGGACATCATCAAACC 710


RESULT 91
US-10-172-399-3
; Sequence 3, Application US/10172399
; Publication No. US20030045495A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Chuan-Yuan
;  APPLICANT:  Dewhirst, Mark
;  APPLICANT:  Huang, Qian
;  TITLE OF INVENTION: A METHOD FOR SELECTIVE EXPRESSION OF THERAPEUTIC GENES BY HYPERTH
;  FILE REFERENCE: 180-129
;  CURRENT APPLICATION NUMBER: US/10/172,399
;  CURRENT FILING DATE:  2002-06-14
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 1840
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (35)..(1042)
US-10-172-399-3

  Query Match             3.0%;  Score 30;  DB 6;  Length 1840;
  Best Local Similarity   100.0%;  Pred. No. 0.0001;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||
Db        703 CAGCTTCTTCATCAGGGACATCATCAAACC 732


RESULT 92
US-10-603-064-11
; Sequence 11, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
;  APPLICANT: Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION: Multiple Cytokine Protein Complexes
;  FILE REFERENCE: LEX-010
;  CURRENT APPLICATION NUMBER: US/10/603,064
;  CURRENT FILING DATE:  2003-06-24
;  PRIOR APPLICATION NUMBER: US/09/634,368
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: 60/147,924
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 2013
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p35-linker-p40-IL-2 fusion protein coding sequence
US-10-603-064-11

  Query Match             3.0%;  Score 30;  DB 8;  Length 2013;
  Best Local Similarity   100.0%;  Pred. No. 0.0001;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||
Db       1230 CAGCTTCTTCATCAGGGACATCATCAAACC 1259


RESULT 93
US-10-603-064-13
; Sequence 13, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
;  APPLICANT: Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION: Multiple Cytokine Protein Complexes
;  FILE REFERENCE: LEX-010
;  CURRENT APPLICATION NUMBER: US/10/603,064
;  CURRENT FILING DATE:  2003-06-24
;  PRIOR APPLICATION NUMBER: US/09/634,368
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: 60/147,924
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
;   LENGTH: 2709
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: Fc-p35-linker-p40-IL-2 fusion protein coding
;   OTHER INFORMATION: sequence
US-10-603-064-13
```

```
  Query Match             3.0%;  Score 30;  DB 8;  Length 2709;
  Best Local Similarity   100.0%;  Pred. No. 0.0001;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||
Db       1926 CAGCTTCTTCATCAGGGACATCATCAAACC 1955


RESULT 94
US-10-136-837-3
; Sequence 3, Application US/10136837
; Publication No. US20030181405A1
; GENERAL INFORMATION:
;  APPLICANT: NORDSTROM, Jeffrey L
;  APPLICANT:  PERICLE, Federica
;  APPLICANT:  ROLLAND, Alain
;  APPLICANT:  RALSTON, Robert
;  TITLE OF INVENTION: Interferon Alpha Plasmids and Delivery Systems, and Methods of Ma
;  TITLE OF INVENTION:  Using the Same
;  FILE REFERENCE: 273/082 (GM15-1USC1)
;  CURRENT APPLICATION NUMBER: US/10/136,837
;  CURRENT FILING DATE:  2002-04-29
;  PRIOR APPLICATION NUMBER: US 09/268,135
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 5966
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Mouse IL-12 pIN0961
US-10-136-837-3

  Query Match             3.0%;  Score 30;  DB 7;  Length 5966;
  Best Local Similarity   100.0%;  Pred. No. 0.00011;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||
Db       5342 CAGCTTCTTCATCAGGGACATCATCAAACC 5371


RESULT 95
US-10-511-237-2
; Sequence 2, Application US/10511237
; Publication No. US20050233457A1
; GENERAL INFORMATION:
;  APPLICANT: Block, Andreas
;  TITLE OF INVENTION: Recombinant Viral Vectors for the Tetracycline-regulated Expressi
;  TITLE OF INVENTION:  Genes
;  FILE REFERENCE: 66741-043
;  CURRENT APPLICATION NUMBER: US/10/511,237
;  CURRENT FILING DATE:  2004-10-12
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 11458
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Adenoviral expression plasmid pAd.3r.mscIL-12 for regulated
;   OTHER INFORMATION: expression of murine IL-12
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (327)..(713)
;   OTHER INFORMATION: VP16
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (714)..(1352)
;   OTHER INFORMATION: TetR
;   FEATURE:
;   NAME/KEY: Intron
;   LOCATION: (1353)..(1912)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: promoter
;   LOCATION: (1864)..(1902)
;   OTHER INFORMATION: TK-min
;   FEATURE:
;   NAME/KEY: protein_bind
;   LOCATION: (1913)..(2212)
;   OTHER INFORMATION: TetO7
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2213)..(2687)
;   OTHER INFORMATION: CMV-min + Intron
;   FEATURE:
;   NAME/KEY: promoter
;   LOCATION: (2226)..(2264)
;   OTHER INFORMATION: CMV-min
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (2688)..(4325)
;   OTHER INFORMATION: Murine single-chain IL-12
US-10-511-237-2

  Query Match             3.0%;  Score 30;  DB 10;  Length 11458;
  Best Local Similarity   100.0%;  Pred. No. 0.00011;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||
Db       3362 CAGCTTCTTCATCAGGGACATCATCAAACC 3391


RESULT 96
US-09-917-265-85
; Sequence 85, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THER
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 85
;   LENGTH: 28
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-917-265-85

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  Best Local Similarity   100.0%;  Pred. No. 0.0012;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 97
US-10-821-670-85
; Sequence 85, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
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;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
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;   OTHER INFORMATION: Synthetic Primer
US-10-821-670-85

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RESULT 98
US-09-917-265-87
; Sequence 87, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
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;   OTHER INFORMATION: Synthetic Primer
US-09-917-265-87

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; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
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US-10-821-670-87

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; Sequence 86, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERI
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
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;   OTHER INFORMATION: Synthetic Primer
US-09-917-265-86

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OM nucleic - nucleic search, using sw model

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Scoring table: OLIGO_NUC
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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172	15	1.5	4863	7	US-11-217-529-2436	Sequence 2436, Ap
173	15	1.5	4995	7	US-11-217-529-2505	Sequence 2505, Ap
c 174	15	1.5	5262	7	US-11-217-529-76367	Sequence 76367, A
175	15	1.5	5515	6	US-10-524-021-1	Sequence 1, Appli
176	15	1.5	5711	6	US-10-480-434A-15	Sequence 15, Appl
c 177	15	1.5	5934	7	US-11-313-450-13	Sequence 13, Appl
c 178	15	1.5	5997	7	US-11-313-450-1	Sequence 1, Appli
c 179	15	1.5	6003	7	US-11-313-450-5	Sequence 5, Appli
c 180	15	1.5	6018	7	US-11-313-450-3	Sequence 3, Appli
181	15	1.5	6218	6	US-10-505-928-460	Sequence 460, App
c 182	15	1.5	6328	7	US-11-263-326-101	Sequence 101, App
c 183	15	1.5	6328	7	US-11-263-326-102	Sequence 102, App
c 184	15	1.5	6328	7	US-11-263-326-103	Sequence 103, App
c 185	15	1.5	6328	7	US-11-263-326-146	Sequence 146, App
c 186	15	1.5	6328	7	US-11-263-326-147	Sequence 147, App
c 187	15	1.5	6328	7	US-11-263-326-148	Sequence 148, App
c 188	15	1.5	6328	7	US-11-263-326-149	Sequence 149, App
c 189	15	1.5	6328	7	US-11-263-326-150	Sequence 150, App
c 190	15	1.5	6328	7	US-11-263-326-151	Sequence 151, App
c 191	15	1.5	6328	7	US-11-263-326-152	Sequence 152, App
c 192	15	1.5	6371	7	US-11-251-465-8	Sequence 8, Appli
c 193	15	1.5	6596	7	US-11-263-326-105	Sequence 105, App
c 194	15	1.5	6599	7	US-11-263-326-106	Sequence 106, App
c 195	15	1.5	6599	7	US-11-263-326-107	Sequence 107, App
c 196	15	1.5	6599	7	US-11-263-326-109	Sequence 109, App
c 197	15	1.5	6732	7	US-11-217-529-1872	Sequence 1872, Ap
c 198	15	1.5	7280	6	US-10-505-928-842	Sequence 842, App
199	15	1.5	8019	7	US-11-217-529-76544	Sequence 76544, A
c 200	15	1.5	8292	6	US-10-501-814-2	Sequence 2, Appli

ALIGNMENTS

```
RESULT 1
US-11-217-529-5663
; Sequence 5663, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5663
;   LENGTH: 303
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-5663

  Query Match             2.0%;  Score 20;  DB 7;  Length 303;
  Best Local Similarity   100.0%;  Pred. No. 0.37;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 TCATCGCCTGGTTTTCCCTG 39
              ||||||||||||||||||||
Db         35 TCATCGCCTGGTTTTCCCTG 54


RESULT 2
US-10-471-571A-1285/c
; Sequence 1285, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
```

; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 1285
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-471-571A-1285

Query Match 1.8%; Score 18; DB 6; Length 960;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 675 CAGCAGCTTCTTCATCAG 692
||||||||||||||||||
Db 142 CAGCAGCTTCTTCATCAG 125

RESULT 3
US-11-313-450-13
; Sequence 13, Application US/11313450
; Publication No. US20060110778A1
; GENERAL INFORMATION:
; APPLICANT: Adorante, Joeseph S.
; APPLICANT: Ehring, George R.
; TITLE OF INVENTION: High-Throughput Screens For Identifying
; TITLE OF INVENTION: Selective Persistent Sodium Channels Channel Blockers
; FILE REFERENCE: 17407 CIP (AP)
; CURRENT APPLICATION NUMBER: US/11/313,450
; CURRENT FILING DATE: 2005-12-19
; PRIOR APPLICATION NUMBER: 09/989797
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252771
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 5934
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-313-450-13

Query Match 1.8%; Score 18; DB 7; Length 5934;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 316 AAAAAGGAAGATGGAATT 333
||||||||||||||||||
Db 4975 AAAAAGGAAGATGGAATT 4992

RESULT 4
US-11-251-465-8
; Sequence 8, Application US/11251465
; Publication No. US20060094061A1
; GENERAL INFORMATION:
; APPLICANT: Brys, Reginald
; APPLICANT: Vandeghinste, Nick
; APPLICANT: Tomme, Peter
; APPLICANT: Klaassen, Hubertus
; TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
; TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
; TITLE OF INVENTION: Inflammatory Diseases
; FILE REFERENCE: P30,172-A USA
; CURRENT APPLICATION NUMBER: US/11/251,465
; CURRENT FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: 60/619,384
; PRIOR FILING DATE: 2004-10-15
; NUMBER OF SEQ ID NOS: 880
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 6371
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-251-465-8

Query Match 1.8%; Score 18; DB 7; Length 6371;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 316 AAAAAGGAAGATGGAATT 333
||||||||||||||||||
Db 5023 AAAAAGGAAGATGGAATT 5040

RESULT 5
US-10-953-349-15338/c
; Sequence 15338, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15338
; LENGTH: 862
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-15338

Query Match 1.7%; Score 17; DB 6; Length 862;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 942 CTACTATAGCTCATCCT 958
|||||||||||||||||
Db 620 CTACTATAGCTCATCCT 604

RESULT 6
US-11-233-726-17/c
; Sequence 17, Application US/11233726
; Publication No. US20060090216A1
; GENERAL INFORMATION:
; APPLICANT: APUYA, Nestor
; APPLICANT: KWOK, Shing
; APPLICANT: ALEXANDROV, Nickolai
; APPLICANT: TATARINOVA, Tatiana
; APPLICANT: FANG, Yiwen
; APPLICANT: PENNELL, Roger
; APPLICANT: LU, Yu-Ping
; APPLICANT: MEDRANO, Leonard
; APPLICANT: FELDMANN, Kenneth A.
; APPLICANT: COOK, Zhihong C.
; TITLE OF INVENTION: Promoter, Promoter Control Elements, And Combinations, And Uses Th
; FILE REFERENCE: 2750-1619PUS2
; CURRENT APPLICATION NUMBER: US/11/233,726
; CURRENT FILING DATE: 2005-02-23
; PRIOR APPLICATION NUMBER: 60/612,891
; PRIOR FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: 60/613,134
; PRIOR FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: 60/637,174
; PRIOR FILING DATE: 2004-12-16
; NUMBER OF SEQ ID NOS: 46
; SEQ ID NO 17

```
;   LENGTH: 1000
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1000)
;   OTHER INFORMATION: Ceres Promoter construct YP0382 as found in Promoter Report #130
US-11-233-726-17

  Query Match             1.7%;  Score 17;  DB 7;  Length 1000;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        233 AAGTCAAAGAATTTGCA 249
              |||||||||||||||||
Db        623 AAGTCAAAGAATTTGCA 607


RESULT 7
US-10-953-349-3012
; Sequence 3012, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3012
;   LENGTH: 1061
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-3012

  Query Match             1.7%;  Score 17;  DB 6;  Length 1061;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        370 AAAAATAAGATCTTTCT 386
              |||||||||||||||||
Db         63 AAAAATAAGATCTTTCT 79


RESULT 8
US-10-953-349-9710
; Sequence 9710, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9710
;   LENGTH: 1498
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-9710

  Query Match             1.7%;  Score 17;  DB 6;  Length 1498;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        183 CTCTGACCAGAGCAGTG 199
              |||||||||||||||||
Db        553 CTCTGACCAGAGCAGTG 569


RESULT 9
US-11-217-529-190982/c
; Sequence 190982, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 190982
;   LENGTH: 3228
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-190982

  Query Match             1.7%;  Score 17;  DB 7;  Length 3228;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        156 TCCTGAAGAAGATGACA 172
              |||||||||||||||||
Db       1929 TCCTGAAGAAGATGACA 1913


RESULT 10
US-10-471-571A-4869/c
; Sequence 4869, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 4869
;   LENGTH: 231
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-4869

  Query Match             1.6%;  Score 16;  DB 6;  Length 231;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGG 693
              ||||||||||||||||
Db        178 CAGCTTCTTCATCAGG 163


RESULT 11
US-10-548-484-9
; Sequence 9, Application US/10548484
; Publication No. US20060107343A1
; GENERAL INFORMATION:
;  APPLICANT: Ishihara Sangyo Kaisha, Ltd.
;  TITLE OF INVENTION: Plant Cells And Plant Bodies With Modified Cell Growth, Developmer
;  TITLE OF INVENTION:  Differentiation
;  FILE REFERENCE: IS-09PCT
```

```
;  CURRENT APPLICATION NUMBER: US/10/548,484
;  CURRENT FILING DATE:  2005-09-09
;  PRIOR APPLICATION NUMBER: JP 2003-66064
;  PRIOR FILING DATE: 2003-03-12
;  NUMBER OF SEQ ID NOS: 100
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 305
;   TYPE: DNA
;   ORGANISM: Oryza sativa
US-10-548-484-9

  Query Match             1.6%;  Score 16;  DB 6;  Length 305;
  Best Local Similarity   100.0%;  Pred. No. 49;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        160 GAAGAAGATGACATCA 175
              ||||||||||||||||
Db         55 GAAGAAGATGACATCA 70


RESULT 12
US-10-548-484-10
; Sequence 10, Application US/10548484
; Publication No. US20060107343A1
; GENERAL INFORMATION:
;  APPLICANT: Ishihara Sangyo Kaisha, Ltd.
;  TITLE OF INVENTION: Plant Cells And Plant Bodies With Modified Cell Growth, Developme
;  TITLE OF INVENTION:  Differentiation
;  FILE REFERENCE: IS-09PCT
;  CURRENT APPLICATION NUMBER: US/10/548,484
;  CURRENT FILING DATE:  2005-09-09
;  PRIOR APPLICATION NUMBER: JP 2003-66064
;  PRIOR FILING DATE: 2003-03-12
;  NUMBER OF SEQ ID NOS: 100
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 305
;   TYPE: DNA
;   ORGANISM: Oryza sativa
US-10-548-484-10

  Query Match             1.6%;  Score 16;  DB 6;  Length 305;
  Best Local Similarity   100.0%;  Pred. No. 49;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        160 GAAGAAGATGACATCA 175
              ||||||||||||||||
Db         55 GAAGAAGATGACATCA 70


RESULT 13
US-10-488-619-3012
; Sequence 3012, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3012
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-488-619-3012

  Query Match             1.6%;  Score 16;  DB 6;  Length 561;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        905 ACAAGGATGCCAAGAT 920
              ||||||||||||||||
Db        336 ACAAGGATGCCAAGAT 351


RESULT 14
US-10-953-349-38575/c
; Sequence 38575, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38575
;   LENGTH: 577
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-38575

  Query Match             1.6%;  Score 16;  DB 6;  Length 577;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        335 GGTCCACTGATATCTT 350
              ||||||||||||||||
Db        436 GGTCCACTGATATCTT 421


RESULT 15
US-10-953-349-39182
; Sequence 39182, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39182
;   LENGTH: 634
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-39182

  Query Match             1.6%;  Score 16;  DB 6;  Length 634;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        904 CACAAGGATGCCAAGA 919
              ||||||||||||||||
Db        281 CACAAGGATGCCAAGA 296


RESULT 16
US-10-548-484-16
; Sequence 16, Application US/10548484
; Publication No. US20060107343A1
; GENERAL INFORMATION:
;  APPLICANT: Ishihara Sangyo Kaisha, Ltd.
;  TITLE OF INVENTION: Plant Cells And Plant Bodies With Modified Cell Growth, Developmer
;  TITLE OF INVENTION:  Differentiation
;  FILE REFERENCE: IS-09PCT
;  CURRENT APPLICATION NUMBER: US/10/548,484
;  CURRENT FILING DATE:  2005-09-09
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;  PRIOR APPLICATION NUMBER: JP 2003-66064
;  PRIOR FILING DATE: 2003-03-12
;  NUMBER OF SEQ ID NOS: 100
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 726
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (542)..(542)
;   OTHER INFORMATION: n stands for any base
US-10-548-484-16

  Query Match             1.6%;  Score 16;  DB 6;  Length 726;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        160 GAAGAAGATGACATCA 175
              ||||||||||||||||
Db        567 GAAGAAGATGACATCA 582


RESULT 17
US-10-196-749-359
; Sequence 359, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C340
;  CURRENT APPLICATION NUMBER: US/10/196,749
;  CURRENT FILING DATE:  2002-07-16
;  PRIOR APPLICATION NUMBER: 10/052586
;  PRIOR FILING DATE: 2002-01-15
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059266
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063120
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063121
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063486
;  PRIOR FILING DATE: 1997-10-21
;  PRIOR APPLICATION NUMBER: 60/063540
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063541
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063544
;  PRIOR FILING DATE: 1997-10-28
;  Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 359
;   LENGTH: 742
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-196-749-359

  Query Match             1.6%;  Score 16;  DB 6;  Length 742;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GAAGATGACATCACCT 178
              ||||||||||||||||
Db        361 GAAGATGACATCACCT 376


RESULT 18
US-10-471-571A-689/c
; Sequence 689, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 689
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-689

  Query Match             1.6%;  Score 16;  DB 6;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        677 GCAGCTTCTTCATCAG 692
              ||||||||||||||||
Db        398 GCAGCTTCTTCATCAG 383


RESULT 19
US-11-217-529-79675/c
; Sequence 79675, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79675
;   LENGTH: 945
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-79675

  Query Match             1.6%;  Score 16;  DB 7;  Length 945;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        675 CAGCAGCTTCTTCATC 690
              ||||||||||||||||
Db        214 CAGCAGCTTCTTCATC 199


RESULT 20
US-10-953-349-27059
```

```
; Sequence 27059, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27059
;   LENGTH: 1039
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-10-953-349-27059

  Query Match             1.6%;  Score 16;  DB 6;  Length 1039;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        445 AGTACCGATTTGAAAT 460
              ||||||||||||||||
Db        407 AGTACCGATTTGAAAT 422


RESULT 21
US-11-217-529-4517
; Sequence 4517, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4517
;   LENGTH: 1083
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-4517

  Query Match             1.6%;  Score 16;  DB 7;  Length 1083;
  Best Local Similarity   100.0%;  Pred. No. 51;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         74 AACTGGAGAAAAACGT 89
              ||||||||||||||||
Db        467 AACTGGAGAAAAACGT 482


RESULT 22
US-11-217-529-75941
; Sequence 75941, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75941
;   LENGTH: 1098
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-75941

  Query Match             1.6%;  Score 16;  DB 7;  Length 1098;
  Best Local Similarity   100.0%;  Pred. No. 51;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        731 TGAAGCCATTAAAAAA 746
              ||||||||||||||||
Db        254 TGAAGCCATTAAAAAA 269


RESULT 23
US-10-953-349-22082/c
; Sequence 22082, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22082
;   LENGTH: 1145
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-22082

  Query Match             1.6%;  Score 16;  DB 6;  Length 1145;
  Best Local Similarity   100.0%;  Pred. No. 51;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TGCATCCTCAGCAGTT 17
              ||||||||||||||||
Db        473 TGCATCCTCAGCAGTT 458


RESULT 24
US-10-953-349-9694
; Sequence 9694, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9694
;   LENGTH: 1226
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-9694

  Query Match             1.6%;  Score 16;  DB 6;  Length 1226;
  Best Local Similarity   100.0%;  Pred. No. 51;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        376 AAGATCTTTCTAAAAT 391
```

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              ||||||||||||||||
Db        973 AAGATCTTTCTAAAAT 988


RESULT 25
US-10-953-349-3568
; Sequence 3568, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3568
;   LENGTH: 1232
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-3568

  Query Match             1.6%;  Score 16;  DB 6;  Length 1232;
  Best Local Similarity   100.0%;  Pred. No. 51;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        669 CTACACCAGCAGCTTC 684
              ||||||||||||||||
Db        592 CTACACCAGCAGCTTC 607


RESULT 26
US-10-953-349-22615/c
; Sequence 22615, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22615
;   LENGTH: 1621
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-22615

  Query Match             1.6%;  Score 16;  DB 6;  Length 1621;
  Best Local Similarity   100.0%;  Pred. No. 51;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        802 TCCTACTTCTCCTTAA 817
              ||||||||||||||||
Db       1184 TCCTACTTCTCCTTAA 1169


RESULT 27
US-10-953-349-33373
; Sequence 33373, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33373
;   LENGTH: 1747
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-33373

  Query Match             1.6%;  Score 16;  DB 6;  Length 1747;
  Best Local Similarity   100.0%;  Pred. No. 51;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        467 TCAAAAGCAGCAGAGG 482
              ||||||||||||||||
Db       1268 TCAAAAGCAGCAGAGG 1283


RESULT 28
US-11-217-529-4576
; Sequence 4576, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4576
;   LENGTH: 1797
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-4576

  Query Match             1.6%;  Score 16;  DB 7;  Length 1797;
  Best Local Similarity   100.0%;  Pred. No. 51;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        816 AACATTTGGCGTACAG 831
              ||||||||||||||||
Db        729 AACATTTGGCGTACAG 744


RESULT 29
US-11-313-836-53/c
; Sequence 53, Application US/11313836
; Publication No. US20060116508A1
; GENERAL INFORMATION:
;  APPLICANT: Glucksman, Maria Alexandra
;  APPLICANT:  Williamson, Mark J.
;  APPLICANT:  Tsia, Fong-Ying
;  APPLICANT:  Rudolph-Owen, Laura A.
;  APPLICANT:  Kapeller-Libermann, Rosana
;  APPLICANT:  Meyers, Rachel E.
;  APPLICANT:  Chiang, Lillian Wei-Ming
;  APPLICANT:  Hunter, John Joseph
;  APPLICANT:  Wood, Andrew
;  APPLICANT:  Jenkins, Lorayne P.
;  TITLE OF INVENTION: NOVEL 27411, 23413, 22438, 23553,
;  TITLE OF INVENTION:  25278, 26212, NARC SC1, NARC 10A, NARC 1, NARC 12, NARC 13,
;  TITLE OF INVENTION:  NARC17, NARC 25, NARC 3, NARC 4, NARC 7, NARC 8, NARC 11,
;  TITLE OF INVENTION:  NARC 14A, NARC 15, NARC 16, NARC 19, NARC 20, NARC 26, NARC
;  TITLE OF INVENTION:  27, NARC 28, NARC 30, NARC 5, NARC 6, NARC 9, NARC 10C, NARC
;  TITLE OF INVENTION:  8B, NARC 9, NARC2A, NARC 16B, NARC 1C, NARC 1A, NARC 25,
;  TITLE OF INVENTION:  86604 AND 32222 MOLECULES AND USES THEREFOR
;  FILE REFERENCE: MPI03-062OMNIM
;  CURRENT APPLICATION NUMBER: US/11/313,836
```

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;  CURRENT FILING DATE:  2005-12-21
;  PRIOR APPLICATION NUMBER: US/10/426,776
;  PRIOR FILING DATE: 2003-04-30
;  PRIOR APPLICATION NUMBER: 10/229,662
;  PRIOR FILING DATE: 2002-08-28
;  PRIOR APPLICATION NUMBER: 09/795,691
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: 60/185,517
;  PRIOR FILING DATE: 2000-02-28
;  PRIOR APPLICATION NUMBER: 10/105,992
;  PRIOR FILING DATE: 2002-03-25
;  PRIOR APPLICATION NUMBER: 09/406,045
;  PRIOR FILING DATE: 1999-09-27
;  PRIOR APPLICATION NUMBER: 10/314,881
;  PRIOR FILING DATE: 2002-12-09
;  PRIOR APPLICATION NUMBER: 09/773,426
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 09/495,823
;  PRIOR FILING DATE: 2000-01-31
;  PRIOR APPLICATION NUMBER: 09/692,785
;  PRIOR FILING DATE: 2000-10-20
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53
;   LENGTH: 1975
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-313-836-53

  Query Match             1.6%;  Score 16;  DB 7;  Length 1975;
  Best Local Similarity   100.0%;  Pred. No. 51;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        475 AGCAGAGGCTCCTCTG 490
              ||||||||||||||||
Db        225 AGCAGAGGCTCCTCTG 210


RESULT 30
US-10-953-349-37153/c
; Sequence 37153, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37153
;   LENGTH: 2117
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-37153

  Query Match             1.6%;  Score 16;  DB 6;  Length 2117;
  Best Local Similarity   100.0%;  Pred. No. 51;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        868 CTCTCCGTGGACAAGA 883
              ||||||||||||||||
Db       1588 CTCTCCGTGGACAAGA 1573


RESULT 31
US-11-293-697-1627
; Sequence 1627, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1627
;   LENGTH: 2270
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1627

  Query Match             1.6%;  Score 16;  DB 7;  Length 2270;
  Best Local Similarity   100.0%;  Pred. No. 52;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        901 TGCCACAAGGATGCCA 916
              ||||||||||||||||
Db       1151 TGCCACAAGGATGCCA 1166


RESULT 32
US-11-293-697-928/c
; Sequence 928, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 928
;   LENGTH: 2278
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-928

  Query Match             1.6%;  Score 16;  DB 7;  Length 2278;
  Best Local Similarity   100.0%;  Pred. No. 52;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        475 AGCAGAGGCTCCTCTG 490
              ||||||||||||||||
Db        442 AGCAGAGGCTCCTCTG 427


RESULT 33
US-11-293-697-1624/c
; Sequence 1624, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1624
;   LENGTH: 2324
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1624

  Query Match             1.6%;  Score 16;  DB 7;  Length 2324;
```

```
  Best Local Similarity   100.0%;  Pred. No. 52;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        947 ATAGCTCATCCTGGAG 962
              ||||||||||||||||
Db       1957 ATAGCTCATCCTGGAG 1942


RESULT 34
US-11-293-697-1068/c
; Sequence 1068, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1068
;   LENGTH: 2538
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1068

  Query Match             1.6%;  Score 16;  DB 7;  Length 2538;
  Best Local Similarity   100.0%;  Pred. No. 52;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        365 AATCCAAAAATAAGAT 380
              ||||||||||||||||
Db       2405 AATCCAAAAATAAGAT 2390


RESULT 35
US-11-293-697-781
; Sequence 781, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 781
;   LENGTH: 2629
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-781

  Query Match             1.6%;  Score 16;  DB 7;  Length 2629;
  Best Local Similarity   100.0%;  Pred. No. 52;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         38 TGGTTTTGCTGGCACC 53
              ||||||||||||||||
Db        622 TGGTTTTGCTGGCACC 637


RESULT 36
US-11-266-446-7/c
; Sequence 7, Application US/11266446
; Publication No. US20060112452A1
; GENERAL INFORMATION:
;  APPLICANT: Keetman, Ulrich
;  APPLICANT:  Duwenig, Elke
;  APPLICANT:  Loyall, Linda P
;  APPLICANT:  Herbers, Karin
;  APPLICANT:  Hillebrand, Helke
;  TITLE OF INVENTION: EXPRESSION CASSETTES FOR SEED-PREFERENTIAL EXPRESSION IN PLANTS
;  FILE REFERENCE: 12810-00165-US
;  CURRENT APPLICATION NUMBER: US/11/266,446
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04026295.8
;  PRIOR FILING DATE: 2004-11-05
;  PRIOR APPLICATION NUMBER: EP 04029024.9
;  PRIOR FILING DATE: 2004-12-08
;  PRIOR APPLICATION NUMBER: EP 05002262.3
;  PRIOR FILING DATE: 2005-02-03
;  PRIOR APPLICATION NUMBER: EP 05002850.5
;  PRIOR FILING DATE: 2005-02-11
;  NUMBER OF SEQ ID NOS: 156
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
;   LENGTH: 2682
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (93)..(2387)
;   OTHER INFORMATION: coding for 5-methyltetrahydro-pteroyltriglutamate homocysteine
;   OTHER INFORMATION: methyltransferase (At5g17920)
US-11-266-446-7

  Query Match             1.6%;  Score 16;  DB 7;  Length 2682;
  Best Local Similarity   100.0%;  Pred. No. 52;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        868 CTCTCCGTGGACAAGA 883
              ||||||||||||||||
Db       1562 CTCTCCGTGGACAAGA 1547


RESULT 37
US-10-953-349-36221/c
; Sequence 36221, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36221
;   LENGTH: 2703
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-36221

  Query Match             1.6%;  Score 16;  DB 6;  Length 2703;
  Best Local Similarity   100.0%;  Pred. No. 52;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        174 CACCTGGACCTCTGAC 189
              ||||||||||||||||
Db       1550 CACCTGGACCTCTGAC 1535


RESULT 38
US-11-293-697-539/c
; Sequence 539, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
```

; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 539
; LENGTH: 2829
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-539

Query Match 1.6%; Score 16; DB 7; Length 2829;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 360 GAAAGAATCCAAAAAT 375
||||||||||||||||
Db 330 GAAAGAATCCAAAAAT 315

RESULT 39
US-10-505-928-444
; Sequence 444, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 444
; LENGTH: 2846
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-444

Query Match 1.6%; Score 16; DB 6; Length 2846;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 845 ACAACAGAGAAAAGAA 860
||||||||||||||||
Db 599 ACAACAGAGAAAAGAA 614

RESULT 40
US-11-145-307A-3
; Sequence 3, Application US/11145307A
; Publication No. US20060094035A1
; GENERAL INFORMATION:
; APPLICANT: Arcturus Bioscience, Inc.
; APPLICANT: Erlander, Mark G.
; APPLICANT: Ma, Xiao-Jun
; TITLE OF INVENTION: Identification of Tumors
; FILE REFERENCE: 022041-002020US
; CURRENT APPLICATION NUMBER: US/11/145,307A
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 60/577,084
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2872
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-145-307A-3

Query Match 1.6%; Score 16; DB 7; Length 2872;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 314 ACAAAAAGGAAGATGG 329
||||||||||||||||
Db 1864 ACAAAAAGGAAGATGG 1879

RESULT 41
US-10-953-349-5832/c
; Sequence 5832, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5832
; LENGTH: 3271
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5832

Query Match 1.6%; Score 16; DB 6; Length 3271;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 154 ACTCCTGAAGAAGATG 169
||||||||||||||||
Db 824 ACTCCTGAAGAAGATG 809

RESULT 42
US-11-217-529-77298
; Sequence 77298, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77298
; LENGTH: 5310
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77298

Query Match 1.6%; Score 16; DB 7; Length 5310;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 329 GAATTTGGTCCACTGA 344
||||||||||||||||
Db 4376 GAATTTGGTCCACTGA 4391

RESULT 43
US-11-253-190-4/c
; Sequence 4, Application US/11253190

```
; Publication No. US20060115839A1
; GENERAL INFORMATION:
;  APPLICANT: Halazonetis, Thanos D
;  TITLE OF INVENTION: METHODS OF IDENTIFYING AN AGENT THAT MODULATES AN INTERACTION
;  TITLE OF INVENTION:  BETWEEN 53BP1 AND HISTONE H3, AND USES THEREOF
;  FILE REFERENCE: HALA0001-100
;  CURRENT APPLICATION NUMBER: US/11/253,190
;  CURRENT FILING DATE:  2005-10-17
;  PRIOR APPLICATION NUMBER: US 60/620,461
;  PRIOR FILING DATE: 2004-10-19
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
;   LENGTH: 6266
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-253-190-4

  Query Match             1.6%;  Score 16;  DB 7;  Length 6266;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        179 GGACCTCTGACCAGAG 194
              ||||||||||||||||
Db       1220 GGACCTCTGACCAGAG 1205


RESULT 44
US-10-953-349-5546/c
; Sequence 5546, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5546
;   LENGTH: 12659
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-5546

  Query Match             1.6%;  Score 16;  DB 6;  Length 12659;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        214 GGTAAAACTCTGACCA 229
              ||||||||||||||||
Db       5793 GGTAAAACTCTGACCA 5778


RESULT 45
US-10-519-335-37/c
; Sequence 37, Application US/10519335
; Publication No. US20060099210A1
; GENERAL INFORMATION:
;  APPLICANT: Cavarec, Laurent
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Destenaves, Benoit
;  APPLICANT:  Gonthier, Catherine
;  APPLICANT:  Elias, Isabelle
;  TITLE OF INVENTION: NOVEL KCNQ POLYPEPTIDES, MODULATORS THEREOF, AND THEIR USES IN TH
;  TITLE OF INVENTION:  TREATMENT OF MENTAL DISORDERS
;  FILE REFERENCE: G-194US03PCT
;  CURRENT APPLICATION NUMBER: US/10/519,335
;  CURRENT FILING DATE:  2004-12-22
;  PRIOR APPLICATION NUMBER: US 60/391,359
;  PRIOR FILING DATE: 2002-06-25
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
;   LENGTH: 151830
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (10)..(10)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (60402)..(60402)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (61110)..(61110)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (98207)..(98207)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (98208)..(98208)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (98209)..(98209)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (98210)..(98210)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (98211)..(98211)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (99743)..(99743)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (108055)..(108055)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (109094)..(109094)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (109125)..(109125)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (118900)..(118900)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (119024)..(119052)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (119053)..(119112)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (119115)..(119121)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (119123)..(119123)
;   OTHER INFORMATION: n = a or c or g or t
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;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (141674)..(141674)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (142063)..(142063)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (142137)..(142137)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (142967)..(142967)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (143077)..(143077)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (143506)..(143506)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (143587)..(143587)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (143629)..(143629)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (149079)..(149079)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (5363)..(5363)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (8080)..(8080)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (10296)..(10296)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (14528)..(14528)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (15336)..(15336)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (15457)..(15457)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (16288)..(16288)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (16306)..(16307)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (16316)..(16316)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (16397)..(16397)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (56012)..(56012)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (57662)..(57662)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: 5'UTR
;   LOCATION: (1)..(54)
;   OTHER INFORMATION: exon 1
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (55)..(124)
;   OTHER INFORMATION: exon 1
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (91147)..(91244)
;   OTHER INFORMATION: exon 2
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (93669)..(93834)
;   OTHER INFORMATION: exon 3
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (96310)..(96422)
;   OTHER INFORMATION: exon 4
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (99546)..(99723)
;   OTHER INFORMATION: exon 5
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (125441)..(125605)

  Query Match             1.6%;  Score 16;  DB 6;  Length 151830;
  Best Local Similarity   100.0%;  Pred. No. 56;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        584 AGGAGGGCAGTGCCTG 599
              ||||||||||||||||
Db       8739 AGGAGGGCAGTGCCTG 8724


RESULT 46
US-11-266-409-12/c
; Sequence 12, Application US/11266409
; Publication No. US20060093578A1
; GENERAL INFORMATION:
;  APPLICANT: SUZUMURA, AKIO
;  TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATING MULTIPLE SCLEROSIS
;  FILE REFERENCE: 279847US40
;  CURRENT APPLICATION NUMBER: US/11/266,409
;  CURRENT FILING DATE:  2005-11-04
;  PRIOR APPLICATION NUMBER: US 60/624,851
;  PRIOR FILING DATE: 2004-11-04
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA
US-11-266-409-12

  Query Match             1.5%;  Score 15;  DB 7;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy        799 CATTCCTACTTCTCC 813
              ||||||||||||||
Db         17 CATTCCTACTTCTCC 3


RESULT 47
US-11-217-529-28477/c
; Sequence 28477, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28477
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-28477

  Query Match             1.5%;  Score 15;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        353 GGGAACAGAAAGAAT 367
              |||||||||||||||
Db         23 GGGAACAGAAAGAAT 9


RESULT 48
US-11-217-529-94239/c
; Sequence 94239, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 94239
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-94239

  Query Match             1.5%;  Score 15;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        916 AAGATCCGCGTGCAA 930
              |||||||||||||||
Db         24 AAGATCCGCGTGCAA 10


RESULT 49
US-11-217-529-115861/c
; Sequence 115861, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 115861
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-115861

  Query Match             1.5%;  Score 15;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        358 CAGAAAGAATCCAAA 372
              |||||||||||||||
Db         18 CAGAAAGAATCCAAA 4


RESULT 50
US-11-217-529-121503/c
; Sequence 121503, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 121503
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-121503

  Query Match             1.5%;  Score 15;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        811 TCCTTAACATTTGGC 825
              |||||||||||||||
Db         19 TCCTTAACATTTGGC 5


RESULT 51
US-10-857-260-37
; Sequence 37, Application US/10857260
; Publication No. US20060110742A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Lyons, Leslie A.
;  APPLICANT:  Grahn, Robert
;  APPLICANT:  Erdman, Carolyn
;  APPLICANT:  The Regents of the University of California
;  TITLE OF INVENTION: Carrier Tests for Polycystic Kidney Disease in the Cat
;  FILE REFERENCE: 02307O-146800US
;  CURRENT APPLICATION NUMBER: US/10/857,260
;  CURRENT FILING DATE:  2004-05-28
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
;   LENGTH: 209
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: human (Hsap) PKD1 exon 29
US-10-857-260-37

  Query Match             1.5%;  Score 15;  DB 6;  Length 209;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        422 CCTGCTGGTGGCTGA 436
              |||||||||||||||
Db         27 CCTGCTGGTGGCTGA 41


RESULT 52
US-11-217-529-4828
; Sequence 4828, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4828
;   LENGTH: 261
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-4828

  Query Match             1.5%;  Score 15;  DB 7;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        840 CAAGAACAACAGAGA 854
              |||||||||||||||
Db         15 CAAGAACAACAGAGA 29


RESULT 53
US-11-301-554-899
; Sequence 899, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
;  APPLICANT: Henderson, Robert A.
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Watanabe, Yoshihiro
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Sleath, Paul R.
;  APPLICANT:  Johnson, Jeffrey C.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Durham, Margarita
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  McNabb, Andria
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.478C21
;  CURRENT APPLICATION NUMBER: US/11/301,554
;  CURRENT FILING DATE:  2005-12-13
;  PRIOR APPLICATION NUMBER: US 10/283,017
;  PRIOR FILING DATE: 2002-10-28
;  PRIOR APPLICATION NUMBER: US 10/113,872
;  PRIOR FILING DATE: 2002-03-28
;  PRIOR APPLICATION NUMBER: US 10/017,754
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: US 09/902,941
;  PRIOR FILING DATE: 2001-07-10
;  PRIOR APPLICATION NUMBER: US 09/849,626
;  PRIOR FILING DATE: 2001-05-03
;  PRIOR APPLICATION NUMBER: US 09/736,457
;  PRIOR FILING DATE: 2000-12-13
;  PRIOR APPLICATION NUMBER: US 09/702,705
;  PRIOR FILING DATE: 2000-10-30
;  PRIOR APPLICATION NUMBER: US 09/677,419
;  PRIOR FILING DATE: 2000-10-06
;  PRIOR APPLICATION NUMBER: US 09/671,325
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US 09/658,824
;  PRIOR FILING DATE: 2000-09-08
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2157
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 899
;   LENGTH: 277
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-301-554-899

  Query Match             1.5%;  Score 15;  DB 7;  Length 277;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        737 CATTAAAAAATTCTC 751
              |||||||||||||||
Db         10 CATTAAAAAATTCTC 24


RESULT 54
US-11-217-529-82243
; Sequence 82243, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82243
;   LENGTH: 354
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
```

```
US-11-217-529-82243

  Query Match             1.5%;  Score 15;  DB 7;  Length 354;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        854 AAAAGAAAGACAGAC 868
              |||||||||||||||
Db         19 AAAAGAAAGACAGAC 33


RESULT 55
US-11-217-529-80395
; Sequence 80395, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80395
;   LENGTH: 423
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-80395

  Query Match             1.5%;  Score 15;  DB 7;  Length 423;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        156 TCCTGAAGAAGATGA 170
              |||||||||||||||
Db        324 TCCTGAAGAAGATGA 338


RESULT 56
US-10-488-619-382
; Sequence 382, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 382
;   LENGTH: 456
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(456)
;   OTHER INFORMATION: n is g, c, a or t
US-10-488-619-382

  Query Match             1.5%;  Score 15;  DB 6;  Length 456;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        851 GAGAAAAGAAAGACA 865
              |||||||||||||||
Db        251 GAGAAAAGAAAGACA 265


RESULT 57
US-11-217-529-4924
; Sequence 4924, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4924
;   LENGTH: 489
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-4924

  Query Match             1.5%;  Score 15;  DB 7;  Length 489;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 CAGTTGGTCATCGCC 27
              |||||||||||||||
Db        178 CAGTTGGTCATCGCC 192


RESULT 58
US-10-471-571A-5447
; Sequence 5447, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 5447
;   LENGTH: 498
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-5447

  Query Match             1.5%;  Score 15;  DB 6;  Length 498;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        339 CACTGATATCTTAAG 353
              |||||||||||||||
Db        360 CACTGATATCTTAAG 374


RESULT 59
US-10-473-173-325/c
; Sequence 325, Application US/10473173
; Publication No. US20060088823A1
; GENERAL INFORMATION:
;  APPLICANT: VAN ANDEL INSTITUTE
```

```
;  TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell
;  TITLE OF INVENTION:  Carcinoma: Prognosis and Drug Target Identification
;  FILE REFERENCE: 38345-170094
;  CURRENT APPLICATION NUMBER: US/10/473,173
;  CURRENT FILING DATE:  2003-09-29
;  PRIOR APPLICATION NUMBER: US 60/279,411
;  PRIOR FILING DATE: 2001-03-29
;  NUMBER OF SEQ ID NOS: 498
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 325
;   LENGTH: 506
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-473-173-325

  Query Match             1.5%;  Score 15;  DB 6;  Length 506;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        543 AGTGGACAACAGGGA 557
              |||||||||||||||
Db        258 AGTGGACAACAGGGA 244


RESULT 60
US-10-488-619-94/c
; Sequence 94, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 94
;   LENGTH: 506
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-488-619-94

  Query Match             1.5%;  Score 15;  DB 6;  Length 506;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        543 AGTGGACAACAGGGA 557
              |||||||||||||||
Db        258 AGTGGACAACAGGGA 244


RESULT 61
US-10-560-723-10
; Sequence 10, Application US/10560723
; Publication No. US20060115821A1
; GENERAL INFORMATION:
;  APPLICANT: EXONHIT THERAPEUTICALS
;  TITLE OF INVENTION: PROSTATE SPECIFIC GENES AND THE USE THEREOF AS TARGETS FOR PROSTA
;  TITLE OF INVENTION:  CANCER THERAPY AND DIAGNOSIS
;  FILE REFERENCE: B0213WO
;  CURRENT APPLICATION NUMBER: US/10/560,723
;  CURRENT FILING DATE:  2005-12-15
;  NUMBER OF SEQ ID NOS: 185
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 508
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-560-723-10

  Query Match             1.5%;  Score 15;  DB 6;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        877 GACAAGACCTCAGCC 891
              |||||||||||||||
Db        261 GACAAGACCTCAGCC 275


RESULT 62
US-10-953-349-31038
; Sequence 31038, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31038
;   LENGTH: 525
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (511)..(511)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-31038

  Query Match             1.5%;  Score 15;  DB 6;  Length 525;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        883 ACCTCAGCCAAGGTC 897
              |||||||||||||||
Db        410 ACCTCAGCCAAGGTC 424


RESULT 63
US-11-217-529-174237/c
; Sequence 174237, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174237
;   LENGTH: 531
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-174237

  Query Match             1.5%;  Score 15;  DB 7;  Length 531;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        859 AAAGACAGACTCTCC 873
              |||||||||||||||
Db        261 AAAGACAGACTCTCC 247
```

```
RESULT 64
US-10-953-349-13816/c
; Sequence 13816, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13816
;   LENGTH: 566
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-13816

  Query Match             1.5%;  Score 15;  DB 6;  Length 566;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        676 AGCAGCTTCTTCATC 690
              |||||||||||||||
Db        255 AGCAGCTTCTTCATC 241


RESULT 65
US-10-953-349-15128/c
; Sequence 15128, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15128
;   LENGTH: 605
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-15128

  Query Match             1.5%;  Score 15;  DB 6;  Length 605;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        276 AGGAGGCGAGGTTCT 290
              |||||||||||||||
Db        134 AGGAGGCGAGGTTCT 120


RESULT 66
US-10-953-349-1547/c
; Sequence 1547, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1547
;   LENGTH: 621
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-1547

  Query Match             1.5%;  Score 15;  DB 6;  Length 621;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        159 TGAAGAAGATGACAT 173
              |||||||||||||||
Db        148 TGAAGAAGATGACAT 134


RESULT 67
US-10-488-619-1757
; Sequence 1757, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations W
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1757
;   LENGTH: 702
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-488-619-1757

  Query Match             1.5%;  Score 15;  DB 6;  Length 702;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        829 CAGGTCCAGGGCAAG 843
              |||||||||||||||
Db         41 CAGGTCCAGGGCAAG 55


RESULT 68
US-11-217-529-78302/c
; Sequence 78302, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78302
;   LENGTH: 723
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-78302

  Query Match             1.5%;  Score 15;  DB 7;  Length 723;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        358 CAGAAAGAATCCAAA 372
              |||||||||||||||
Db        515 CAGAAAGAATCCAAA 501
```

```
RESULT 69
US-10-953-349-30607
; Sequence 30607, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30607
;   LENGTH: 734
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-10-953-349-30607

  Query Match             1.5%;  Score 15;  DB 6;  Length 734;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        250 GATGCTGGCCAGTAT 264
              |||||||||||||||
Db        328 GATGCTGGCCAGTAT 342


RESULT 70
US-10-488-619-1758/c
; Sequence 1758, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1758
;   LENGTH: 795
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(795)
;   OTHER INFORMATION: n is g, c, a or t
US-10-488-619-1758

  Query Match             1.5%;  Score 15;  DB 6;  Length 795;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        829 CAGGTCCAGGGCAAG 843
              |||||||||||||||
Db        726 CAGGTCCAGGGCAAG 712


RESULT 71
US-10-953-349-3534/c
; Sequence 3534, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3534
;   LENGTH: 798
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-3534

  Query Match             1.5%;  Score 15;  DB 6;  Length 798;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        677 GCAGCTTCTTCATCA 691
              |||||||||||||||
Db        577 GCAGCTTCTTCATCA 563


RESULT 72
US-11-217-529-970
; Sequence 970, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 970
;   LENGTH: 843
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-970

  Query Match             1.5%;  Score 15;  DB 7;  Length 843;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        852 AGAAAAGAAAGACAG 866
              |||||||||||||||
Db        480 AGAAAAGAAAGACAG 494


RESULT 73
US-10-953-349-25
; Sequence 25, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
;   LENGTH: 852
;   TYPE: DNA
;   ORGANISM: Brassica napus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (697)..(697)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (753)..(753)
```

```
;   OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-25

  Query Match             1.5%;  Score 15;  DB 6;  Length 852;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        314 ACAAAAAGGAAGATG 328
              |||||||||||||||
Db        547 ACAAAAAGGAAGATG 561


RESULT 74
US-10-953-349-39
; Sequence 39, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39
;   LENGTH: 865
;   TYPE: DNA
;   ORGANISM: Brassica napus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (529)..(529)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-39

  Query Match             1.5%;  Score 15;  DB 6;  Length 865;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        470 AAAGCAGCAGAGGCT 484
              |||||||||||||||
Db        678 AAAGCAGCAGAGGCT 692


RESULT 75
US-10-953-349-5007
; Sequence 5007, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5007
;   LENGTH: 880
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-5007

  Query Match             1.5%;  Score 15;  DB 6;  Length 880;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        156 TCCTGAAGAAGATGA 170
              |||||||||||||||
Db        478 TCCTGAAGAAGATGA 492


RESULT 76
US-10-953-349-15440
; Sequence 15440, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15440
;   LENGTH: 922
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-15440

  Query Match             1.5%;  Score 15;  DB 6;  Length 922;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        912 TGCCAAGATCCGCGT 926
              |||||||||||||||
Db        791 TGCCAAGATCCGCGT 805


RESULT 77
US-10-953-349-12006/c
; Sequence 12006, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12006
;   LENGTH: 1021
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (682)..(682)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (691)..(691)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (729)..(729)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (761)..(761)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (804)..(804)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-12006

  Query Match             1.5%;  Score 15;  DB 6;  Length 1021;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        477 CAGAGGCTCCTCTGA 491
              |||||||||||||||
Db         74 CAGAGGCTCCTCTGA 60
```

```
RESULT 78
US-11-217-529-78549
; Sequence 78549, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78549
;   LENGTH: 1041
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-78549

  Query Match             1.5%;  Score 15;  DB 7;  Length 1041;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        729 ACTGAAGCCATTAAA 743
              |||||||||||||||
Db        376 ACTGAAGCCATTAAA 390


RESULT 79
US-11-217-529-173436
; Sequence 173436, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 173436
;   LENGTH: 1077
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-173436

  Query Match             1.5%;  Score 15;  DB 7;  Length 1077;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        232 CAAGTCAAAGAATTT 246
              |||||||||||||||
Db        283 CAAGTCAAAGAATTT 297


RESULT 80
US-11-217-529-6206
; Sequence 6206, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6206
;   LENGTH: 1089
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-6206

  Query Match             1.5%;  Score 15;  DB 7;  Length 1089;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        622 CCCATTGAAGTCGTG 636
              |||||||||||||||
Db        478 CCCATTGAAGTCGTG 492


RESULT 81
US-10-953-349-32952/c
; Sequence 32952, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32952
;   LENGTH: 1101
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-32952

  Query Match             1.5%;  Score 15;  DB 6;  Length 1101;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        877 GACAAGACCTCAGCC 891
              |||||||||||||||
Db       1092 GACAAGACCTCAGCC 1078


RESULT 82
US-10-953-349-31251/c
; Sequence 31251, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31251
```

```
;   LENGTH: 1122
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-10-953-349-31251

  Query Match             1.5%;  Score 15;  DB 6;  Length 1122;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        305 TCCTGATACACAAAA 319
              |||||||||||||||
Db       1044 TCCTGATACACAAAA 1030


RESULT 83
US-10-953-349-17431
; Sequence 17431, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17431
;   LENGTH: 1129
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-17431

  Query Match             1.5%;  Score 15;  DB 6;  Length 1129;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        155 CTCCTGAAGAAGATG 169
              |||||||||||||||
Db        893 CTCCTGAAGAAGATG 907


RESULT 84
US-10-953-349-19240/c
; Sequence 19240, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19240
;   LENGTH: 1157
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-19240

  Query Match             1.5%;  Score 15;  DB 6;  Length 1157;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        477 CAGAGGCTCCTCTGA 491
              |||||||||||||||
Db         74 CAGAGGCTCCTCTGA 60


RESULT 85
US-10-953-349-19188/c
; Sequence 19188, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19188
;   LENGTH: 1178
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-19188

  Query Match             1.5%;  Score 15;  DB 6;  Length 1178;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        239 AAGAATTTGCAGATG 253
              |||||||||||||||
Db        280 AAGAATTTGCAGATG 266


RESULT 86
US-11-217-529-81713/c
; Sequence 81713, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81713
;   LENGTH: 1194
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-81713

  Query Match             1.5%;  Score 15;  DB 7;  Length 1194;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        372 AAATAAGATCTTTCT 386
              |||||||||||||||
Db        719 AAATAAGATCTTTCT 705


RESULT 87
US-10-953-349-25037/c
; Sequence 25037, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25037
```

```
;   LENGTH: 1228
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-25037

  Query Match             1.5%;  Score 15;  DB 6;  Length 1228;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        239 AAGAATTTGCAGATG 253
              |||||||||||||||
Db        399 AAGAATTTGCAGATG 385


RESULT 88
US-10-953-349-37059
; Sequence 37059, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37059
;   LENGTH: 1243
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-37059

  Query Match             1.5%;  Score 15;  DB 6;  Length 1243;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        154 ACTCCTGAAGAAGAT 168
              |||||||||||||||
Db        823 ACTCCTGAAGAAGAT 837


RESULT 89
US-10-953-349-21963/c
; Sequence 21963, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21963
;   LENGTH: 1244
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-21963

  Query Match             1.5%;  Score 15;  DB 6;  Length 1244;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        790 AGCACCCCACATTCC 804
              |||||||||||||||
Db        362 AGCACCCCACATTCC 348


RESULT 90
US-11-217-529-77875
; Sequence 77875, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77875
;   LENGTH: 1257
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-77875

  Query Match             1.5%;  Score 15;  DB 7;  Length 1257;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        447 TACCGATTTGAAATT 461
              |||||||||||||||
Db       1017 TACCGATTTGAAATT 1031


RESULT 91
US-10-953-349-21887/c
; Sequence 21887, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21887
;   LENGTH: 1259
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-21887

  Query Match             1.5%;  Score 15;  DB 6;  Length 1259;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        211 TCTGGTAAAACTCTG 225
              |||||||||||||||
Db        137 TCTGGTAAAACTCTG 123


RESULT 92
US-10-953-349-28383
; Sequence 28383, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28383
```

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;   LENGTH: 1262
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-10-953-349-28383

  Query Match             1.5%;  Score 15;  DB 6;  Length 1262;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        154 ACTCCTGAAGAAGAT 168
              |||||||||||||||
Db        831 ACTCCTGAAGAAGAT 845


RESULT 93
US-11-217-529-191180/c
; Sequence 191180, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 191180
;   LENGTH: 1290
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-191180

  Query Match             1.5%;  Score 15;  DB 7;  Length 1290;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        806 ACTTCTCCTTAACAT 820
              |||||||||||||||
Db        571 ACTTCTCCTTAACAT 557


RESULT 94
US-10-953-349-5441
; Sequence 5441, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5441
;   LENGTH: 1301
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-5441

  Query Match             1.5%;  Score 15;  DB 6;  Length 1301;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        749 CTCGGCATGTGGAAG 763
              |||||||||||||||
Db        878 CTCGGCATGTGGAAG 892


RESULT 95
US-10-471-571A-569
; Sequence 569, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 569
;   LENGTH: 1335
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-569

  Query Match             1.5%;  Score 15;  DB 6;  Length 1335;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 TCAGCAGTTGGTCAT 23
              |||||||||||||||
Db        688 TCAGCAGTTGGTCAT 702


RESULT 96
US-10-953-349-14176
; Sequence 14176, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14176
;   LENGTH: 1343
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (84)..(84)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-14176

  Query Match             1.5%;  Score 15;  DB 6;  Length 1343;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        470 AAAGCAGCAGAGGCT 484
              |||||||||||||||
Db        652 AAAGCAGCAGAGGCT 666


RESULT 97
US-10-953-349-29639
; Sequence 29639, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
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; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29639
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-953-349-29639

Query Match 1.5%; Score 15; DB 6; Length 1344;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 226 ACCATCCAAGTCAAA 240
||||||||||||||||
Db 800 ACCATCCAAGTCAAA 814

RESULT 98
US-10-953-349-34749
; Sequence 34749, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34749
; LENGTH: 1364
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
US-10-953-349-34749

Query Match 1.5%; Score 15; DB 6; Length 1364;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 158 CTGAAGAAGATGACA 172
||||||||||||||||
Db 583 CTGAAGAAGATGACA 597

RESULT 99
US-10-953-349-23846/c
; Sequence 23846, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23846
; LENGTH: 1415
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-23846

Query Match 1.5%; Score 15; DB 6; Length 1415;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 469 AAAAGCAGCAGAGGC 483
||||||||||||||||
Db 1010 AAAAGCAGCAGAGGC 996

RESULT 100
US-11-217-529-2039/c
; Sequence 2039, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2039
; LENGTH: 1428
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-2039

Query Match 1.5%; Score 15; DB 7; Length 1428;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 353 GGGAACAGAAAGAAT 367
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Db 1051 GGGAACAGAAAGAAT 1037

Search completed: June 9, 2006, 23:43:19
Job time : 25.7903 secs

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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 12, 2006, 15:14:42 ; Search time 4447.57 Seconds
(without alignments)
7073.997 Million cell updates/sec

Title: US-10-821-670A-56
Perfect score: 1757
Sequence: 1 MHPQQLVIAWFSLVLLAPPL.....VQARDRYYSSSWSNWASVSC 328

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-Q=/abss/ABSSWEB_spool/US10821670/runat_07062006_110102_26152/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss06h
-USER=US10821670_@CGN_1_1_5308_@runat_07062006_110102_26152 -NCPU=6 -ICPU=3
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
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2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		1757	100.0	985	2	AR595967	AR595967 Sequence
2	c	1757	100.0	985	2	AR595968	AR595968 Sequence
3		1757	100.0	987	2	AR595950	AR595950 Sequence
4	c	1757	100.0	987	2	AR595951	AR595951 Sequence
5		1757	100.0	990	2	AX076200	AX076200 Sequence
6		1757	100.0	990	2	AX076482	AX076482 Sequence
7		1757	100.0	4522	2	AX076209	AX076209 Sequence
8		1757	100.0	4522	2	AX076476	AX076476 Sequence
9		1752	99.7	990	14	FCU83184	U83184 Felis catus
10		1751	99.7	2193	2	AR242435	AR242435 Sequence
11		1751	99.7	2193	2	AR280203	AR280203 Sequence
12		1751	99.7	2193	2	AR322418	AR322418 Sequence
13		1743	99.2	1006	14	FCIL12P40	Y07762 Felis catus
14		1743	99.2	1599	2	AR595956	AR595956 Sequence
15	c	1743	99.2	1599	2	AR595957	AR595957 Sequence
16		1653	94.1	987	2	AR595969	AR595969 Sequence
17	c	1653	94.1	987	2	AR595970	AR595970 Sequence
18		1653	94.1	990	2	AR151071	AR151071 Sequence
19		1653	94.1	990	2	BD014663	BD014663 Process f
20		1653	94.1	990	2	E15017	E15017 Canine mRNA
21		1653	94.1	990	2	AR316470	AR316470 Sequence
22		1653	94.1	1599	2	AR595971	AR595971 Sequence
23	c	1653	94.1	1599	2	AR595972	AR595972 Sequence
24		1653	94.1	2267	2	AR596011	AR596011 Sequence
25	c	1653	94.1	2267	2	AR596012	AR596012 Sequence
26		1643	93.5	921	2	AR242436	AR242436 Sequence
27		1643	93.5	921	2	AR242437	AR242437 Sequence
28		1643	93.5	921	2	AR280204	AR280204 Sequence
29		1643	93.5	921	2	AR280205	AR280205 Sequence
30		1643	93.5	921	2	AR322419	AR322419 Sequence
31		1643	93.5	921	2	AR322420	AR322420 Sequence
32		1642	93.5	1015	14	CFU49100	U49100 Canis famil
33		1635	93.1	921	2	AR595948	AR595948 Sequence
34	c	1635	93.1	921	2	AR595949	AR595949 Sequence
35		1635	93.1	1533	2	AR595959	AR595959 Sequence
36	c	1635	93.1	1533	2	AR595960	AR595960 Sequence
37		1624	92.4	990	2	BD014653	BD014653 Process f
38		1620	92.2	990	2	AR151061	AR151061 Sequence
39		1620	92.2	990	2	AR316460	AR316460 Sequence
40		1618.5	92.1	2154	2	BD171281	BD171281 Novel can
41		1579	89.9	990	2	AX154603	AX154603 Sequence
42		1554	88.4	1626	8	AF401989	AF401989 Synthetic
43		1553	88.4	1058	14	ECIL12P40	Y11129 Equus cabal
44		1550	88.2	921	2	AR595965	AR595965 Sequence
45	c	1550	88.2	921	2	AR595966	AR595966 Sequence

ALIGNMENTS

RESULT 1
AR595967
LOCUS AR595967 985 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 55 from patent US 6818444.
ACCESSION AR595967
VERSION AR595967.1 GI:56646948
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 985)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 55 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .985
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.: 1.11e-185 Length: 985
Score: 1757.00 Matches: 328
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0

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DB:                    2             Gaps:          0

US-10-821-670A-56 (1-328) x AR595967 (1-985)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984

RESULT 2
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AR595968/c
LOCUS       AR595968                985 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 57 from patent US 6818444.
ACCESSION   AR595968
VERSION     AR595968.1  GI:56646949
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 985)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 57 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .985
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.11e-185      Length:         985
Score:                  1757.00        Matches:        328
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-56 (1-328) x AR595968 (1-985)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326
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Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGC 2

RESULT 3
AR595950
LOCUS       AR595950                987 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 29 from patent US 6818444.
ACCESSION   AR595950
VERSION     AR595950.1  GI:56646931
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 29 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.11e-185      Length:          987
Score:                  1757.00        Matches:         328
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            100.0%         Indels:          0
DB:                     2              Gaps:            0

US-10-821-670A-56 (1-328) x AR595950 (1-987)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984

RESULT 4
AR595951/c
LOCUS       AR595951                987 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 31 from patent US 6818444.
ACCESSION   AR595951
VERSION     AR595951.1  GI:56646932
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 31 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
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Pred. No.:              1.11e-185      Length:         987
Score:                  1757.00        Matches:        328
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-56 (1-328) x AR595951 (1-987)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        321 SerAsnTrpAlaSerValSerCys 328
              ||||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGC 4

RESULT 5
AX076200
LOCUS       AX076200                 990 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 1 from Patent WO0104155.
ACCESSION   AX076200
VERSION     AX076200.1  GI:12710825
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 1 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="feline IL-12 p40"
ORIGIN

Alignment Scores:
Pred. No.:              1.12e-185      Length:         990
Score:                  1757.00        Matches:        328
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-56 (1-328) x AX076200 (1-990)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
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Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
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Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984

RESULT 6
AX076482
LOCUS       AX076482                990 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 8 from Patent WO0104280.
ACCESSION   AX076482
VERSION     AX076482.1  GI:12711034
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 8 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Sequence coding for SEQ ID NO 2, IL-12 p40"
ORIGIN

Alignment Scores:
Pred. No.:              1.12e-185      Length:         990
Score:                  1757.00        Matches:        328
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-56 (1-328) x AX076482 (1-990)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuAlaProProLeu 20
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Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
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Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
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Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
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Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
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Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
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Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
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Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
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Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
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Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984

RESULT 7
AX076209
LOCUS       AX076209                4522 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 10 from Patent WO0104155.
ACCESSION   AX076209
VERSION     AX076209.1  GI:12710834
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
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          other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 10 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .4522
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Plasmid pMol-fil12p40"
ORIGIN

Alignment Scores:
Pred. No.:              1.02e-184       Length:         4522
Score:                  1757.00         Matches:        328
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-56 (1-328) x AX076209 (1-4522)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
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Db       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
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Db       3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
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Db       3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
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Db       3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
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Db       3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
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Db       3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
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Db       3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
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Db       3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db       4007 AGCAACTGGGCATCCGTGTCCTGC 4030

RESULT 8
AX076476
LOCUS       AX076476                4522 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 2 from Patent WO0104280.
ACCESSION   AX076476
VERSION     AX076476.1  GI:12711028
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 2 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .4522
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="IL-12p40"
ORIGIN

Alignment Scores:
Pred. No.:              1.02e-184       Length:         4522
Score:                  1757.00         Matches:        328
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-56 (1-328) x AX076476 (1-4522)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
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Db       3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
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Db       3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
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Db       3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
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Db         3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy          101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy          121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
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Db         3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy          141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
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Db         3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy          161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
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Db         3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

Qy          181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
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Db         3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy          201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy          221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
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Db         3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy          241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
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Db         3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy          261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
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Db         3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy          281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
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Db         3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy          301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
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Db         3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

Qy          321 SerAsnTrpAlaSerValSerCys 328
                |||||||||||||||||||||||
Db         4007 AGCAACTGGGCATCCGTGTCCTGC 4030

RESULT 9
FCU83184
LOCUS       FCU83184                990 bp    mRNA    linear   MAM 16-JUL-1999
DEFINITION  Felis catus interleukin-12 p40 subunit (IL-12) mRNA, complete cds.
ACCESSION   U83184
VERSION     U83184.1  GI:2735050
KEYWORDS    .
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Nucleotide and predicted peptide sequence of feline interleukin-12
            (IL-12)
  JOURNAL   DNA Seq. 8 (1-2), 77-82 (1997)
   PUBMED   9522125
REFERENCE   2  (bases 1 to 990)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal
            Veterinary Medicine, University of Zurich, Winterthurerstrasse 260,
            Zurich, ZH 8057, Switzerland
FEATURES             Location/Qualifiers
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                     LIHKKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFTVKSSR
                     GSSDPQGVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPAAEESLPIEVVVDAIHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFGV
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ORIGIN

Alignment Scores:
Pred. No.:                4.04e-185       Length:          990
Score:                    1752.00         Matches:         327
Percent Similarity:       100.0%          Conservative:    1
Best Local Similarity:    99.7%           Mismatches:      0
Query Match:              99.7%           Indels:          0
DB:                       14              Gaps:            0

US-10-821-670A-56 (1-328) x FCU83184 (1-990)

Qy            1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            1 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy           21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy           41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
                ||||||||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||
Db          121 GCCCCCGGAGAAATGGTGGTCCTCACCTGTGACACGCCTGAAGAAGATGACATCACCTGG 180

Qy           61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy           81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy          101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy          121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy          141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy          161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy          181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984

RESULT 10
AR242435
LOCUS       AR242435                2193 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 5 from patent US 6472509.
ACCESSION   AR242435
VERSION     AR242435.1  GI:27288852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2193)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 5 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .2193
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.66e-184       Length:         2193
Score:                  1751.00         Matches:        327
Percent Similarity:     99.7%           Conservative:   0
Best Local Similarity:  99.7%           Mismatches:     1
Query Match:            99.7%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-56 (1-328) x AR242435 (1-2193)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db         64 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTACCTGGTTTTGCTGGCACCTCCTCTC 123

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 183

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 243

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 303

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 363

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 423

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 483

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 543

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 603

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 663

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 723

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 783

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 843

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 903

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 963

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 1023

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db       1024 AGCAACTGGGCATCCGTGTCCTGC 1047

RESULT 11
AR280203
LOCUS       AR280203                2193 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 5 from patent US 6518045.
ACCESSION   AR280203
VERSION     AR280203.1  GI:29715593
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2193)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 5 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
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FEATURES             Location/Qualifiers
     source          1. .2193
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:                1.66e-184      Length:          2193
Score:                    1751.00        Matches:         327
Percent Similarity:       99.7%          Conservative:    0
Best Local Similarity:    99.7%          Mismatches:      1
Query Match:              99.7%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-56 (1-328) x AR280203 (1-2193)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db         64 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTACCTGGTTTTGCTGGCACCTCCTCTC 123

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 183

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 243

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 303

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 363

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 423

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 483

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 543

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 603

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 663

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 723

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 783

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 843

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 903

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 963

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 1023

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db       1024 AGCAACTGGGCATCCGTGTCCTGC 1047

RESULT 12
AR322418
LOCUS       AR322418               2193 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 5 from patent US 6566097.
ACCESSION   AR322418
VERSION     AR322418.1  GI:33708171
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2193)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 5 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .2193
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:                1.66e-184      Length:          2193
Score:                    1751.00        Matches:         327
Percent Similarity:       99.7%          Conservative:    0
Best Local Similarity:    99.7%          Mismatches:      1
Query Match:              99.7%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-56 (1-328) x AR322418 (1-2193)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db         64 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTACCTGGTTTTGCTGGCACCTCCTCTC 123

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 183

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 243

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 303

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 363

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 423

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 483

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 543

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 603

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 663

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 723

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 783

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 843

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 903

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 963

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 1023

Qy        321 SerAsnTrpAlaSerValSerCys 328
                 |||||||||||||||||||||||
Db       1024 AGCAACTGGGCATCCGTGTCCTGC 1047

RESULT 13
FCIL12P40
LOCUS       FCIL12P40                1006 bp    mRNA    linear   MAM 18-APR-2005
DEFINITION  Felis catus mRNA for interleukin-12 p40 chain.
ACCESSION   Y07762
VERSION     Y07762.1  GI:2102664
KEYWORDS    interleukin-12 p40.
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1
  AUTHORS   Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
  TITLE     Molecular cloning of cat interleukin-12
  JOURNAL   Immunogenetics 45 (6), 462-463 (1997)
   PUBMED   9089110
REFERENCE   2  (bases 1 to 1006)
  AUTHORS   Schijns,V.E.C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
            Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
            Utrecht, NETHERLANDS
FEATURES             Location/Qualifiers
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ORIGIN

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Percent Similarity:     99.4%           Conservative:   0
Best Local Similarity:  99.4%           Mismatches:     2
Query Match:            99.2%           Indels:         0
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US-10-821-670A-56 (1-328) x FCIL12P40 (1-1006)

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RESULT 14
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 38 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:              8.18e-184      Length:         1599
Score:                  1743.00        Matches:        326
Percent Similarity:     99.4%          Conservative:   0
Best Local Similarity:  99.4%          Mismatches:     2
Query Match:            99.2%          Indels:         0
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US-10-821-670A-56 (1-328) x AR595956 (1-1599)

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VERSION     AR595957.1  GI:56646938
KEYWORDS    .
SOURCE      Unknown.
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            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 40 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
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Alignment Scores:
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US-10-821-670A-56 (1-328) x AR595957 (1-1599)

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	1757	100.0	985	6	ABK98961	Abk98961 Feline in
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c	4	1757	100.0	985	14	ADV34709	Adv34709 Feline N-
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	14	1743	99.2	1599	6	ABK98950	Abk98950 Feline in
c	15	1743	99.2	1599	6	ABK98951	Abk98951 Feline in
	16	1743	99.2	1599	14	ADV34691	Adv34691 Feline si
c	17	1743	99.2	1599	14	ADV34693	Adv34693 Feline si
	18	1653	94.1	987	6	ABK98963	Abk98963 Canine in
c	19	1653	94.1	987	6	ABK98964	Abk98964 Canine in
c	20	1653	94.1	987	14	ADV34712	Adv34712 Canine si
	21	1653	94.1	987	14	ADV34710	Adv34710 Canine si
	22	1653	94.1	990	2	AAV13817	Aav13817 Canine IL
	23	1653	94.1	990	2	AAX03162	Aax03162 Nucleic a
	24	1653	94.1	990	2	AAX35625	Aax35625 Nucleic a
	25	1653	94.1	990	4	AAI64388	Aai64388 Canine co
	26	1653	94.1	1599	6	ABK98965	Abk98965 Canine in
c	27	1653	94.1	1599	6	ABK98966	Abk98966 Canine in
c	28	1653	94.1	1599	14	ADV34715	Adv34715 Canine si
	29	1653	94.1	1599	14	ADV34713	Adv34713 Canine si
c	30	1653	94.1	2267	6	ABK99006	Abk99006 Canine in
	31	1653	94.1	2267	6	ABK99005	Abk99005 Canine in
	32	1653	94.1	2267	14	ADV34757	Adv34757 Canine si
c	33	1653	94.1	2267	14	ADV34759	Adv34759 Canine si
	34	1643	93.5	921	2	AAV56627	Aav56627 Feline FL
	35	1643	93.5	921	2	AAV56626	Aav56626 Feline FL
	36	1642	93.5	1015	13	ADT04849	Adt04849 Canine in
	37	1635	93.1	921	6	ABK98942	Abk98942 Feline in
c	38	1635	93.1	921	6	ABK98943	Abk98943 Feline in
c	39	1635	93.1	921	14	ADV34681	Adv34681 Feline si
	40	1635	93.1	921	14	ADV34679	Adv34679 Feline si
c	41	1635	93.1	1533	6	ABK98954	Abk98954 Feline in
	42	1635	93.1	1533	6	ABK98953	Abk98953 Feline in
c	43	1635	93.1	1533	14	ADV34697	Adv34697 Feline si
	44	1635	93.1	1533	14	ADV34695	Adv34695 Feline si
	45	1624	92.4	990	2	AAV13816	Aav13816 Canine IL

ALIGNMENTS

RESULT 1
ABK98962/c
ID ABK98962 standard; cDNA; 985 BP.
XX
AC ABK98962;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p40-N985 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX

```
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 3; Page 75-76; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 985 BP; 207 A; 245 C; 250 G; 283 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.22e-164      Length:          985
Score:                  1757.00        Matches:         328
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            100.0%         Indels:          0
DB:                     6              Gaps:            0

US-10-821-670A-56 (1-328) x ABK98962 (1-985)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGC 2

RESULT 2
ABK98961
ID   ABK98961 standard; cDNA; 985 BP.
XX
AC   ABK98961;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p40-N985 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69311.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 3; Page 73-74; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
```

```
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 985 BP; 283 A; 250 C; 245 G; 207 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.22e-164       Length:         985
Score:                  1757.00         Matches:        328
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-56 (1-328) x ABK98961 (1-985)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984

RESULT 3
ADV34707
ID   ADV34707 standard; cDNA; 985 BP.
XX
AC   ADV34707;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline N-terminal IL-12p40 protein encoding cDNA, nFeIL-12p40-N985.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .984
FT                   /*tag=  a
FT                   /product= "PCaIL-12P40-N328 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34708.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 55; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline N-terminal single chain IL-12p40 protein
CC   encoding cDNA.
XX
SQ   Sequence 985 BP; 283 A; 250 C; 245 G; 207 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.:              1.22e-164       Length:         985
Score:                  1757.00         Matches:        328
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-56 (1-328) x ADV34707 (1-985)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
              ||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984

RESULT 4
ADV34709/c
ID   ADV34709 standard; DNA; 985 BP.
XX
AC   ADV34709;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline N-terminal IL-12p40 protein complementary DNA, nFeIL-12p40-N985.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 57; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline N-terminal single chain IL-12p40
CC   complementary DNA.
XX
SQ   Sequence 985 BP; 207 A; 245 C; 250 G; 283 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.22e-164       Length:         985
Score:                  1757.00         Matches:        328
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-56 (1-328) x ADV34709 (1-985)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGC 2
```

RESULT 5
ABK98944
ID ABK98944 standard; cDNA; 987 BP.
XX
AC ABK98944;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p40-987 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69303.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 1; Page 51-53; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 987 BP; 283 A; 250 C; 246 G; 208 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.22e-164	Length:	987
Score:	1757.00	Matches:	328
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-56 (1-328) x ABK98944 (1-987)

```
Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
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Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984

RESULT 6
ABK98945/c
ID   ABK98945 standard; cDNA; 987 BP.
XX
AC   ABK98945;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p40-987 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 3; Page 54; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 987 BP; 208 A; 246 C; 250 G; 283 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.22e-164       Length:          987
Score:                    1757.00         Matches:         328
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              100.0%          Indels:          0
DB:                       6               Gaps:            0

US-10-821-670A-56 (1-328) x ABK98945 (1-987)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388
```

```
Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGC 4
```

RESULT 7
ADV34682
ID ADV34682 standard; cDNA; 987 BP.
XX
AC ADV34682;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain IL-12p40 full-length cDNA, nFeIL-12p40 987.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; gene; ss.
XX
OS Felis catus.
XX
FH Key   Location/Qualifiers
FT CDS   1. .987
FT   /*tag= a
FT   /product= "PFeIL-12p40 329 protein "
FT   /partial
FT   /note= "No stop codon"
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
DR P-PSDB; ADV34683.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Claim 23; SEQ ID NO 29; 103pp; English.

XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain IL-12p40 subunit protein
CC encoding full-length cDNA.
XX
SQ Sequence 987 BP; 283 A; 250 C; 246 G; 208 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.22e-164	Length:	987
Score:	1757.00	Matches:	328
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-56 (1-328) x ADV34682 (1-987)

```
Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
```

```
Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984

RESULT 8
ADV34684/c
ID   ADV34684 standard; DNA; 987 BP.
XX
AC   ADV34684;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12p40 complementary DNA, nFeIL-12p40 987.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 31; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12p40 subunit full-length
CC   complementary DNA.
XX
SQ   Sequence 987 BP; 208 A; 246 C; 250 G; 283 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.22e-164      Length:          987
Score:                  1757.00        Matches:         328
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            100.0%         Indels:          0
DB:                     14             Gaps:            0

US-10-821-670A-56 (1-328) x ADV34684 (1-987)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGC 4

RESULT 9
AAF26082
ID   AAF26082 standard; DNA; 990 BP.
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XX
AC   AAF26082;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p40 encoding DNA SEQ ID 8.
XX
KW   Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW   interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS   Felis sp.
XX
PN   WO200104280-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002262.
XX
PR   08-JUL-1999;   99CH-00001258.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
XX
PI   Leutenegger C,  Schroff M,  Wittig B,  Lutz H;
XX
DR   WPI; 2001-147190/15.
XX
PT   Vaccine for treating or preventing lentivirus infection in cats, contains
PT   nucleic acid sequence encoding viral protein under control of eukaryotic
PT   promoter.
XX
PS   Claim 14; Page 36; 37pp; German.
XX
CC   This invention describes a novel vaccine (A) for prevention or treatment
CC   of lentivirus infection in felines which comprises an immunizing nucleic
CC   acid sequence (I) that contains, or comprises, at least part of a gene
CC   encoding a protein (II) of the virus, under control of a eukaryotic
CC   promoter functional in the relevant animal. (II) is especially the
CC   envelope (env) protein. The invention also describes (1) vaccine (A)
CC   containing an immunizing protein, or fragment, from a lentivirus plus at
CC   least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC   lentivirus protein, or fragment, especially derived from feline immune
CC   deficiency virus (FIV), by expressing the corresponding nucleic acid
CC   sequence in a host cell. The products of the invention have antiviral
CC   activity. The vaccine (A) and related protein-based vaccines, are
CC   particularly used to treat or prevent lentivirus infections in domestic
CC   cats, especially feline immune deficiency virus (FIV). Vaccination with
CC   (A) allows differentiation between vaccinated and infected animals, from
CC   the antibody status. The vaccines may be formulated with an adjuvant
CC   (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC   immune response, particularly a Th1 response
XX
SQ   Sequence 990 BP; 283 A; 249 C; 248 G; 210 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.22e-164       Length:         990
Score:                  1757.00         Matches:        328
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     4               Gaps:           0

US-10-821-670A-56 (1-328) x AAF26082 (1-990)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984

RESULT 10
AAF26085
ID   AAF26085 standard; DNA; 990 BP.
XX
AC   AAF26085;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p40 encoding DNA.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
```

OS Felis sp.
XX
PN WO200104155-A2.
XX
PD 18-JAN-2001.
XX
PF 08-JUL-2000; 2000WO-DE002263.
XX
PR 08-JUL-1999; 99CH-00001259.
XX
PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA (UYZU-) UNIV ZUERICH.
PA (REGC) UNIV CALIFORNIA.
XX
PI Lutz H, Leutenegger C, Pedersen N, Schroff M, Wittig B;
XX
DR WPI; 2001-147178/15.
XX
PT Recombinant feline interleukin-12, useful as immunostimulant and for
PT treating e.g. viral infections in cats, and related nucleic acid
PT constructs.
XX
PS Claim 3; Page 30; 35pp; German.
XX
CC This invention describes a novel feline interleukin-12 (fIL-12)
CC polypeptide (I) that is expressed, by recombinant gene expression in
CC eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC of subunits p35 and p40. These proteins are formed so that, in equimolar
CC concentrations and in presence of an immunizing antigen, they can be
CC administered to carnivores, particularly domestic cats. The invention
CC also describes a nucleic acid construct (II) encoding fIL-12 containing
CC sequences at least 95% identical with the p40- and p35-encoding sequences
CC (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC as immunostimulants for immunization against infectious diseases and/or
CC for treating infections or tumors in felines, especially domestic cats.
CC The products of the invention have immunostimulatory, antiviral and
CC antitumor activity. Nucleic acid constructs that encode (II) are useful
CC as adjuvants for prophylactic immunization against viral diseases and for
CC treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC is useful for carnivores, and particularly domestic cats in the
CC following: (i) as immunostimulant, for preventative or therapeutic use;
CC and (ii) treating tumors and autoimmune diseases, or diseases associated
CC with a Th1 defect, especially pre-existing infections by feline immune
CC deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ Sequence 990 BP; 283 A; 249 C; 248 G; 210 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.22e-164	Length:	990
Score:	1757.00	Matches:	328
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	4	Gaps:	0

US-10-821-670A-56 (1-328) x AAF26085 (1-990)

```
Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984
```

RESULT 11
AAF26076
ID AAF26076 standard; DNA; 4522 BP.
XX
AC AAF26076;
XX
DT 24-APR-2001 (first entry)
XX
DE Feline IL-12p40 encoding DNA SEQ ID 2.
XX
KW Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS Felis sp.
XX
PN WO200104280-A2.
XX
PD 18-JAN-2001.
XX
PF 08-JUL-2000; 2000WO-DE002262.

```
XX
PR   08-JUL-1999;   99CH-00001258.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
XX
PI   Leutenegger C,  Schroff M,  Wittig B,  Lutz H;
XX
DR   WPI; 2001-147190/15.
XX
PT   Vaccine for treating or preventing lentivirus infection in cats, contains
PT   nucleic acid sequence encoding viral protein under control of eukaryotic
PT   promoter.
XX
PS   Disclosure; Page 29-31; 37pp; German.
XX
CC   This invention describes a novel vaccine (A) for prevention or treatment
CC   of lentivirus infection in felines which comprises an immunizing nucleic
CC   acid sequence (I) that contains, or comprises, at least part of a gene
CC   encoding a protein (II) of the virus, under control of a eukaryotic
CC   promoter functional in the relevant animal. (II) is especially the
CC   envelope (env) protein. The invention also describes (1) vaccine (A)
CC   containing an immunizing protein, or fragment, from a lentivirus plus at
CC   least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC   lentivirus protein, or fragment, especially derived from feline immune
CC   deficiency virus (FIV), by expressing the corresponding nucleic acid
CC   sequence in a host cell. The products of the invention have antiviral
CC   activity. The vaccine (A) and related protein-based vaccines, are
CC   particularly used to treat or prevent lentivirus infections in domestic
CC   cats, especially feline immune deficiency virus (FIV). Vaccination with
CC   (A) allows differentiation between vaccinated and infected animals, from
CC   the antibody status. The vaccines may be formulated with an adjuvant
CC   (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC   immune response, particularly a Th1 response
XX
SQ   Sequence 4522 BP; 1180 A; 1126 C; 1106 G; 1110 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                9.28e-164      Length:          4522
Score:                    1757.00        Matches:         328
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       4              Gaps:            0

US-10-821-670A-56 (1-328) x AAF26076 (1-4522)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db       4007 AGCAACTGGGCATCCGTGTCCTGC 4030

RESULT 12
AAF26094
ID   AAF26094 standard; DNA; 4522 BP.
XX
AC   AAF26094;
XX
DT   24-APR-2001  (first entry)
XX
DE   Plasmid pMol-fil12p40 DNA SEQ ID 10.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS   Synthetic.
XX
PN   WO200104155-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002263.
XX
PR   08-JUL-1999;   99CH-00001259.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Lutz H,  Leutenegger C,  Pedersen N,  Schroff M,  Wittig B;
XX
DR   WPI; 2001-147178/15.
```

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XX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs.
XX
PS   Example 1c; Page 33-35; 35pp; German.
XX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
CC   following: (i) as immunostimulant, for preventative or therapeutic use;
CC   and (ii) treating tumors and autoimmune diseases, or diseases associated
CC   with a Th1 defect, especially pre-existing infections by feline immune
CC   deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ   Sequence 4522 BP; 1180 A; 1126 C; 1106 G; 1110 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                9.28e-164       Length:          4522
Score:                    1757.00         Matches:         328
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              100.0%          Indels:          0
DB:                       4               Gaps:            0

US-10-821-670A-56 (1-328) x AAF26094 (1-4522)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db       4007 AGCAACTGGGCATCCGTGTCCTGC 4030

RESULT 13
AAV56625
ID   AAV56625 standard; cDNA; 2193 BP.
XX
AC   AAV56625;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp40 cDNA.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             64. .1053
FT                   /*tag=  a
FT   sig_peptide     64. .129
FT                   /*tag=  b
FT   mat_peptide     130. .1050
FT                   /*tag=  c
FT                   /product= "FLAFp40"
FT                   /note= "feline cytokine"
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP001824.
XX
PR   04-JUN-1996;   96JP-00165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
XX
```

```
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76173.
XX
PT   Novel feline cytokine protein - useful for treating feline auto:immune
PT   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS   Claim 19; Page 52-54; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine protein, FLAFp40. This
CC   protein can be used in the production of a FLAFp35/FLAFp40 heterodimer
CC   which can potentiate the cytotoxic activity of feline cytotoxic T
CC   lymphocyte cells. Such proteins are used for treatment of feline
CC   autoimmune diseases e.g. as caused by feline herpes virus or feline
CC   calcivirus
XX
SQ   Sequence 2193 BP; 680 A; 451 C; 493 G; 569 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.39e-163      Length:         2193
Score:                  1751.00        Matches:        327
Percent Similarity:     99.7%          Conservative:   0
Best Local Similarity:  99.7%          Mismatches:     1
Query Match:            99.7%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-56 (1-328) x AAV56625 (1-2193)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||
Db         64 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTACCTGGTTTTGCTGGCACCTCCTCTC 123

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 183

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 243

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 303

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 363

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 423

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 483

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 543

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 603

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 663

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 723

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        724 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 783

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 843

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 903

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 963

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 1023

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db       1024 AGCAACTGGGCATCCGTGTCCTGC 1047

RESULT 14
ABK98950
ID   ABK98950 standard; cDNA; 1599 BP.
XX
AC   ABK98950;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1599 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69306.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 58-60; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
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XX
SQ   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              5.7e-163        Length:         1599
Score:                  1743.00         Matches:        326
Percent Similarity:     99.4%           Conservative:   0
Best Local Similarity:  99.4%           Mismatches:     2
Query Match:            99.2%           Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-56 (1-328) x ABK98950 (1-1599)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984

RESULT 15
ABK98951/c
ID   ABK98951 standard; cDNA; 1599 BP.
XX
AC   ABK98951;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1599 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 61-62; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              5.7e-163        Length:         1599
Score:                  1743.00         Matches:        326
Percent Similarity:     99.4%           Conservative:   0
Best Local Similarity:  99.4%           Mismatches:     2
Query Match:            99.2%           Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-56 (1-328) x ABK98951 (1-1599)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
```

```
Db       1599 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 1540

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 1420

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1359 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 1300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1299 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 1240

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
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Db       1239 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
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Db       1179 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 1120

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db       1119 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 1060

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        999 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 940

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        939 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 880

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        879 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 820

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 760

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        759 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 640

Qy        321 SerAsnTrpAlaSerValSerCys 328
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Db        639 AGCAACTGGGCATCCGTGTCCTGC 616


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GenCore version 5.1.9
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Total number of hits satisfying chosen parameters: 12732272

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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AR595956
LOCUS AR595956 1599 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 38 from patent US 6818444.
ACCESSION AR595956
VERSION AR595956.1 GI:56646937
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1599)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 38 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .1599
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 100.0%; Score 1599; DB 2; Length 1599;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Qy       241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
Db       241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy       301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
Db       301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy       361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
Db       361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy       421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
Db       421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy       481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
Db       481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy       541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
Db       541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy       601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
Db       601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy       661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
Db       661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy       721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
Db       721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy       781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
Db       781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy       841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
Db       841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy       901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
Db       901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy       961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020
Db       961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020

Qy      1021 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 1080
Db      1021 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 1080

Qy      1081 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 1140
Db      1081 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 1140

Qy      1141 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200
Db      1141 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200

Qy      1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 1260
Db      1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 1260

Qy      1261 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 1320
Db      1261 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 1320

Qy      1321 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 1380
Db      1321 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 1380

Qy      1381 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 1440
Db      1381 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 1440

Qy      1441 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 1500
Db      1441 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 1500

Qy      1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 1560
Db      1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 1560

Qy      1561 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
Db      1561 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
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RESULT 2
AR595957/c
LOCUS AR595957 1599 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 40 from patent US 6818444.
ACCESSION AR595957
VERSION AR595957.1 GI:56646938
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1599)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 40 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .1599
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 100.0%; Score 1599; DB 2; Length 1599;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
Db      1599 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 1540

Qy        61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
Db      1539 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy       121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
Db      1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 1420

Qy       181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
Db      1419 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy       241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
Db      1359 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 1300

Qy       301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
Db      1299 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 1240

Qy       361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
Db      1239 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180
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Qy       421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
Db      1179 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 1120

Qy       481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
Db      1119 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 1060

Qy       541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
Db      1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy       601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
Db       999 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 940

Qy       661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
Db       939 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 880

Qy       721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
Db       879 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 820

Qy       781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
Db       819 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 760

Qy       841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
Db       759 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy       901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
Db       699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 640

Qy       961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020
Db       639 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 580

Qy      1021 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 1080
Db       579 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 520

Qy      1081 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 1140
Db       519 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 460

Qy      1141 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200
Db       459 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 400

Qy      1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 1260
Db       399 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 340

Qy      1261 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 1320
Db       339 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 280

Qy      1321 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 1380
Db       279 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 220

Qy      1381 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 1440
Db       219 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 160

Qy      1441 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 1500
Db       159 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 100

Qy      1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 1560
Db        99 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 40

Qy      1561 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
Db        39 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
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RESULT 3
AR595959
LOCUS AR595959 1533 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 43 from patent US 6818444.
ACCESSION AR595959
VERSION AR595959.1 GI:56646940
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1533)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 43 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .1533
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 95.9%; Score 1533; DB 2; Length 1533;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
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Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
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Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026
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Db        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy       1027 ACTCCATCCCCGGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1086
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Db        961 ACTCCATCCCCGGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020

Qy       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1146
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Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080

Qy       1147 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206
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Db       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1266
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Qy       1267 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1326
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Db       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260

Qy       1327 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1386
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320

Qy       1387 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1446
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Db       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380

Qy       1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1506
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Db       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440

Qy       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1566
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500

Qy       1567 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
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Db       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533


RESULT 4
AR595960/c
LOCUS       AR595960               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 45 from patent US 6818444.
ACCESSION   AR595960
VERSION     AR595960.1  GI:56646941
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 45 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
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ORIGIN

  Query Match             95.9%;  Score 1533;  DB 2;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1533;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy         367 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
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Db        1233 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy         427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy         487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy         547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
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Db        1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy         607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy         667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
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Db         933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy         727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy         847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694
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Qy       907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
Db       693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy       967 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026
Db       633 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy      1027 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1086
Db       573 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy      1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1146
Db       513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy      1147 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206
Db       453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy      1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1266
Db       393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy      1267 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1326
Db       333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy      1327 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1386
Db       273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy      1387 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1446
Db       213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy      1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1506
Db       153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy      1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1566
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy      1567 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
Db         33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1


RESULT 5
AR595971
LOCUS       AR595971                1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 61 from patent US 6818444.
ACCESSION   AR595971
VERSION     AR595971.1  GI:56646952
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 61 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             89.4%;  Score 1429.4;  DB 2;  Length 1599;
  Best Local Similarity   93.4%;  Pred. No. 0;
  Matches 1493;  Conservative    0;  Mismatches  106;  Indels    0;  Gaps    0;
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Qy         1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
Db         1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

Qy        61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
Db        61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy       121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
Db       121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy       181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
Db       181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy       241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
Db       241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy       301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
Db       301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360

Qy       361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
Db       361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy       421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
Db       421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Qy       481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
Db       481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540

Qy       541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
Db       541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy       601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
Db       601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Qy       661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
Db       661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy       721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
Db       721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy       781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
Db       781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Qy       841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
Db       841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy       901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
Db       901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960

Qy       961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020
Db       961 AGCGACTGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020

Qy      1021 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 1080
Db      1021 ACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGA 1080
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Qy       1081 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 1140
             ||| |||||||||||||||||||||||||||||||||||||||||| || ||||||||||||
Db       1081 GCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCC 1140

Qy       1141 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200
             |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db       1141 GAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200

Qy       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 1260
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACT 1260

Qy       1261 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 1320
             || ||||||||||||||||  ||||| |||||||||||||  ||||||||||||||||
Db       1261 AACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGC 1320

Qy       1321 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 1380
             |||||||||||||||||||||||||| |||| |||||||||||||| ||||||||| |||
Db       1321 ATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTA 1380

Qy       1381 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 1440
             |||||||| || ||||||||||||||||||||||||||||||||||||| |||||||||
Db       1381 ATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTG 1440

Qy       1441 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 1500
             ||||||||||||||| |||||||||||||||||||||||| |||||| | ||||| |||
Db       1441 TTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCG 1500

Qy       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 1560
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCG 1560

Qy       1561 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
             |||||||||||||||||||  |||  ||||  |||||
Db       1561 GTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1599


RESULT 6
AR595972/c
LOCUS       AR595972                1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 63 from patent US 6818444.
ACCESSION   AR595972
VERSION     AR595972.1  GI:56646953
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 63 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             89.4%;  Score 1429.4;  DB 2;  Length 1599;
  Best Local Similarity   93.4%;  Pred. No. 0;
  Matches 1493;  Conservative    0;  Mismatches  106;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||| |||||||||||||||| ||||| ||||||| |||||||||||  ||||||||
Db       1599 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 1540

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||||||||||||| |||| |||||||||||||||||||| |||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 1420

Qy         181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
               ||||| |  |||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1419 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy         241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
               ||||||| |||||||||||||||||||| |||||||||||| |||||||||||  ||
Db       1359 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 1300

Qy         301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
               ||||  |||| |||||||| ||||||||||||||||||||||||||||||| |||||||
Db       1299 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 1240

Qy         361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
               |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy         421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
               || |||||||||||||||||||||||| |||||||||||| ||||||||| |||||
Db       1179 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 1120

Qy         481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
               |||| |||||||||||||| |||||| |||||||||| |||||| |||||||||| ||||
Db       1119 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 1060

Qy         541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy         601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
               ||  |||||||||||||||||||| || |||||||||| ||||||||||||||||||||
Db       999 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 940

Qy         661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
               || |||||||||||||||||||||||||||||| |||||||||||||| ||||||||||
Db       939 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 880

Qy         721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
               |||||||| |||||||||| |||||||||||||| ||||| || ||||||||||||||
Db       879 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 820

Qy         781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
               |||||||||||||||||||||||||||||||| | |||||| || |||||| |||||||
Db       819 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 760

Qy         841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
               |||||||| |||||||||||||| ||||||| |||||||||||||||||||||||||||
Db       759 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy         901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
               |||||||||||||||||||||||||||||||| |||||||||||||| ||||||||| |||
Db       699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 640

Qy         961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020
               ||| |||||||||| ||||| |||||||||||||||||||||||||||||||||||||||
Db       639 AGCGACTGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 580

Qy        1021 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 1080
               |||||||||||||||||||| ||||||||  ||  | ||||||||||||||| || || ||
Db       579 ACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGA 520

Qy        1081 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 1140
               ||| |||||||||||||||||||||||||||||||||||||||||| || ||||||||||||
Db       519 GCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCC 460

Qy        1141 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200
               |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db       459 GAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTA 400

Qy        1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 1260
               |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db       399 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACT 340
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Qy       1261 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 1320
             || ||||||||||||||||  ||||| ||||||||||||||  ||||||||||||||||
Db        339 AACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGC 280

Qy       1321 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 1380
             |||||||||||||||||||||||||| |||| |||||||||||||| |||||||| |||
Db        279 ATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTA 220

Qy       1381 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 1440
             |||||||| || ||||||||||||||||||||||||||||||||||||| |||||||||
Db        219 ATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTG 160

Qy       1441 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 1500
             |||||||||||||| |||||||||||||||||||||||| |||||| | ||||| |||
Db        159 TTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCG 100

Qy       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCG 40

Qy       1561 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
             |||||||||||||||||||  |||  ||||  |||||
Db         39 GTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1


RESULT 7
AR595973
LOCUS       AR595973               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 66 from patent US 6818444.
ACCESSION   AR595973
VERSION     AR595973.1  GI:56646954
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 66 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
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ORIGIN

  Query Match             85.9%;  Score 1373;  DB 2;  Length 1533;
  Best Local Similarity   93.5%;  Pred. No. 0;
  Matches 1433;  Conservative    0;  Mismatches  100;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              |||||||||||||||| | ||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              |||||||||||||||||||||||| |||| ||||||||||||||||||| |||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              | ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              | |||||||||||||||||||| |||||||||||| |||||||||||  ||  ||||
Db        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              |||| |||||||| |||||||||||||||||||||||||||||||||| ||||||||||
Db        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||| |||
Db        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              |||||||||||||||||||||| |||||||||||| ||||||||| |||||||||| |
Db        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420

Qy        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||| |||||| |||||||||| |||||| |||||||||| ||||||||||
Db        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              |||||||||||||||||| || |||||||||| |||||||||||||||||||||| |||
Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              |||||||||||||||||||||||| |||||||||||| |||||||||| ||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              || |||||||||| |||||||||||| ||||| || |||||||||||||| ||||||
Db        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              |||||||||||||||||||||||||| | |||||| || |||||| ||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              || |||||||||||||| ||||||| ||||||||||||||||||||||||||||||||||
Db        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              |||||||||||||||||||||||||||||| |||||||||||||||| ||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900

Qy        967 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026
              |||||||| ||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy       1027 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1086
              |||||||||||||| |||||||| ||  | |||||||||||||| || || ||||| ||
Db        961 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 1020

Qy       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1146
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 1080

Qy       1147 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1081 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1266
              |||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||
Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1200

Qy       1267 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1326
              |||||||||||||  |||||  |||||||||||||  ||||||||||||||  ||||||
Db       1201 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1260

Qy       1327 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1386
              |||||||||||||||||||| |||| |||||||||||||| |||||||| |||||||||
Db       1261 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1320

Qy       1387 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1446
              || || |||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       1321 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 1380

Qy       1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1506
              ||||||||| |||||||||||||||||||||||||||||| |||||| | ||||| |||||||||
Db       1381 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1440
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Qy       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1566
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1500

Qy       1567 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
             ||||||||||||||| ||| |||| |||||
Db       1501 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1533


RESULT 8
AR595974/c
LOCUS       AR595974               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 68 from patent US 6818444.
ACCESSION   AR595974
VERSION     AR595974.1  GI:56646955
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 68 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           85.9%;  Score 1373;  DB 2;  Length 1533;
  Best Local Similarity   93.5%;  Pred. No. 0;
  Matches 1433;  Conservative    0;  Mismatches  100;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              |||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              |||||||||||||||||||||||| |||| ||||||||||||||||||||| ||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1414

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              | |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       1413 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              | |||||||||||||||||||| |||||||||||| |||||||||||   ||  ||||
Db       1353 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1294

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
               |||| |||||||| |||||||||||||||||||||||||||||| ||||||||||||
Db       1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

Qy        367 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||| |||
Db       1233 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              |||||||||||||||||||||| |||||||||||| ||||||||| |||||||||| |
Db       1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||||| |||||| |||||||||| |||||| |||||||||| ||||||||||
Db       1113 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1054

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
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Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 994

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              |||||||||||||||||||| || |||||||||| |||||||||||||||||||| |||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934
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Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              |||||||||||||||||||||||||| |||||||||||||| |||||||||| ||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 874

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              || |||||||||||| |||||||||||||| ||||| || |||||||||||||| ||||||
Db        873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
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Db        813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
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Db        753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
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Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 634

Qy        967 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026
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Db        633 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy       1027 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1086
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Db        573 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 514

Qy       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1146
              |||||||||||||||||||||||||||||||||||||||||||| || ||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 454

Qy       1147 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1266
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||| |||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 334

Qy       1267 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1326
              |||||||||||||| ||||| |||||||||||||| |||||||||||||| ||||||
Db        333 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 274

Qy       1327 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1386
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Db        273 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 214

Qy       1387 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1446
              || || |||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        213 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 154

Qy       1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1506
              ||||||||| |||||||||||||||||||||||| |||||| | ||||| ||||||||||
Db        153 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 94

Qy       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1566
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 34

Qy       1567 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
              ||||||||||||||| ||| |||| |||||
Db         33 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1


RESULT 9
AF401989
LOCUS       AF401989               1626 bp    mRNA    linear   SYN 14-FEB-2002
DEFINITION  Synthetic construct single chain interleukin-12 mRNA, complete cds.
ACCESSION   AF401989
VERSION     AF401989.1  GI:18656516
KEYWORDS    .
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SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 1626)
  AUTHORS   McMonagle,E.L.J., Taylor,S., van Zuilekom,H., Sanders,L.,
            Scholtes,N., Keanie,L.J., Hopkins,C.A., Logan,N.A., Bain,D.,
            Argyle,D.J., Onions,D.E., Schijns,V.E. and Nicolson,L.
  TITLE     Production of biologically active equine interleukin 12 through
            expression of p35, p40 and single chain IL-12 in mammalian and
            baculovirus expression systems
  JOURNAL   Equine Vet. J. 33 (7), 693-698 (2001)
   PUBMED   11770992
REFERENCE   2  (bases 1 to 1626)
  AUTHORS   McMonagle,L.J., Taylor,S., Keanie,L.J., Hopkins,C.A., Logan,N.A.,
            Argyle,D.J., Onions,D.E. and Nicolson,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUL-2001) Veterinary Pathology, Glasgow Veterinary
            School, Bearsden Rd, Glasgow G61 1QH, UK
FEATURES             Location/Qualifiers
     source          1. .1626
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                     /mol_type="mRNA"
                     /db_xref="taxon:32630"
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                     /note="derived from Equus caballus; N-terminal p40 subunit
                     linked by (Gly4Ser)3 linker to signal-peptide deleted p35
                     subunit"
                     /codon_start=1
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                     /translation="MGHQWLVLSWFSLVLLASPLMAIWELEKDVYVVELDWYPDAPGE
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                     GSSDPRGVTCGAATLSAERVSVDDREYKKYTVECQEGSACPAAEESLPIEIVVDAVHK
                     LKYENYTSGFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPETWSTPHSYFSLTFSI
                     QVQGKNKKERKDRLFMDETSATVTCHKDGQIRVQARDRYYSSSWSEWASVSCSGGGGS
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                     HEDITKDKSSTVAACLPLELAPNESCLASREISFITNGSCLTPGKASSMMTLCLSSIY
                     EDLKMYQVEFKAMNAKLLIDPQRQIFLDENMLTAIDKLMQALNFNSETVPQKPSLEGL
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     primer_bind     1. .14
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     misc_feature    988. .1032
                     /note="linker"
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ORIGIN

  Query Match             79.0%;  Score 1262.6;  DB 8;  Length 1626;
  Best Local Similarity   86.9%;  Pred. No. 0;
  Matches 1410;  Conservative    0;  Mismatches  189;  Indels   24;  Gaps    1;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              |||  ||  |||  ||||||| || ||||| ||||||||||||||||||  ||||||||
Db          1 ATGGGTCACCAGTGGTTGGTCCTCTCCTGGTTTTCCCTGGTTTTGCTGGCGTCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||||||||| | || |||||||||| ||||| ||| ||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTGTATGTTGTAGAATTGGATTGGTACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||| |||||||||||||||||||||||||| |||||||||| | ||||||||||
Db        121 GCCCCTGGAGAAATGGTGGTCCTCACCTGCAATACCCCTGAAGAAGAAGGCATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||| | |||||||| ||| ||| |||||||||| |||||  ||||||||||||||||
Db        181 ACCTCGGCCCAGAGCAATGAGGTCTTAGGCTCTGGCAAAACCTTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              || |||| |||||||||  ||| |||||||| ||||||||||||||||||||||||||||
Db        241 GAGTTTGGAGATGCTGGCTGGTACACCTGTCACAAAGGAGGCGAGGTTCTGAGCCATTCT 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              |||  ||| | ||||| ||||||||||||||||||||||||||| || ||||  || |||
Db        301 CACCTGCTGCTTCACAAGAAGGAAGATGGAATTTGGTCCACTGACATTTTAAAAGACCAG 360

Qy        361 AAAGAATCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Db        361 AAAGAATCCAAAAATAAGACCTTTCTAAAATGTGAGGCAAAGAATTATTCCGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db        421 ACATGCTGGTGGCTGACAGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              || |||||||||||||| || |||||| |||||||||||||||||||| ||||||| ||||
Db        481 GGTTCCTCTGACCCCCGAGGGGTGACGTGTGGAGCAGCGACACTCTCCGCAGAGAGGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              || |||||| ||||||| |||||||||||||| |||||||||||||||||||||||||||
Db        541 AGCGTGGACGACAGGGAGTATAAGAAGTACACGGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||| |||||||||||||| ||||||||  |||||||||| ||| ||||||||||||||
Db        601 CCGGCCGCCGAGGAGAGCCTGCCCATTGAGATCGTGGTGGATGCTGTTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Db        661 TATGAAAACTACACCAGCGGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              |||||||| |||||||||||||| |||||||||| ||||| || |||||||| |||||
Db        721 AACCTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCC 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              || |||||||||||||||||||||||||||||| | |||||     | ||||||||||||
Db        781 GAGACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTCTCTATTCAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||||||| |  |||| ||||||||||||||| | ||||  |||| |||||||  |||
Db        841 AAGAACAAGAAGGAAAGGAAAGACAGACTCTTCATGGATGAGACTTCAGCCACAGTCACA 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              |||||||||||| | ||||||| || |||||||| |||||||||| ||||||||||||
Db        901 TGCCACAAGGATGGCCAGATCCGTGTCCAAGCCAGGGACCGCTACTACAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGG----------------------CGGT 996
              ||| | ||||||||||| ||||||||||||||                      ||||
Db        961 AGCGAATGGGCATCCGTATCCTGCAGTGGTGGCGGTGGCTCGGGCGGTGGTGGATCCGGT 1020

Qy        997 GGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTC 1056
              ||||||||||||||| ||| | || ||  | || |||  ||| || ||||||||||||||
Db       1021 GGCGGCGGATCTAGGAACCTCCCCACAGCCACACCAGGCCCAGGAATGTTCCAGTGCCTC 1080

Qy       1057 AACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACT 1116
              |||||||||||||| ||||||| |  || |||||||||||||||||||||||||| |||||
Db       1081 AACCACTCCCAAAACCTGCTGAGGACCGTCAGCAACACGCTTCAGAAGGCCAGGCAAACC 1140

Qy       1117 CTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAA 1176
              |||||||| |||||||||||||| |||||||| |||||||| |||||||||||||| ||
Db       1141 CTAGAATTCTACTCCTGCACTTCTGAAGAGATCGATCATGAGGATATCACAAAAGACAAG 1200

Qy       1177 ACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCT 1236
              | |||||| |||| ||||||| | || |||||  ||  ||| ||||||||||||||||
Db       1201 AGCAGCACCGTGGCGGCCTGCCTCCCCCTGGAACTCGCCCCGAACGAGAGTTGCCTGGCT 1260

Qy       1237 TCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTT 1296
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Db       1261 TCCAGAGAGATCTCTTTCATAACTAATGGGAGTTGCCTGACCCCCGGAAAGGCCTCTTCT 1320

Qy       1297 ATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTC 1356
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Db       1381 AAGGCCATGAATGCCAAGCTGTTGATAGATCCTCAGAGGCAGATCTTTCTGGATGAGAAC 1440

Qy       1417 ATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCA 1476

Db       1441 ATGCTGACAGCCATTGACAAGCTGATGCAGGCCCTGAACTTCAACAGTGAGACTGTGCCA 1500

Qy       1477 CAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTT 1536

Db       1501 CAAAAGCCCTCCCTTGAAGGACTGGATTTTTATAAAACTAAAGTCAAGCTCTGCATCCTT 1560

Qy       1537 CTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCT 1596

Db       1561 CTTCATGCCTTCAGAATCCGCGCAGTGACCATCAACAGGATGATGGGCTATCTGAATGCT 1620

Qy       1597 TCC 1599

Db       1621 TCC 1623


RESULT 10
AR091394
LOCUS       AR091394                1623 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 9 from patent US 5994104.
ACCESSION   AR091394
VERSION     AR091394.1  GI:10018149
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1623)
  AUTHORS   Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
  TITLE     Interleukin-12 fusion protein
  JOURNAL   Patent: US 5994104-A 9 30-NOV-1999;
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             78.1%;  Score 1248.2;  DB 2;  Length 1623;
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  Matches 1408;  Conservative    0;  Mismatches  188;  Indels   27;  Gaps    2;

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Db          1 ATGGGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Db         61 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Db        121 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Db        181 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Db        241 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Db        301 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Db        361 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Db        421 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Db        481 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Db        541 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 597

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Db        598 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 657

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Db        658 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 717

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Db        718 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 777

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Db        778 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 837

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Db        838 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 897

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Db        898 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 957

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGT---------------------------- 996

Db        958 AGCGAATGGGCATCTGTGCCCTGCAGTGGTGGCGGTGGAAGCGGCGGTGGCGGAAGCGGC 1017

Qy        997 GGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTC 1056

Db       1018 GGTGGCGGCAGCAGAAACCTCCCCCTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTT 1077

Qy       1057 AACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACT 1116

Db       1078 CACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACT 1137

Qy       1117 CTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAA 1176

Db       1138 CTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAA 1197

Qy       1177 ACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCT 1236

Db       1198 ACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAAT 1257

Qy       1237 TCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTT 1296

Db       1258 TCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTT 1317

Qy       1297 ATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTC 1356

Db       1318 ATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTC 1377

Qy       1357 AAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAAC 1416

Db       1378 AAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAAC 1437

Qy       1417 ATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCA 1476

Db       1438 ATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCA 1497
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Qy       1477 CAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTT 1536
Db       1498 CAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTT 1557

Qy       1537 CTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCT 1596
Db       1558 CTTCATGCTTTCAGAATTCGGGCAGTGACTATTGACAGAGTGACGAGCTATCTGAATGCT 1617

Qy       1597 TCC 1599
Db       1618 TCC 1620


RESULT 11
AR091393
LOCUS       AR091393                6139 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 7 from patent US 5994104.
ACCESSION   AR091393
VERSION     AR091393.1  GI:10018148
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 6139)
  AUTHORS   Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
  TITLE     Interleukin-12 fusion protein
  JOURNAL   Patent: US 5994104-A 7 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .6139
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                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             78.1%;  Score 1248.2;  DB 2;  Length 6139;
  Best Local Similarity   86.8%;  Pred. No. 0;
  Matches 1408;  Conservative    0;  Mismatches  188;  Indels   27;  Gaps    2;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
Db       3222 ATGGGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 3281

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
Db       3282 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 3341

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
Db       3342 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 3401

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
Db       3402 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 3461

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
Db       3462 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 3521

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
Db       3522 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 3581

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
Db       3582 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 3641

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
Db       3642 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 3701

Qy        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
Db       3702 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 3761

Qy         541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
Db       3762 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 3818

Qy         601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
Db       3819 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 3878

Qy         661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
Db       3879 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 3938

Qy         721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
Db       3939 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 3998

Qy         781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
Db       3999 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 4058

Qy         841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
Db       4059 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 4118

Qy         901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
Db       4119 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 4178

Qy         961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGT---------------------- 996
Db       4179 AGCGAATGGGCATCTGTGCCCTGCAGTGGTGGCGGTGGAAGCGGCGGTGGCGGAAGCGGC 4238

Qy         997 GGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTC 1056
Db       4239 GGTGGCGGCAGCAGAAACCTCCCCCTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTT 4298

Qy        1057 AACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACT 1116
Db       4299 CACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACT 4358

Qy        1117 CTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAA 1176
Db       4359 CTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAA 4418

Qy        1177 ACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCT 1236
Db       4419 ACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAAT 4478

Qy        1237 TCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTT 1296
Db       4479 TCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTT 4538

Qy        1297 ATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTC 1356
Db       4539 ATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTC 4598

Qy        1357 AAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAAC 1416
Db       4599 AAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAAC 4658

Qy        1417 ATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCA 1476
Db       4659 ATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCA 4718

Qy        1477 CAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTT 1536
Db       4719 CAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTT 4778

Qy        1537 CTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCT 1596
Db       4779 CTTCATGCTTTCAGAATTCGGGCAGTGACTATTGACAGAGTGACGAGCTATCTGAATGCT 4838
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Qy       1597 TCC 1599
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Db       4839 TCC 4841


RESULT 12
AR091395
LOCUS       AR091395               1560 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 11 from patent US 5994104.
ACCESSION   AR091395
VERSION     AR091395.1  GI:10018150
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1560)
  AUTHORS   Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
  TITLE     Interleukin-12 fusion protein
  JOURNAL   Patent: US 5994104-A 11 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .1560
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ORIGIN

  Query Match             75.1%;  Score 1201.2;  DB 2;  Length 1560;
  Best Local Similarity   86.9%;  Pred. No. 0;
  Matches 1355;  Conservative    0;  Mismatches  178;  Indels   27;  Gaps    2;

Qy         64 GCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCC 123
              |||||||||||||||| ||||| | |||||||| ||||| ||||| ||| | || ||||||
Db          1 GCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCC 60

Qy        124 CCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACC 183
              || |||||||||||||||||||||   | || ||||||||||||   ||||||||||||
Db         61 CCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACC 120

Qy        184 TCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAA 243
              |  |||||||||||||| ||| |||||||||| ||||| ||||||||||||||||||||
Db        121 TTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAG 180

Qy        244 TTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTC 303
              |||| ||||||||||||||| |||||||| |||||||||||||||||| ||||||||| ||
Db        181 TTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTC 240

Qy        304 CTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAA 363
              || ||| | |||||||||||||||||||||||||||||||||||| |||| ||| ||||||
Db        241 CTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAA 300

Qy        364 GAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACC 423
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Db        301 GAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACC 360

Qy        424 TGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGC 483
              |||||||||||||| |||||||||| ||||||| ||||| ||||||||||||||||||||
Db        361 TGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGC 420

Qy        484 TCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGA 543
              || |||||||||||||| |||||| || ||||| || |||||||| |||||||  ||||||
Db        421 TCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGA 480

Qy        544 GTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCG 603
              | |||||||| ||| |||     ||||| |||||||||| ||||||| ||||||||||||
Db        481 GGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCA 537

Qy        604 GCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTAC 663
              ||||| |||||||| || |||||||| ||| ||||||| ||  ||||||||||||||||
Db        538 GCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTAT 597

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAAC 723
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Db        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAAC 657

Qy        724 CTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGAC 783
              |||| |||||||||||||| |||||||||| ||||| || |||||||| |||||||||
Db        658 TTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGAC 717

Qy        784 ACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAG 843
              |||||||  || |||||||||||||||||| | |||||   |||| ||||||||||||||
Db        718 ACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAG 777

Qy        844 AACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGC 903
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Db        778 AGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGC 837

Qy        904 CACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGC 963
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Db        838 CGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGC 897

Qy        964 AACTGGGCATCCGTGTCCTGCAGTGGTGGCGGT-----------------------GGC 999
              | ||||||| ||| |||||||||||||||||                       ||
Db        898 GAATGGGCATCTGTGCCCTGCAGTGGTGGCGGTGGAAGCGGCGGTGGCGGAAGCGGCGGT 957

Qy       1000 GGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAAC 1059
              |||||    |||||| | ||     | ||||||  ||| || |||||||  |||||  ||
Db        958 GGCGGCAGCAGAAACCTCCCCCTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCAC 1017

Qy       1060 CACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTA 1119
              |||||||||| ||||||| | ||| |||||||| ||| ||||||||||||||||||||||
Db       1018 CACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTA 1077

Qy       1120 GAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACC 1179
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Db       1078 GAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACC 1137

Qy       1180 AGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCC 1239
              |||||||||||||||| |||||| |||||||||||| ||||||||||||||    ||||
Db       1138 AGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCC 1197

Qy       1240 AGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATG 1299
              ||||||| |||| | ||||||||||||||||||||||||||||||||||||||||||||||
Db       1198 AGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATG 1257

Qy       1300 ACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAG 1359
              | | |||||||||||||| ||||| ||||| ||||||||||||||||||||||||||||||
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Qy       1360 GCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATG 1419
              |||||||||||||||  | |||||||||| |||||||||||||| ||||||||||||
Db       1318 ACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATG 1377

Qy       1420 CTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAG 1479
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Db       1378 CTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAA 1437

Qy       1480 AACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTT 1539
              || |||||| | ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1438 AAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTT 1497

Qy       1540 CATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
              |||||||||||||||| |||||||| ||  | ||| ||| ||||||||||||||||||
Db       1498 CATGCTTTCAGAATTCGGGCAGTGACTATTGACAGAGTGACGAGCTATCTGAATGCTTCC 1557


RESULT 13
FCIL12P40
LOCUS       FCIL12P40              1006 bp    mRNA    linear   MAM 18-APR-2005
DEFINITION  Felis catus mRNA for interleukin-12 p40 chain.
ACCESSION   Y07762
VERSION     Y07762.1  GI:2102664
KEYWORDS    interleukin-12 p40.
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
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REFERENCE   1
  AUTHORS   Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
  TITLE     Molecular cloning of cat interleukin-12
  JOURNAL   Immunogenetics 45 (6), 462-463 (1997)
   PUBMED   9089110
REFERENCE   2  (bases 1 to 1006)
  AUTHORS   Schijns,V.E.C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
            Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
            Utrecht, NETHERLANDS
FEATURES             Location/Qualifiers
     source          1. .1006
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                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
                     /cell_type="lymphocyte"
                     /tissue_type="peripheral blood"
     gene            1. .1006
                     /gene="IL-12.p40"
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                     GSSDPQEVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPAAEESLPIEVVVDAIHK
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                     QVQGKNNREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSNWASVSCS"
ORIGIN

  Query Match           61.7%;  Score 987;  DB 14;  Length 1006;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-284;
  Matches  987;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
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Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
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Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
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Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Qy        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
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Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
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Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
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Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
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Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
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Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987


RESULT 14
AR595950
LOCUS       AR595950                 987 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 29 from patent US 6818444.
ACCESSION   AR595950
VERSION     AR595950.1  GI:56646931
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 29 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           61.5%;  Score 983.8;  DB 2;  Length 987;
  Best Local Similarity  99.8%;  Pred. No. 2.4e-283;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
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Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
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Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
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Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

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Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
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Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987


RESULT 15
AR595951/c
LOCUS       AR595951                 987 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 31 from patent US 6818444.
ACCESSION   AR595951
VERSION     AR595951.1  GI:56646932
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.

REFERENCE   1  (bases 1 to 987)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 31 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             61.5%;  Score 983.8;  DB 2;  Length 987;
  Best Local Similarity   99.8%;  Pred. No. 2.4e-283;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
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Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
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Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
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Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
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Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
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Db         27 AGCAACTGGGCATCCGTGTCCTGCAGT 1
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OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1599	100.0	1599	6	ABK98950	Abk98950 Feline in
c	2	1599	100.0	1599	6	ABK98951	Abk98951 Feline in
	3	1599	100.0	1599	14	ADV34691	Adv34691 Feline si
c	4	1599	100.0	1599	14	ADV34693	Adv34693 Feline si
c	5	1533	95.9	1533	6	ABK98954	Abk98954 Feline in
	6	1533	95.9	1533	6	ABK98953	Abk98953 Feline in
c	7	1533	95.9	1533	14	ADV34697	Adv34697 Feline si
	8	1533	95.9	1533	14	ADV34695	Adv34695 Feline si
	9	1429.4	89.4	1599	6	ABK98965	Abk98965 Canine in
c	10	1429.4	89.4	1599	6	ABK98966	Abk98966 Canine in
c	11	1429.4	89.4	1599	14	ADV34715	Adv34715 Canine si
	12	1429.4	89.4	1599	14	ADV34713	Adv34713 Canine si
	13	1373	85.9	1533	6	ABK98967	Abk98967 Canine in
c	14	1373	85.9	1533	6	ABK98968	Abk98968 Canine in
c	15	1373	85.9	1533	14	ADV34718	Adv34718 Canine si
	16	1373	85.9	1533	14	ADV34716	Adv34716 Canine si
	17	1287	80.5	11569	10	ADG25150	Adg25150 Vector pA
	18	1285.4	80.4	11453	10	ADG25152	Adg25152 Vector pS
	19	1258.8	78.7	8608	6	AAD31548	Aad31548 pIRES-hB7
	20	1258.8	78.7	8629	6	AAD31552	Aad31552 pIRES-IL1
	21	1248.2	78.1	6139	3	AAZ40023	Aaz40023 Interleuk
	22	1243.8	77.8	8578	6	AAD31546	Aad31546 pIRES-hB7
	23	1243.8	77.8	8578	6	AAD31545	Aad31545 pIRES-hB7
	24	1243.8	77.8	8623	6	AAD31547	Aad31547 pIRES-hB7
	25	1243.8	77.8	8644	6	AAD31551	Aad31551 pIRES-IL1
	26	1228.8	76.8	8638	6	AAD31549	Aad31549 pIRES-hB7
	27	1228.8	76.8	8659	6	AAD31550	Aad31550 pIRES-IL1
	28	983.8	61.5	987	6	ABK98944	Abk98944 Feline in
c	29	983.8	61.5	987	6	ABK98945	Abk98945 Feline in
	30	983.8	61.5	987	14	ADV34682	Adv34682 Feline si
c	31	983.8	61.5	987	14	ADV34684	Adv34684 Feline si
c	32	981.8	61.4	985	6	ABK98962	Abk98962 Feline in
	33	981.8	61.4	985	6	ABK98961	Abk98961 Feline in
	34	981.8	61.4	985	14	ADV34707	Adv34707 Feline N-
c	35	981.8	61.4	985	14	ADV34709	Adv34709 Feline N-
	36	980.6	61.3	990	4	AAF26082	Aaf26082 Feline IL
	37	980.6	61.3	990	4	AAF26085	Aaf26085 Feline IL
	38	980.6	61.3	4522	4	AAF26076	Aaf26076 Feline IL
	39	980.6	61.3	4522	4	AAF26094	Aaf26094 Plasmid p
	40	979	61.2	2193	2	AAV56625	Aav56625 Feline FL
	41	921	57.6	921	6	ABK98942	Abk98942 Feline in
c	42	921	57.6	921	6	ABK98943	Abk98943 Feline in
c	43	921	57.6	921	14	ADV34681	Adv34681 Feline si
	44	921	57.6	921	14	ADV34679	Adv34679 Feline si
	45	919.4	57.5	921	2	AAV56626	Aav56626 Feline FL

ALIGNMENTS

RESULT 1
ABK98950
ID ABK98950 standard; cDNA; 1599 BP.
XX
AC ABK98950;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12-1599 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69306.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 58-60; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain

```
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1599;  DB 6;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1599;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020

Qy       1021 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 1080

Qy       1081 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 1140

Qy       1141 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200

Qy       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 1260

Qy       1261 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 1320

Qy       1321 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 1380

Qy       1381 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 1440

Qy       1441 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 1500

Qy       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 1560

Qy       1561 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
              |||||||||||||||||||||||||||||||||||||||
Db       1561 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599


RESULT 2
ABK98951/c
ID   ABK98951 standard; cDNA; 1599 BP.
XX
AC   ABK98951;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1599 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
```

PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 61-62; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

Query Match 100.0%; Score 1599; DB 6; Length 1599;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1599 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 1540

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 1420

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1359 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 1300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1299 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 1240

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1179 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 1120

Qy        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1119 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 1060

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        999 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 940

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        939 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 880

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        879 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 820

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 760

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        759 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 640

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        639 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 580

Qy       1021 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        579 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 520

Qy       1081 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        519 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 460

Qy       1141 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        459 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 400

Qy       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        399 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 340

Qy       1261 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        339 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 280

Qy       1321 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        279 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 220

Qy       1381 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 160

Qy       1441 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        159 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 100

Qy       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 40

Qy       1561 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
              |||||||||||||||||||||||||||||||||||||||
Db         39 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
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RESULT 3
ADV34691
ID   ADV34691 standard; cDNA; 1599 BP.
XX
AC   ADV34691;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1599
FT                   /*tag=  a
FT                   /product= "PFeIL-12p533 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34692.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 38; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1599;  DB 14;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1599;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020

Qy       1021 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 1080

Qy       1081 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 1140

Qy       1141 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200

Qy       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 1260

Qy       1261 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 1320
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Qy       1321 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 1380

Qy       1381 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 1440

Qy       1441 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 1500

Qy       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 1560

Qy       1561 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
             |||||||||||||||||||||||||||||||||||||||
Db       1561 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
```

RESULT 4
ADV34693/c
ID ADV34693 standard; DNA; 1599 BP.
XX
AC ADV34693;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain IL-12 complementary DNA, nFeIL-12 1599.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Felis catus.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 3; SEQ ID NO 40; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain IL-12 complementary DNA.
XX
SQ Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

Query Match 100.0%; Score 1599; DB 14; Length 1599;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1599 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 1540

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 1420

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1359 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 1300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1299 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 1240

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1179 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 1120

Qy        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1119 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 1060

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        999 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 940

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        939 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 880

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        879 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 820

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 760

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        759 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 640

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        639 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 580

Qy       1021 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        579 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 520

Qy       1081 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 1140
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        519 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 460

Qy       1141 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        459 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 400

Qy       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 1260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        399 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 340

Qy       1261 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 1320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        339 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 280

Qy       1321 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 1380
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        279 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 220

Qy       1381 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 1440
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 160

Qy       1441 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 1500
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        159 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 100

Qy       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 1560
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          99 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 40

Qy       1561 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
                |||||||||||||||||||||||||||||||||||||
Db          39 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
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RESULT 5
ABK98954/c
ID   ABK98954 standard; cDNA; 1533 BP.
XX
AC   ABK98954;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1533 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 66-67; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

  Query Match             95.9%;  Score 1533;  DB 6;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1533;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy         367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy         427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy         487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy         547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy         607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy         667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy         727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy         787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy         847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        967 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy       1027 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1086
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1146
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy       1147 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1266
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy       1267 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1326
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy       1327 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1386
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy       1387 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1446
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy       1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1506
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1566
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy       1567 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
                ||||||||||||||||||||||||||||||||
Db          33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
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RESULT 6
ABK98953
ID ABK98953 standard; cDNA; 1533 BP.
XX
AC ABK98953;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12-1533 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69307.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 63-64; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

```
  Query Match             95.9%;  Score 1533;  DB 6;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1533;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy         367 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy         427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy         487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy         547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy       1027 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020

Qy       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080

Qy       1147 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200

Qy       1267 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260

Qy       1327 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1386
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320

Qy       1387 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380

Qy       1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1506
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440

Qy       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1566
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500

Qy       1567 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
              |||||||||||||||||||||||||||||||||
Db       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
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RESULT 7
ADV34697/c
ID ADV34697 standard; DNA; 1533 BP.
XX

AC ADV34697;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain IL-12 complementary DNA, nFeIL-12 1533.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Felis catus.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 3; SEQ ID NO 45; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain IL-12 complementary DNA.
XX
SQ Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

Query Match 95.9%; Score 1533; DB 14; Length 1533;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        367 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        967 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy       1027 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy       1147 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy       1267 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy       1327 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1386
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy       1387 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy       1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1506
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1566
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy       1567 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
              |||||||||||||||||||||||||||||||||
Db         33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1


RESULT 8
ADV34695
ID   ADV34695 standard; cDNA; 1533 BP.
XX
AC   ADV34695;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1533
FT                   /*tag=  a
FT                   /product= "PFeIL-12 511 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34696.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 43; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

  Query Match             95.9%;  Score 1533;  DB 14;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1533;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
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Qy       187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
Db       121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy       247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
Db       181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy       307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
Db       241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy       367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
Db       301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy       427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
Db       361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy       487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
Db       421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy       547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
Db       481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy       607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
Db       541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy       667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
Db       601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy       727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
Db       661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy       787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
Db       721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy       847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
Db       781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy       907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
Db       841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy       967 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026
Db       901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy      1027 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1086
Db       961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020

Qy      1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1146
Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080

Qy      1147 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206
Db       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy      1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1266
Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200

Qy      1267 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1326
Db       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260

Qy      1327 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1386
Db       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320

Qy      1387 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1446
Db       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380

Qy      1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1506
Db       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440

Qy      1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1566
Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500

Qy      1567 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
Db       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
```

RESULT 9
ABK98965
ID ABK98965 standard; cDNA; 1599 BP.
XX
AC ABK98965;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12-1599 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69313.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 79-80; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid

```
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 452 A; 392 C; 383 G; 372 T; 0 U; 0 Other;

  Query Match             89.4%;  Score 1429.4;  DB 6;  Length 1599;
  Best Local Similarity   93.4%;  Pred. No. 0;
  Matches 1493;  Conservative    0;  Mismatches  106;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              |||||| |||||||||||||||| ||||| ||||||| |||||||||||  ||||||||
Db          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||||||||||| | ||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||||||||||| |||| |||||||||||||||||||| |||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||| | |||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||| |||||||||||||||||||| |||||||||||| ||||||||||||  ||
Db        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
                ||||  |||| |||||||| |||||||||||||||||||||||||||||| |||||||
Db        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              || |||||||||||||||||||||||||| |||||||||||| ||||||||| ||||||
Db        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              |||| |||||||||||||| |||||| |||||||||| |||||| |||||||||| ||||
Db        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||  |||||||||||||||||||| || |||||||||| ||||||||||||||||||||
Db        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              || |||||||||||||||||||||||||| |||||||||||| |||||||||
Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              |||||||| |||||||||| |||||||||||||| ||||| || ||||||||||||||
Db        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              |||||||||||||||||||||||||||||| | |||||| || |||||| |||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||||||| |||||||||||||| ||||||| ||||||||||||||||||||||||||||
Db        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              |||||||||||||||||||||||||||||||||| |||||||||||||| |||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020
              ||| |||||||||| ||||| ||||||||||||||||||||||||||||||||||||||
Db        961 AGCGACTGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020

Qy       1021 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 1080
              |||||||||||||||||||| |||||||| ||  | |||||||||||||| || || ||
Db       1021 ACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGA 1080

Qy       1081 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 1140
              ||| |||||||||||||||||||||||||||||||||||||||| || ||||||||||||
Db       1081 GCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCC 1140

Qy       1141 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1141 GAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200

Qy       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 1260
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACT 1260

Qy       1261 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 1320
              || |||||||||||||||  ||||| |||||||||||||  ||||||||||||||||
Db       1261 AACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGC 1320

Qy       1321 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 1380
              |||||||||||||||||||||||||||||| |||| |||||||||||||| ||||||| |||
Db       1321 ATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTA 1380

Qy       1381 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 1440
              |||||||| || |||||||||||||||||||||||||||||||||| |||||||||
Db       1381 ATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTG 1440

Qy       1441 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 1500
              |||||||||||||| |||||||||||||||||||||||| |||||| | ||||| |||
Db       1441 TTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCG 1500

Qy       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCG 1560

Qy       1561 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
              |||||||||||||||||||  |||  ||||  |||||
Db       1561 GTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1599


RESULT 10
ABK98966/c
ID   ABK98966 standard; cDNA; 1599 BP.
XX
AC   ABK98966;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1599 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
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XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 82-83; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 372 A; 383 C; 392 G; 452 T; 0 U; 0 Other;

  Query Match             89.4%;  Score 1429.4;  DB 6;  Length 1599;
  Best Local Similarity   93.4%;  Pred. No. 0;
  Matches 1493;  Conservative    0;  Mismatches  106;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||| |||||||||||||||||| ||||| ||||||| |||||||||| ||||||||
Db       1599 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 1540

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||||||||||| | ||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||||||||||||| |||| |||||||||||||||||||| |||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 1420

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||| |  |||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1419 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||| |||||||||||||||||||||| |||||||||||| |||||||||||   ||
Db       1359 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 1300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||  |||| |||||||| |||||||||||||||||||||||||||||| |||||||
Db       1299 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 1240

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              || |||||||||||||||||||||||| |||||||||||| |||||||| ||||||
Db       1179 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 1120

Qy        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              |||| |||||||||||||| |||||| |||||||||| |||||| |||||||||| ||||
Db       1119 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 1060

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||  |||||||||||||||||||| || |||||||||| ||||||||||||||||||||
Db        999 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 940

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              || |||||||||||||||||||||||||||||||| |||||||||||||| |||||||||
Db        939 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 880

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||| |||||||||| |||||||||||||| ||||| || ||||||||||||||
Db        879 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 820

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              |||||||||||||||||||||||||||||||| | |||||| || |||||| |||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 760

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||||||| |||||||||||||| ||||||| |||||||||||||||||||||||||||
Db        759 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              |||||||||||||||||||||||||||||||| |||||||||||||| |||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 640

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020
              ||| |||||||||| ||||| ||||||||||||||||||||||||||||||||||||||
Db        639 AGCGACTGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 580

Qy       1021 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 1080
              |||||||||||||||||| |||||||| ||  | ||||||||||||||| || || ||
Db        579 ACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGA 520

Qy       1081 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 1140
              ||| |||||||||||||||||||||||||||||||||||||||| || ||||||||||||
Db        519 GCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCC 460

Qy       1141 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        459 GAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTA 400

Qy       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 1260
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        399 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACT 340

Qy       1261 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 1320
              || |||||||||||||||  ||||| |||||||||||||  ||||||||||||||||
Db        339 AACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGC 280

Qy       1321 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 1380
              |||||||||||||||||||||||| |||| |||||||||||||| ||||||| |||
Db        279 ATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTA 220

Qy       1381 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 1440
              |||||||| || ||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        219 ATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTG 160

Qy       1441 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 1500
              |||||||||||||| |||||||||||||||||||||||| |||||| | ||||| |||
Db        159 TTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCG 100

Qy       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCG 40

Qy       1561 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
              |||||||||||||||||||  |||  ||||  |||||
Db          39 GTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1

RESULT 11
ADV34715/c
ID   ADV34715 standard; DNA; 1599 BP.
XX
AC   ADV34715;
XX
DT   24-FEB-2005  (first entry)
XX
```

DE Canine single chain IL-12 complementary DNA, nCaIL-12 1599.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Canis familiaris.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 4; SEQ ID NO 63; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the canine single chain IL-12 complementary DNA.
XX
SQ Sequence 1599 BP; 372 A; 383 C; 392 G; 452 T; 0 U; 0 Other;

Query Match 89.4%; Score 1429.4; DB 14; Length 1599;
Best Local Similarity 93.4%; Pred. No. 0;
Matches 1493; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||| |||||||||||||||||| ||||| ||||||| |||||||||||  ||||||||
Db       1599 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 1540

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||||||||||| | ||||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||||||||||||| |||| |||||||||||||||||||| |||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 1420

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||| |  |||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1419 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||| |||||||||||||||||||| |||||||||||| ||||||||||||  ||
Db       1359 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 1300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
                ||||  |||| |||||||| |||||||||||||||||||||||||||||||| |||||||
Db       1299 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 1240

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              || |||||||||||||||||||||||||| |||||||||||| ||||||||| ||||||
Db       1179 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 1120

Qy        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              |||| |||||||||||||| |||||| |||||||||| |||||| |||||||||| ||||
Db       1119 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 1060

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||  |||||||||||||||||||| || |||||||||| ||||||||||||||||||||
Db        999 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 940

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              || |||||||||||||||||||||||||||||| |||||||||||| ||||||||||
Db        939 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 880

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              |||||||| |||||||||| |||||||||||||| ||||| || ||||||||||||||
Db        879 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 820

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              |||||||||||||||||||||||||||||||| | |||||| || |||||| |||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 760

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||||||| |||||||||||||| ||||||| |||||||||||||||||||||||||||||
Db        759 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              |||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 640

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020
              ||| |||||||||| ||||| ||||||||||||||||||||||||||||||||||||||
Db        639 AGCGACTGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 580

Qy       1021 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 1080
              |||||||||||||||||| |||||||| ||  | |||||||||||||| || || ||
Db        579 ACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGA 520

Qy       1081 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 1140
              ||| |||||||||||||||||||||||||||||||||||||||||||| || ||||||||||
Db        519 GCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCC 460

Qy       1141 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        459 GAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTA 400

Qy       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 1260
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        399 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACT 340

Qy       1261 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 1320
              || |||||||||||||||| ||||| |||||||||||||| ||||||||||||||||||
Db        339 AACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGC 280

Qy       1321 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 1380
              |||||||||||||||||||||||||||||| |||| |||||||||||||| |||||||| |||
Db        279 ATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTA 220

Qy       1381 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 1440
              |||||||| || |||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        219 ATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTG 160

Qy       1441 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 1500
              |||||||||||||| |||||||||||||||||||||||||||||||| |||||| | ||||| |||
Db        159 TTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCG 100

Qy       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCG 40
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Qy       1561 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
              ||||||||||||||||||||  |||  ||||  |||||
Db         39 GTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1

RESULT 12
ADV34713
ID   ADV34713 standard; cDNA; 1599 BP.
XX
AC   ADV34713;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12 protein cDNA, nCaIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1599
FT                   /*tag=  a
FT                   /product= "PCaIL-12 533 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34714.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 61; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1599 BP; 452 A; 392 C; 383 G; 372 T; 0 U; 0 Other;

  Query Match             89.4%;  Score 1429.4;  DB 14;  Length 1599;
  Best Local Similarity   93.4%;  Pred. No. 0;
  Matches 1493;  Conservative    0;  Mismatches  106;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              |||||  |||||||||||||||||  |||||  |||||||  ||||||||||  ||||||||
Db          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||||||||||||||| |||| |||||||||||||||||| |||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||| | |||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||| |||||||||||||||||||| |||||||||||| |||||||||||  ||
Db        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||  |||| |||||||| |||||||||||||||||||||||||||||| |||||||
Db        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              || |||||||||||||||||||||||| |||||||||||| ||||||||| ||||||
Db        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              |||| |||||||||||||| |||||| |||||||||| |||||| |||||||||| ||||
Db        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||  |||||||||||||||||||| || |||||||||| ||||||||||||||||||||
Db        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              || |||||||||||||||||||||||||||||| |||||||||||||| ||||||||||
Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              |||||||| |||||||||| |||||||||||||| ||||| || ||||||||||||||
Db        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              |||||||||||||||||||||||||||||| | |||||| || |||||| |||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||||||| |||||||||||| |||||| |||||||||||||||||||||||||||||||
Db        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              |||||||||||||||||||||||||||||| |||||||||||||| ||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020
              ||| |||||||||| ||||| ||||||||||||||||||||||||||||||||||||||
Db        961 AGCGACTGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020

Qy       1021 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 1080
              |||||||||||||||||||| |||||||| ||  | |||||||||||||| || ||
Db       1021 ACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGA 1080

Qy       1081 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 1140
              ||| |||||||||||||||||||||||||||||||||||||| || ||||||||||||
Db       1081 GCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCC 1140

Qy       1141 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1141 GAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200

Qy       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 1260
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACT 1260

Qy       1261 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 1320
                || ||||||||||||||||  ||||| ||||||||||||||  ||||||||||||||||
Db       1261 AACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGC 1320

Qy       1321 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 1380
                |||||||||||||||||||||||||| |||| |||||||||||||| |||||||| |||
Db       1321 ATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTA 1380

Qy       1381 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 1440
                |||||||| || |||||||||||||||||||||||||||||||||||||||| |||||||||
Db       1381 ATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTG 1440

Qy       1441 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 1500
                |||||||||||||||| |||||||||||||||||||||||| |||||| | ||||| |||
Db       1441 TTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCG 1500

Qy       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 1560
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCG 1560

Qy       1561 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
                ||||||||||||||||||  |||  ||||  |||||
Db       1561 GTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1599


RESULT 13
ABK98967
ID   ABK98967 standard; cDNA; 1533 BP.
XX
AC   ABK98967;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1533 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69314.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 83-85; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 446 A; 368 C; 369 G; 350 T; 0 U; 0 Other;

  Query Match             85.9%;  Score 1373;  DB 6;  Length 1533;
  Best Local Similarity   93.5%;  Pred. No. 0;
  Matches 1433;  Conservative    0;  Mismatches  100;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              |||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              |||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              | |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              | |||||||||||||||||||| |||||||||||| |||||||||||   ||  ||||
Db        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||  |||||||| ||||||||||||||||||||||||||||||| ||||||||||||
Db        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||| |||
Db        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              |||||||||||||||||||| |||||||||||| ||||||||| |||||||||| |
Db        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420

Qy        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||| |||||| |||||||||| |||||| |||||||||| ||||||||||
Db        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              |||||||||||||||||| || |||||||||| |||||||||||||||||||||| |||
Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              |||||||||||||||||||||||| |||||||||||| ||||||||||  ||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              || |||||||||| |||||||||||| ||||| || |||||||||||||| ||||||
Db        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              |||||||||||||||||||||||| | |||||| || |||||| ||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              || |||||||||||||| ||||||| |||||||||||||||||||||||||||||||||
Db        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              |||||||||||||||||||||||||| |||||||||||||||| |||||||||||| ||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
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Qy        967 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026
              ||||||||| ||||| |||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy       1027 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1086
              |||||||||||||| |||||||| ||  | ||||||||||||||| || || ||||| ||
Db        961 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 1020

Qy       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1146
              |||||||||||||||||||||||||||||||||| || ||||||||||||||||||||
Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 1080

Qy       1147 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       1081 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1266
              |||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||
Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1200

Qy       1267 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1326
              |||||||||||||  ||||| ||||||||||||||  |||||||||||||||| ||||||
Db       1201 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1260

Qy       1327 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1386
              |||||||||||||||||||| |||| |||||||||||||| |||||||| |||||||||
Db       1261 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1320

Qy       1387 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1446
              || || ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db       1321 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 1380

Qy       1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1506
              |||||||| |||||||||||||||||||||||| |||||| | ||||| |||||||||
Db       1381 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1440

Qy       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1566
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1500

Qy       1567 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
              |||||||||||||  |||  ||||  |||||
Db       1501 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1533


RESULT 14
ABK98968/c
ID   ABK98968 standard; cDNA; 1533 BP.
XX
AC   ABK98968;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1533 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
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XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 86-87; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

  Query Match             85.9%;  Score 1373;  DB 6;  Length 1533;
  Best Local Similarity   93.5%;  Pred. No. 0;
  Matches 1433;  Conservative    0;  Mismatches  100;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              |||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              |||||||||||||||||||||||||| |||| |||||||||||||||||| |||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1414

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              |  |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       1413 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              | ||||||||||||||||||||| |||||||||||| |||||||||||||  ||  ||||
Db       1353 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1294

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||  |||||||| ||||||||||||||||||||||||||||||| ||||||||||||
Db       1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||| |||
Db       1233 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              |||||||||||||||||||| |||||||||||| ||||||||| |||||||||| |
Db       1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||| |||||| |||||||||| |||||| |||||||||| ||||||||||
Db       1113 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1054

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 994

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              |||||||||||||||||| || |||||||||| |||||||||||||||||||| |||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              |||||||||||||||||||||||||| |||||||||||| |||||||||  ||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 874
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Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              || |||||||||| |||||||||||||| ||||| || |||||||||||||| ||||||
Db        873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              |||||||||||||||||||||||||| | |||||| || |||||| ||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              || |||||||||||| ||||||| ||||||||||||||||||||||||||||||||||
Db        753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              |||||||||||||||||||||||||| ||||||||||||||| |||||||||||| ||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 634

Qy        967 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026
              |||||||| ||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy       1027 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1086
              ||||||||||||| |||||||| ||  | |||||||||||||| || || ||||| ||
Db        573 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 514

Qy       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1146
              |||||||||||||||||||||||||||||||||||||||| || ||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 454

Qy       1147 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1266
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 334

Qy       1267 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1326
              |||||||||||||| ||||| |||||||||||||| |||||||||||||||| ||||||
Db        333 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 274

Qy       1327 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1386
              |||||||||||||||||||| |||| |||||||||||||| |||||||| |||||||||
Db        273 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 214

Qy       1387 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1446
              || || |||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        213 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 154

Qy       1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1506
              ||||||||| |||||||||||||||||||||||||||||||| |||||| | ||||| |||||||||
Db        153 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 94

Qy       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1566
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 34

Qy       1567 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
              |||||||||||||||  |||  ||||  |||||
Db         33 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1


RESULT 15
ADV34718/c
ID   ADV34718 standard; DNA; 1533 BP.
XX
AC   ADV34718;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12 complementary DNA, nCaIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 68; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 complementary DNA.
XX
SQ   Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

  Query Match           85.9%;  Score 1373;  DB 14;  Length 1533;
  Best Local Similarity  93.5%;  Pred. No. 0;
  Matches 1433;  Conservative    0;  Mismatches  100;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              |||||||||||||||||| | |||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              |||||||||||||||||||||| |||| |||||||||||||||||| ||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1414

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              | |||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1413 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              | |||||||||||||||||| |||||||||||| |||||||||||  ||  ||||
Db       1353 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1294

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              |||| |||||||| ||||||||||||||||||||||||||||||| ||||||||||||
Db       1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              |||||||||||||||||| |||||||||||||||||||||||||||||||| |||
Db       1233 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              |||||||||||||||||||||| |||||||||||| ||||||||| |||||||||| |
Db       1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||| |||||| |||||||||| |||||| |||||||||| ||||||||||
Db       1113 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1054

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
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Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 994

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              |||||||||||||||||||| || |||||||||| |||||||||||||||||||| |||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              |||||||||||||||||||||||||| |||||||||||| ||||||||| ||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 874

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              || |||||||||| |||||||||||||| ||||| || |||||||||||||| ||||||
Db        873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              |||||||||||||||||||||||||| | |||||| || |||||| ||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              || |||||||||||||| ||||||| ||||||||||||||||||||||||||||||||||
Db        753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              |||||||||||||||||||||||||| |||||||||||||| |||||||||||| ||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 634

Qy        967 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026
              |||||||| ||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy       1027 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1086
              |||||||||||||| |||||||| ||  | ||||||||||||||| || || ||||| ||
Db        573 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 514

Qy       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1146
              |||||||||||||||||||||||||||||||||||| || ||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 454

Qy       1147 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1266
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||| |||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 334

Qy       1267 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1326
              |||||||||||||  ||||| |||||||||||||  |||||||||||||| ||||||
Db        333 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 274

Qy       1327 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1386
              |||||||||||||||||||| |||| |||||||||||||| |||||||| |||||||||
Db        273 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 214

Qy       1387 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1446
              || || ||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        213 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 154

Qy       1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1506
              |||||||| |||||||||||||||||||||| |||||| | ||||| |||||||||
Db        153 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 94

Qy       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1566
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db          93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 34

Qy       1567 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
              |||||||||||||||  |||  ||||  |||||
Db          33 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1


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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	578.4	36.2	756	5	CK130264	CK130264 AGENCOURT
	2	576.4	36.0	735	5	CD559605	CD559605 AGENCOURT
	3	566.8	35.4	747	5	CD559607	CD559607 AGENCOURT
	4	565.4	35.4	772	5	CD559604	CD559604 AGENCOURT
	5	509.6	31.9	745	5	CD559602	CD559602 AGENCOURT
	6	508.4	31.8	1839	6	AK162981	AK162981 Mus muscu
c	7	507.6	31.7	785	5	CD559448	CD559448 AGENCOURT
c	8	506.4	31.7	772	5	CD559450	CD559450 AGENCOURT
c	9	501.4	31.4	736	5	CD559453	CD559453 AGENCOURT
c	10	499.8	31.3	762	5	CD559451	CD559451 AGENCOURT
	11	497.4	31.1	2908	6	AK155593	AK155593 Mus muscu
	12	495.4	31.0	762	14	DQ033872	DQ033872 Homo sapi
	13	490.6	30.7	762	14	DQ033873	DQ033873 Pan trogl
c	14	477.4	29.9	754	5	CD559452	CD559452 AGENCOURT
c	15	471.8	29.5	766	5	CD559449	CD559449 AGENCOURT
c	16	436	27.3	725	5	CD559454	CD559454 AGENCOURT
	17	415.6	26.0	724	5	CD559603	CD559603 AGENCOURT
	18	409.4	25.6	935	4	CD013914	CD013914 90138124
	19	408.8	25.6	1136	4	CD013915	CD013915 90138132
	20	400	25.0	1042	5	CD559606	CD559606 AGENCOURT
	21	353.8	22.1	649	5	CJ134671	CJ134671 CJ134671
	22	331.2	20.7	863	4	CD013916	CD013916 90138296
	23	264.2	16.5	475	7	BF704417	BF704417 MI-P-E6-a
	24	258	16.1	1938	6	BC035571	BC035571 Homo sapi
	25	248.2	15.5	417	8	CO949904	CO949904 UMC-pd12c
	26	227.6	14.2	387	4	BY167742	BY167742 BY167742
	27	227.4	14.2	812	2	BG702253	BG702253 602683459
	28	218.8	13.7	423	4	BY218447	BY218447 BY218447
	29	218	13.6	589	1	AI050362	AI050362 ub30a07.r
	30	215.8	13.5	432	4	BY154173	BY154173 BY154173
	31	215.8	13.5	563	3	BU698113	BU698113 LL2in1206
c	32	215	13.4	1099	2	BI523344	BI523344 603175938
	33	208.4	13.0	375	4	BY222535	BY222535 BY222535
c	34	207.6	13.0	778	1	AJ820622	AJ820622 AJ820622
	35	205.8	12.9	346	4	BY164658	BY164658 BY164658
	36	201.2	12.6	355	4	BY221814	BY221814 BY221814
	37	200	12.5	373	7	BF552757	BF552757 UI-R-C0-i
	38	198.2	12.4	700	12	CE093997	CE093997 tigr-gss-
	39	190	11.9	561	3	BU699383	BU699383 LL2in1157
	40	180.4	11.3	535	11	AZ441303	AZ441303 1M0232M24
	41	180.2	11.3	252	10	DV799576	DV799576 est_t_tru
	42	175.2	11.0	412	4	CB801533	CB801533 AMGNNUC:S
c	43	173.8	10.9	777	4	CB168830	CB168830 CWI602769
	44	173	10.8	427	10	DT930939	DT930939 S13.1784
c	45	169.8	10.6	569	11	AZ853726	AZ853726 2M0157M01

ALIGNMENTS

RESULT 1
CK130264
LOCUS CK130264 756 bp mRNA linear EST 02-DEC-2003
DEFINITION AGENCOURT_14496566 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971871 5', mRNA sequence.
ACCESSION CK130264
VERSION CK130264.1 GI:38622200
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 756)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: h column: 02
High quality sequence start: 5
High quality sequence stop: 731.
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971871"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:

loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 36.2%; Score 578.4; DB 5; Length 756;
Best Local Similarity 88.3%; Pred. No. 1.6e-158;
Matches 640; Conservative 0; Mismatches 82; Indels 3; Gaps 1;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              |||  ||  |||||||||||||||| | ||| ||||||||||||| |||||| ||||||||
Db         34 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 93

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||||| ||||| | |||||||| ||||| ||||| ||| | || |||
Db         94 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 153

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||| |||||||||||||||||||||||  | || ||||||||||||  |||||||||
Db        154 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 213

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||  |||||||||||||| ||| |||||||||| ||||| ||||||||||||||||||
Db        214 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 273

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              || |||| |||||||||||||||| |||||||| |||||||||||||||||| |||||||||
Db        274 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 333

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              |||| ||| | ||||||||||||||||||||||||||||||||||| |||| ||| |||
Db        334 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 393

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||| |||||||||||| |||||||| ||| ||||| ||||||||||||||||||||
Db        394 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 453

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              |||||||||||||||||| |||||||||| ||||||| ||||| ||||||||||||||||
Db        454 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 513

Qy        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||| |||||||||||| |||||| || ||||| || |||||||| |||||||   |||
Db        514 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 573

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||| |||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||
Db        574 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 630

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              || ||||| |||||||| || |||||||| ||| ||||||| ||  ||||||||||||||
Db        631 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 690

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              || ||||||||||||||||||||||||||||||||||||||||| |||| ||||||||||
Db        691 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCNAACCTGACCCACCCAAG 750

Qy        721 AACCT 725
              ||| |
Db        751 AACTT 755
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RESULT 2
CD559605

```
LOCUS       CD559605                735 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496534 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971870 5', mRNA sequence.
ACCESSION   CD559605
VERSION     CD559605.2  GI:38558937
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 735)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585673.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 01
            High quality sequence stop: 709.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971870"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN
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Query Match 36.0%; Score 576.4; DB 5; Length 735;
Best Local Similarity 88.4%; Pred. No. 6.1e-158;
Matches 638; Conservative 0; Mismatches 81; Indels 3; Gaps 1;

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Db         17 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 76

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||||| ||||| | |||||||| ||||| ||||| ||| | || |||
Db         77 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 136
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Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||| |||||||||||||||||||||||||  | || ||||||||||||||  |||||||||
Db        137 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 196

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||  |||||||||||||| ||| |||||||||| ||||| ||||||||||||||||||
Db        197 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 256

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              || |||| ||||||||||||||| |||||||| |||||||||||||||| |||||||||
Db        257 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 316

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
               |||| ||| | ||||||||||||||||||||||||||||||||||| |||| ||| |||
Db        317 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 376

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Db        377 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 436

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db        437 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAGAGCAGCAGA 496

Qy        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||| |||||||||||||| |||||| || ||||| || |||||||| |||||||  |||
Db        497 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 556

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||| |||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||
Db        557 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 613

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              || ||||| |||||||| || |||||||| ||| ||||||| ||  ||||||||||||||
Db        614 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 673

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              || ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        674 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 733

Qy        721 AA 722
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Db        734 AA 735
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RESULT 3
CD559607

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LOCUS       CD559607                747 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14497061 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971868 5', mRNA sequence.
ACCESSION   CD559607
VERSION     CD559607.2  GI:38558941
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 747)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585675.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: g  column: 11
            High quality sequence start: 14
            High quality sequence stop: 671.
FEATURES              Location/Qualifiers
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                      /clone="IMAGE:6971868"
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                      /lab_host="DH5A (T1 phage-resistant)"
                      /clone_lib="NIH_MGC_195"
                      /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                      loxP-HindIII; Clones from this library have been
                      PCR-amplified using gene-specific primers to contain the
                      complete open reading frame (based on known gene sequences
                      available from NCBI's RefSeq). Template for PCR is cDNA
                      derived from either pooled cytoplasmic polyA RNA from 30
                      cells lines or pooled total RNA from 10 different tissues
                      (from BD Biosciences/Clontech and Washington University).
                      PCR products are directionally cloned into the loxP sites
                      of the pDNR-Dual vector. Library constructed by Dr.
                      Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                      Expression Laboratory, Research Technology Program, SAIC
                      Frederick, NCI-Frederick, Frederick, MD 21702). For
                      information on which gene each clone represents, please
                      visit our anonymous ftp site at
                      ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                      a Note: this is a NIH_MGC Library."
ORIGIN
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Query Match 35.4%; Score 566.8; DB 5; Length 747;
Best Local Similarity 88.1%; Pred. No. 4.2e-155;
Matches 629; Conservative 0; Mismatches 82; Indels 3; Gaps 1;

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Qy          8 CTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCA 67
              | |||||||||||||| | ||| |||||||||||||| |||||| |||||||| ||||||
Db         36 CCCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTCGTGGCCA 95

Qy         68 TATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCG 127
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Db         96 TATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCTG 155

Qy        128 GAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCTG 187
              |||||||||||||||||||||  | || ||||||||||||  ||||||||||||  |
Db        156 GAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTGG 215

Qy        188 ACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTG 247
              |||||||||||| ||| |||||||||| ||||| |||||||||||||||||||| ||||
Db        216 ACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTTG 275

Qy        248 CAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCC 307
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Db        276 GAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTGC 335

Qy        308 TGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAAT 367
              || | |||||||||||||||||||||||||||||||||||| |||| ||| |||||||||
Db        336 TGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAAC 395

Qy        368 CCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCT 427
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Db        396 CCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCT 455

Qy        428 GGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCT 487
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Qy        488 CTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGG 547
              |||||||||||| |||||| || ||||| || |||||||| |||||||  ||||||| ||
Db        516 CTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGG 575
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Qy        548 ACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTG 607
              |||||| ||| |||    ||||| |||||||||| ||||||| |||||||||||| ||||
Db        576 ACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTG 632

Qy        608 CCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAA 667
              | |||||||| || |||||||| ||| |||||||     |||||||||||| |||| ||||
Db        633 CTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATTGCGTTCACAAGCTCCAGTATGAAA 692

Qy        668 ACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGA 721
              |||||||| |||||||||||||||||||||||||||||||| |||||||||| |
Db        693 ACTACACCCGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAAA 746
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RESULT 4
CD559604

```
LOCUS       CD559604                772 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496598 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971872 5', mRNA sequence.
ACCESSION   CD559604
VERSION     CD559604.2  GI:38558934
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 772)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585672.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 03
            High quality sequence start: 13
            High quality sequence stop: 750.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971872"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
```

ORIGIN

```
  Query Match             35.4%;  Score 565.4;  DB 5;  Length 772;
  Best Local Similarity   87.6%;  Pred. No. 1.1e-154;
  Matches  630;  Conservative    0;  Mismatches   86;  Indels    3;  Gaps    1;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              |||  ||  |||||||||||||||| | ||| |||||||||||||| |||||| ||||||||
Db         38 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 97

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||| ||||| | |||||||| ||||| ||||| ||| | || |||
Db         98 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 157

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||| |||||||||||||||||||||  | || |||||||||||||  |||||||||
Db        158 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 217

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||  |||||||||||||| |||||||||||| ||||| ||||||||||||||||||||
Db        218 ACCTTGGACCAGAGCAGTGAGGTCCTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 277

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              || |||| |||||||||||||| |||||||| |||||||||||||||| |||||||||
Db        278 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 337

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||  ||| | |||||||||||||||||||||||||||||||||| |||| ||| |||
Db        338 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 397

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||| |||||||||||| |||||||| ||| ||||| ||||||||||||||||||||
Db        398 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 457

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              |||||||||||||||| |||||||| ||||||| ||||| ||||||||||||||||||
Db        458 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 517

Qy        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||| |||||||||||| |||||| || ||||| || |||||||| |||||||  |||
Db        518 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 577

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||| |||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||
Db        578 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 634

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              || ||||| |||||||| || |||||||| ||| ||||||| ||  ||||||||||||||
Db        635 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 694

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAA 719
              || |||||||||||||||||||||||||||||||||||||||| | |  |   || ||
Db        695 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAACCTGACCAACCCAAA 753
```

RESULT 5
CD559602

```
LOCUS       CD559602                745 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496684 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971874 5', mRNA sequence.
ACCESSION   CD559602
VERSION     CD559602.2  GI:38558930
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 745)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585670.
```

```
           Contact: Daniela S. Gerhard, Ph.D.
           Office of Cancer Genomics
           National Cancer Institute / NIH
           Bldg. 31 Rm10A07 Bethesda, MD 20892
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: IRBK2  row: h  column: 05
           High quality sequence start: 2
           High quality sequence stop: 644.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /clone="IMAGE:6971874"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match           31.9%;  Score 509.6;  DB 5;  Length 745;
  Best Local Similarity  86.3%;  Pred. No. 3.2e-138;
  Matches  587;  Conservative    0;  Mismatches   89;  Indels    4;  Gaps    2;

Qy          8 CTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCA 67
              | |||||||||||||| | ||| |||||||||||| |||||| |||||||| ||||||
Db         13 CCCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTCGTGGCCA 72

Qy         68 TATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCG 127
              |||||||||| ||||| | |||||||| ||||| ||||| ||| | || ||||||||| |
Db         73 TATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCTG 132

Qy        128 GAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCTG 187
              |||||||||||||||||||||  | || ||||||||||||  ||||||||||||  |
Db        133 GAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTGG 192

Qy        188 ACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTG 247
              |||||||||||||| ||| |||||||||| ||||| ||||||||||||||||||| ||||
Db        193 ACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTTG 252

Qy        248 CAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCC 307
              |||||||||||||||| |||||||| |||||||||||||||| ||||||||| |||| |
Db        253 GAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTGC 312

Qy        308 TGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAAT 367
              || | ||||||||||||||||||||||||||||||||||| |||| ||| |||||||||
Db        313 TGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAAC 372

Qy        368 CCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCT 427
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Db        373 CCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCT 432

Qy        428 GGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCT 487
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Db        433 GGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTT 492

Qy        488 CTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGG 547
              |||||||||||| |||||| || ||||| || |||||||| |||||||  ||||||| ||
Db        493 CTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGG 552

Qy        548 ACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTG 607
              |||||| ||| |||     ||||| |||||||||| ||||||| |||||||||||| ||||
Db        553 ACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTG 609

Qy        608 CCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAA 667
              | |||||||| || |||||||| ||| ||||||| ||    |||||||||| ||   |||
Db        610 CTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGC-CGTCACAAGCTCATGTTGAAAA 668

Qy        668 ACTACACCAGCAGCTTCTTC 687
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Db        669 TACACCACGGCTTCTTTCTC 688


RESULT 6
AK162981
LOCUS       AK162981               1839 bp    mRNA    linear   HTC 21-SEP-2005
DEFINITION  Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched
            library, clone:A430014H12 product:interleukin 12b, full insert
            sequence.
ACCESSION   AK162981
VERSION     AK162981.1  GI:74188061
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
            Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
            Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
            Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
            Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
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Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

CONSRTM RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409 (6821), 685-690 (2001)

PUBMED 11217851

REFERENCE 5

AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420 (6915), 563-573 (2002)

PUBMED 12466851

REFERENCE 6

AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE The transcriptional landscape of the mammalian genome

JOURNAL Science 309 (5740), 1559-1563 (2005)

PUBMED 16141072

REFERENCE 7

AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.

CONSRTM RIKEN Genome Exploration Research Group

TITLE Antisense transcription in the mammalian transcriptome

JOURNAL Science 309 (5740), 1564-1566 (2005)

PUBMED 16141073

REFERENCE 8 (bases 1 to 1839)

AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

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ORIGIN

Query Match 31.8%; Score 508.4; DB 6; Length 1839;
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Matches 732; Conservative 0; Mismatches 241; Indels 39; Gaps 4;

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RESULT 7
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LOCUS CD559448 785 bp mRNA linear EST 19-NOV-2003
DEFINITION AGENCOURT_14496712 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971874 5', mRNA sequence.
ACCESSION CD559448
VERSION CD559448.2 GI:38453466
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 785)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585516.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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ORIGIN

Query Match 31.7%; Score 507.6; DB 5; Length 785;
Best Local Similarity 85.7%; Pred. No. 1.3e-137;
Matches 588; Conservative 0; Mismatches 94; Indels 4; Gaps 2;

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RESULT 8
CD559450/c
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DEFINITION  AGENCOURT_14496612 NIH_MGC_195 Homo sapiens cDNA clone
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ACCESSION   CD559450
VERSION     CD559450.2  GI:38453469
KEYWORDS    EST.
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  ORGANISM  Homo sapiens
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            Hominidae; Homo.
REFERENCE   1  (bases 1 to 772)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585518.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
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                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match           31.7%;  Score 506.4;  DB 5;  Length 772;
  Best Local Similarity  86.5%;  Pred. No. 2.8e-137;
  Matches  582;  Conservative    0;  Mismatches   87;  Indels    4;  Gaps    2;

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RESULT 9
CD559453/c
LOCUS       CD559453                736 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14497154 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971869 5', mRNA sequence.
ACCESSION   CD559453
VERSION     CD559453.2  GI:38453475
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 736)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585521.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
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                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN
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  Best Local Similarity  87.1%;  Pred. No. 8.4e-136;
  Matches  574;  Conservative    0;  Mismatches   81;  Indels    4;  Gaps    2;

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Qy        509 GTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGT 568
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Db        553 GCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAACAAGGAGTAT---GAGT 497

Qy        569 ACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTG 628
              || |||||||||| ||||||| |||||||||||| ||||| |||||||| || |||||||
Db        496 ACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCTGAGGAGAGTCTGCCCATTG 437

Qy        629 AAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCA 688
              | ||| ||||||| ||  ||||||||||||||| ||||||||||||||||||||||||||
Db        436 AGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCA 377

Qy        689 TCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATT 748
              |||||||||||||||||| |||||||||||||| |||| ||||||||||||||| ||||
Db        376 TCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATT 317

Qy        749 CTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACT 808
              ||||||| ||||| || |||||||| |||||||||||||||| || ||||||||||||
Db        316 CTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACATTCCTACT 257

Qy        809 TCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGAC 868
              ||||| | |||||  |||| |||||||||||||||| ||| ||||||||||||| |||
Db        256 TCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGCAAGAGAGAAAAGAAAGATAGAG 197

Qy        869 TCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGC 928
              ||| |  |||||||||||||||| |||| | |||| ||| ||||||  || ||||||
Db        196 TCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGCAAAAATGCCAGCATTAGCGTGC 137

Qy        929 AAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987
              |||   |||||||||||||||||| |||||| | |||||||| ||| ||||||||
Db        136 GGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAATGGGCATCTGTGCCCTGCAGT 78


RESULT 10
CD559451/c
LOCUS       CD559451                762 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496580 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971871 5', mRNA sequence.
ACCESSION   CD559451
VERSION     CD559451.2  GI:38453471
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585519.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
```

```
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: IRBK2  row: h  column: 02
           High quality sequence start: 38
           High quality sequence stop: 761.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971871"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match            31.3%;  Score 499.8;  DB 5;  Length 762;
  Best Local Similarity  86.9%;  Pred. No. 2.5e-135;
  Matches  573;  Conservative    0;  Mismatches   82;  Indels    4;  Gaps    2;

Qy        329 GAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAA 388
              | | ||||||||||||||| |||| ||| ||||||||| |||||||||||| || |||||
Db        753 GGAATTGGTCCACTGATAT-TTAAAGGACCAGAAAGAACCCAAAAATAAGACCTCTCTAA 695

Qy        389 AATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTA 448
              ||| ||||| ||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        694 GATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGACAATCAGTA 635

Qy        449 CCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTT 508
              | ||||||| ||||| |||||||||||||||||||| |||||||||||| |||||| |
Db        634 CTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGT 575

Qy        509 GTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGT 568
              | ||||| || |||||||| |||||||  ||||||| |||||||| ||| |||    |||
Db        574 GCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAACAAGGAGTAT---GAGT 518

Qy        569 ACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTG 628
              || |||||||||| ||||||| |||||||||||| ||||| |||||||| || |||||||
Db        517 ACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCTGAGGAGAGTCTGCCCATTG 458

Qy        629 AAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCA 688
              | ||| ||||||| ||  |||||||||||||||| ||||||||||||||||||||||||
Db        457 AGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCA 398

Qy        689 TCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATT 748
              |||||||||||||||||| |||||||||||||| |||| ||||||||||||| ||||
Db        397 TCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATT 338

Qy        749 CTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACT 808
              ||||||| ||||| || |||||||| |||||||||||||||| || ||||||||||||
Db        337 CTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACATTCCTACT 278

Qy        809 TCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGAC 868
              ||||| | ||||| |||| |||||||||||||||| ||| |||||||||||||| |||
Db        277 TCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGCAAGAGAGAAAAGAAAGATAGAG 218

Qy        869 TCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGC 928
              ||| | |||||||||||||||| |||| | |||| ||| |||||| || ||||||
Db        217 TCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGCAAAAATGCCAGCATTAGCGTGC 158

Qy        929 AAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987
                |||  ||||||||||||||||||||| |||||| | |||||||| ||| ||||||||
Db        157 GGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAATGGGCATCTGTGCCCTGCAGT 99


RESULT 11
AK155593
LOCUS       AK155593               2908 bp    mRNA    linear   HTC 21-SEP-2005
DEFINITION  Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN
            full-length enriched library, clone:F730005O03 product:interleukin
            12b, full insert sequence.
ACCESSION   AK155593
VERSION     AK155593.1  GI:74212721
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
            Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
            Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
            Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
            Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
            Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
            Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
            Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
            Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  CONSRTM   RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium
```

TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
PUBMED 11217851
REFERENCE 5
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
CONSRTM FANTOM Consortium
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420 (6915), 563-573 (2002)
PUBMED 12466851
REFERENCE 6
AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.
CONSRTM FANTOM Consortium
TITLE The transcriptional landscape of the mammalian genome
JOURNAL Science 309 (5740), 1559-1563 (2005)
PUBMED 16141072
REFERENCE 7
AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.
CONSRTM RIKEN Genome Exploration Research Group
TITLE Antisense transcription in the mammalian transcriptome
JOURNAL Science 309 (5740), 1564-1566 (2005)
PUBMED 16141073
REFERENCE 8 (bases 1 to 2908)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers
source 1. .2908
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:F730005O03"
/db_xref="taxon:10090"
/clone="F730005O03"
/cell_type="B6-derived CD11 +ve dendritic cells"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
misc_feature 1. .2908
/note="interleukin 12b (MGD|MGI:96540 GB|M86671, evidence: BLASTN, 99%, match=1807)
putative"

ORIGIN

Query Match 31.1%; Score 497.4; DB 6; Length 2908;
Best Local Similarity 72.3%; Pred. No. 2.2e-134;
Matches 732; Conservative 0; Mismatches 241; Indels 40; Gaps 5;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              |||  ||||||| || |   |||| ||||| || || | ||||||||||   |||| |||
Db        461 ATGTGTCCTCAGAAGCTAACCATCTCCTGGTTTGCCATCGTTTTGCTGGTGTCTCCACTC 520

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||| ||||| ||||||||| |||||||||||||||||| ||||||||   || |||
Db        521 ATGGCCATGTGGGAGCTGGAGAAAGACGTTTATGTTGTAGAGGTGGACTGGACTCCCGAT 580

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
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Db        581 GCCCCTGGAGAAACAGTGAACCTCACCTGTGACACGCCTGAAGAAGATGACATCACCTGG 640

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              ||||| ||||||||    || |||| |||||||||| || || |||||||||   ||||||
Db        641 ACCTCAGACCAGAGACATGGAGTCATAGGCTCTGGAAAGACCCTGACCATCACTGTCAAA 700

Qy        241 GAATTTGCAGATGCTGGCCAG-TATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTC 299
              || |||  ||||||||||||| || ||||| || ||||||||||||  ||||||||| ||
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Qy        360 GAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTT 419
               ||| | | |||||| |||| || || || ||||| |||   ||||| || ||||| ||
Db        813 -AAAAATTTCAAAAACAAGACTTTCCTGAAGTGTGAAGCACCAAATTACTCCGGACGGTT 871

Qy        420 CACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAG 479
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Db        872 CACGTGCTCATGGCTGGTGCAAAGAAACATGGACTTGAAGTTCAACATCAAGAGCAGTAG 931

Qy        480 AGGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGT 539
                | ||| ||||| | |  |  ||||| ||||||   ||| | || || ||||||||||
Db        932 CAGTTCCCCTGACTCTCGGGCAGTGACATGTGGAATGGCGTCTCTGTCTGCAGAGAAGGT 991

Qy        540 CAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTG 599
              || | ||||| | ||||| ||| |||||||  |||||   || |||||||     ||||
Db        992 CACACTGGACCAAAGGGACTATGAGAAGTATTCAGTGTCCTGCCAGGAGGATGTCACCTG 1051

Qy        600 CCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAA 659
              |||  ||||||||||| ||| |||||||| | | | |||| ||    ||  ||   ||
Db       1052 CCCAACTGCCGAGGAGACCCTGCCCATTGAACTGGCGTTGGAAGCACGGCAGCAGAATAA 1111

Qy        660 GTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAA 719
              || || ||||||| || |||||||||||||||||||||||||||| ||||| |||||
Db       1112 ATATGAGAACTACAGCACCAGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAA 1171

Qy        720 GAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCC 779
              |||| ||||  |||||| || || || ||    || ||||| || |||||||| |||||
Db       1172 GAACTTGCAGATGAAGCCTTTGAAGAACTC---ACAGGTGGAGGTCAGCTGGGAGTACCC 1228

Qy        780 TGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGG 839
              |||| |||||||||| || |||||||||||||| | |  ||    || |   ||||| |
Db       1229 TGACTCCTGGAGCACTCCCCATTCCTACTTCTCCCTCAAGTTCTTTGTTCGAATCCAGCG 1288

Qy        840 CAAGAACAACA----------------------GAGAAAAGAAAGACAGACTCTCCGT 875
              ||||||  | |                      |  |  ||||||      ||  |||
Db       1289 CAAGAAAGAAAAGATGAAGGAGACAGAGGAGGGGTGTAACCAGAAAGGTGCGTTCCTCGT 1348

Qy        876 GGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAG 935
              || ||||| ||  || | |||    ||   ||| |  |  ||  || ||||||||||
Db       1349 AGAGAAGACATCTACCGAAGTCCAATG---CAAAGGCGGGAATGTCTGCGTGCAAGCTCA 1405

Qy        936 AGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGTG 988
              || ||||| || |  || || || ||||| |||||||  ||  ||||||| |
Db       1406 GGATCGCTATTACAATTCCTCATGCAGCAAGTGGGCATGTGTTCCCTGCAGGG 1458


RESULT 12
DQ033872
LOCUS       DQ033872               762 bp    DNA     linear   GSS 02-JUN-2005
DEFINITION  Homo sapiens IL12A gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   DQ033872
VERSION     DQ033872.1  GI:66885081
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     A Scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
  JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
   PUBMED   15869325
REFERENCE   2  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.  Translation starts at the beginning of
            alignment.
FEATURES             Location/Qualifiers
     source          1. .762
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="3"
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                     /gene="IL12A"
                     /locus_tag="HC3464"
ORIGIN

  Query Match           31.0%;  Score 495.4;  DB 14;  Length 762;
  Best Local Similarity   89.7%;  Pred. No. 5e-134;
  Matches  532;  Conservative    0;  Mismatches   61;  Indels    0;  Gaps    0;

Qy       1007 CTAGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCC 1066
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Db        167 CCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCC 226

Qy       1067 AAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTT 1126
              ||| ||||||| | ||| ||||||||| ||| ||||||||||||||||||||||||||||
Db        227 AAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTTT 286

Qy       1127 ACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAG 1186
              || | |||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        287 ACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAG 346

Qy       1187 TGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGA 1246
              |||||||||| |||||| |||||||||||||| ||||||||||||||    ||||||||||
Db        347 TGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGAGAGA 406

Qy       1247 TCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCC 1306
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Db        407 CCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATGGCCC 466

Qy       1307 TGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGA 1366
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Db        467 TGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGA 526

Qy       1367 ATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAG 1426
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Db        527 ATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCAG 586

Qy       1427 CTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCT 1486
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Db        587 TTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCT 646

Qy       1487 CCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTT 1546
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Db        647 CCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTT 706

Qy       1547 TCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
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Db        707 TCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTCC 759
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RESULT 13
DQ033873
LOCUS       DQ033873               762 bp    DNA     linear   GSS 02-JUN-2005
DEFINITION  Pan troglodytes IL12A gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   DQ033873
VERSION     DQ033873.1  GI:66885082
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     A Scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
  JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
   PUBMED   15869325
REFERENCE   2  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.  Translation starts at the beginning of
            alignment.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     gene            <1. .>762
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ORIGIN

  Query Match             30.7%;  Score 490.6;  DB 14;  Length 762;
  Best Local Similarity   89.2%;  Pred. No. 1.3e-132;
  Matches  529;  Conservative    0;  Mismatches   64;  Indels    0;  Gaps    0;

Qy       1007 CTAGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCC 1066
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Db        167 CCAGAAACCTCCCCGTGGCCACCCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCC 226

Qy       1067 AAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTT 1126
             ||| ||||||| | ||| |||||||||| ||| ||||||||||||||||||||||||||||
Db        227 AAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTTT 286

Qy       1127 ACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAG 1186
             || | |||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        287 ACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAG 346

Qy       1187 TGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGA 1246
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Db        347 TGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGAGAGA 406

Qy       1247 TCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCC 1306
              |||| | ||||||||||||||||||||||||||||||||||||||||||||| | |||
Db        407 CCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATGGCCC 466

Qy       1307 TGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGA 1366
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Db        467 TGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGA 526

Qy       1367 ATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAG 1426
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Db        527 ATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCAG 586

Qy       1427 CTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCT 1486
              |||||| |||||| | |||||||||||| |||||||| |||||||||||| || ||||
Db        587 TTATTGACGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCT 646

Qy       1487 CCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTT 1546
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Db        647 CCCTTGAAGAACTGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTT 706

Qy       1547 TCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
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Db        707 TCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTCC 759


RESULT 14
CD559452/c
LOCUS       CD559452               754 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496548 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971870 5', mRNA sequence.
ACCESSION   CD559452
VERSION     CD559452.2  GI:38453473
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 754)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585520.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 01
            High quality sequence start: 130
            High quality sequence stop: 572.
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                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
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ORIGIN

Query Match 29.9%; Score 477.4; DB 5; Length 754;
Best Local Similarity 84.8%; Pred. No. 1e-128;
Matches 559; Conservative 0; Mismatches 96; Indels 4; Gaps 2;

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Db        752 GAATTTGGTCCAATGATAT-TTAAAGGACCAGAAAGAACCCAAAAATAAGACCTTTCTAA 694

Qy        389 AATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTA 448
              ||| ||||| ||||||||||||||||||||||||||||||||||||||| |||||||||
Db        693 GATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGACAATCAGTA 634

Qy        449 CCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTT 508
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Db        633 CTGATTTGACATTCAGTGTCAAGAGCAGCAGAGGCTTTTTTGACCCCCAAGGGGTGACGT 574

Qy        509 GTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGT 568
              | ||||| || |||||||  |||||||  ||||||| |||||||| ||| |||    |||
Db        573 GCGGAGCTGCTACACTCTTTGCAGAGAGAGTCAGAGGGGACAACAAGGAGTAT---GAGT 517

Qy        569 ACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTG 628
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Db        516 ACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGGTGAGGAGAGTTTGCCCATTG 457

Qy        629 AAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCA 688
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Db        456 AGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACCAGCAGGTTTTTCA 397

Qy        689 TCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATT 748
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Db        396 TCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATT 337

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Qy        809 TCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGAC 868
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              |||   ||||| |||||||||||||  |||||| | |||||||  ||| ||||||||
Db        156 GGGCCCAGGACCGGTACTATAGCTCATTTTGGAGCGAATGGGCATTTGTGCCCTGCAGT 98
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RESULT 15
CD559449/c
LOCUS CD559449 766 bp mRNA linear EST 19-NOV-2003
DEFINITION AGENCOURT_14496649 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971873 5', mRNA sequence.
ACCESSION CD559449
VERSION CD559449.2 GI:38453467
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 766)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585517.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: h column: 04
High quality sequence stop: 641.

FEATURES Location/Qualifiers
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/organism="Homo sapiens"
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/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 29.5%; Score 471.8; DB 5; Length 766;
Best Local Similarity 85.6%; Pred. No. 4.6e-127;
Matches 537; Conservative 0; Mismatches 87; Indels 3; Gaps 1;

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Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Db        714 AGAAGAACCCAGAAATAGTACTTTCTAAGATGCGAGGCCAAGAAGTATTCTGGACGTTTC 655

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db        654 ACCTGGTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 595

Qy        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Db        594 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 535

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||  ||||||||  |||  |||    ||||| |||||||||| |||||||  ||||||||||
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Search completed: June 10, 2006, 17:40:18
Job time : 9339.05 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 10, 2006, 04:51:14 ; Search time 345.172 Seconds
(without alignments)
8667.862 Million cell updates/sec

Title: US-10-821-670A-38
Perfect score: 1599
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	2	1599	100.0	1599	3	US-09-917-265A-40	Sequence 40, Appl
	3	1533	95.9	1533	3	US-09-917-265A-43	Sequence 43, Appl
c	4	1533	95.9	1533	3	US-09-917-265A-45	Sequence 45, Appl
	5	1429.4	89.4	1599	3	US-09-917-265A-61	Sequence 61, Appl
c	6	1429.4	89.4	1599	3	US-09-917-265A-63	Sequence 63, Appl
	7	1373	85.9	1533	3	US-09-917-265A-66	Sequence 66, Appl
c	8	1373	85.9	1533	3	US-09-917-265A-68	Sequence 68, Appl
	9	1248.2	78.1	1623	2	US-08-751-767A-9	Sequence 9, Appli
	10	1248.2	78.1	6139	2	US-08-751-767A-7	Sequence 7, Appli
	11	1201.2	75.1	1560	2	US-08-751-767A-11	Sequence 11, Appl
	12	983.8	61.5	987	3	US-09-917-265A-29	Sequence 29, Appl
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	14	981.8	61.4	985	3	US-09-917-265A-55	Sequence 55, Appl
c	15	981.8	61.4	985	3	US-09-917-265A-57	Sequence 57, Appl
	16	979	61.2	2193	3	US-09-011-143-5	Sequence 5, Appli
	17	979	61.2	2193	3	US-09-302-495-5	Sequence 5, Appli
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	43	777.4	48.6	1018	3	US-09-535-370-194	Sequence 194, App
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ALIGNMENTS

RESULT 1
US-09-917-265A-38
; Sequence 38, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1599)
US-09-917-265A-38

Query Match 100.0%; Score 1599; DB 3; Length 1599;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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RESULT 2
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; Sequence 40, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265A-40

Query Match 100.0%; Score 1599; DB 3; Length 1599;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       819 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 760

Qy       841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Qy       901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
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RESULT 3
US-09-917-265A-43
; Sequence 43, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)
US-09-917-265A-43

Query Match 95.9%; Score 1533; DB 3; Length 1533;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
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Qy       427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
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Qy       487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
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Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
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Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy       1027 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020

Qy       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080

Qy       1147 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200

Qy       1267 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260

Qy       1327 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1386
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320

Qy       1387 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380

Qy       1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1506
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440

Qy       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1566
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500

Qy       1567 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
              |||||||||||||||||||||||||||||||
Db       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
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RESULT 4
US-09-917-265A-45/c
; Sequence 45, Application US/09917265A
; Patent No. 6818444

```
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-45

  Query Match             95.9%;  Score 1533;  DB 3;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1533;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy         367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy         427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy         487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy         547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy         607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy         667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy         727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy         787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754
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Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        967 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy       1027 ACTCCATCCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy       1147 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy       1267 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy       1327 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1386
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy       1387 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy       1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1506
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1566
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy       1567 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
              |||||||||||||||||||||||||||||||||
Db          33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
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RESULT 5
US-09-917-265A-61
; Sequence 61, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-09-917-265A-61

  Query Match             89.4%;  Score 1429.4;  DB 3;  Length 1599;
  Best Local Similarity   93.4%;  Pred. No. 0;
  Matches 1493;  Conservative    0;  Mismatches  106;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||| |||||||||||||||||| ||||| ||||||| |||||||||| ||||||||
Db          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||||||||||||| |||| ||||||||||||||||||| |||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||| |  |||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||| |||||||||||||||||||| |||||||||| |||||||||||  ||
Db        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||  |||| |||||||| ||||||||||||||||||||||||||||||| |||||||
Db        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              || |||||||||||||||||||||||| |||||||||||| ||||||||| ||||||
Db        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              |||| |||||||||||||| |||||| |||||||||| |||||| |||||||||| ||||
Db        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||  |||||||||||||||||||| || |||||||||| ||||||||||||||||||||
Db        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              || |||||||||||||||||||||||||| |||||||||||||| ||||||||||
Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||| |||||||||| |||||||||||||| ||||| || ||||||||||||||
Db        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              |||||||||||||||||||||||||||||||| | |||||| || |||||| |||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||| |||||||||||||| ||||||| ||||||||||||||||||||||||||
Db        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              |||||||||||||||||||||||||||||||| |||||||||||||| |||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
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Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020
              ||| |||||||||| ||||| ||||||||||||||||||||||||||||||||||||||||
Db        961 AGCGACTGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020

Qy       1021 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 1080
              |||||||||||||||||||| |||||||| ||   | ||||||||||||||| || || ||
Db       1021 ACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGA 1080

Qy       1081 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 1140
              ||| ||||||||||||||||||||||||||||||||||||||| || ||||||||||||
Db       1081 GCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCC 1140

Qy       1141 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1141 GAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200

Qy       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 1260
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACT 1260

Qy       1261 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 1320
              || |||||||||||||||  ||||| |||||||||||||  ||||||||||||||||
Db       1261 AACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGC 1320

Qy       1321 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 1380
              |||||||||||||||||||||||| |||| |||||||||||||| |||||||| |||
Db       1321 ATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTA 1380

Qy       1381 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 1440
              |||||||| || ||||||||||||||||||||||||||||||||||||| |||||||||
Db       1381 ATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTG 1440

Qy       1441 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 1500
              |||||||||||||||  |||||||||||||||||||||||| |||||| | ||||| |||
Db       1441 TTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCG 1500

Qy       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCG 1560

Qy       1561 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
              |||||||||||||||||||  |||  ||||  |||||
Db       1561 GTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1599


RESULT 6
US-09-917-265A-63/c
; Sequence 63, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-63

  Query Match             89.4%;  Score 1429.4;  DB 3;  Length 1599;
  Best Local Similarity   93.4%;  Pred. No. 0;
  Matches 1493;  Conservative    0;  Mismatches  106;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              |||||  |||||||||||||||||  |||||  |||||||  ||||||||||  ||||||||
Db       1599 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 1540

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||||||||||||| |||| ||||||||||||||||||| |||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 1420

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||| |  |||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1419 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||| |||||||||||||||||||||| |||||||||||||  ||||||||||||  ||
Db       1359 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 1300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||  |||| |||||||| ||||||||||||||||||||||||||||| |||||||
Db       1299 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 1240

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              || |||||||||||||||||||||||||||||||||||||| |||||||||| ||||||
Db       1179 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 1120

Qy        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              |||| |||||||||||||| |||||| |||||||||| |||||| |||||||||| ||||
Db       1119 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 1060

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||  |||||||||||||||||||||||| || |||||||||| ||||||||||||||||||
Db        999 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 940

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              || |||||||||||||||||||||||||||||| |||||||||||||| ||||||||||
Db        939 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 880

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              |||||||| |||||||||| |||||||||||||| ||||| || ||||||||||||||
Db        879 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 820

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              |||||||||||||||||||||||||||||||||||||||| | |||||| || |||||| |||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 760

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||||||| |||||||||||||| |||||||| |||||||||||||||||||||||||||||
Db        759 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              |||||||||||||||||||||||||||||||||||||| |||||||||||||||| |||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 640

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020
              ||| |||||||||| ||||| ||||||||||||||||||||||||||||||||||||||||
Db        639 AGCGACTGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 580

Qy       1021 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 1080
              |||||||||||||||||||| |||||||| ||   | ||||||||||||||| || || ||
Db        579 ACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGA 520

Qy       1081 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 1140
              ||| ||||||||||||||||||||||||||||||||||||||| || ||||||||||||
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Db        519 GCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCC 460

Qy       1141 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        459 GAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTA 400

Qy       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        399 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACT 340

Qy       1261 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 1320
              || |||||||||||||||||  ||||| ||||||||||||||  ||||||||||||||||
Db        339 AACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGC 280

Qy       1321 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 1380
              |||||||||||||||||||||||||| |||| |||||||||||||| |||||||| |||
Db        279 ATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTA 220

Qy       1381 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 1440
              |||||||| || ||||||||||||||||||||||||||||||||||||| |||||||||
Db        219 ATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTG 160

Qy       1441 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 1500
              |||||||||||||||| |||||||||||||||||||||||| |||||| | ||||| |||
Db        159 TTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCG 100

Qy       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCG 40

Qy       1561 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
              |||||||||||||||||||  |||  ||||  |||||
Db         39 GTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1
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RESULT 7
US-09-917-265A-66
; Sequence 66, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)
US-09-917-265A-66

Query Match 85.9%; Score 1373; DB 3; Length 1533;
Best Local Similarity 93.5%; Pred. No. 0;
Matches 1433; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

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Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              |||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              |||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              | ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              | |||||||||||||||||||| |||||||||||| |||||||||||  ||  ||||
Db        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              |||| |||||||| |||||||||||||||||||||||||||||| ||||||||||||
Db        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||| |||
Db        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              |||||||||||||||||||||||||| |||||||||||| ||||||||| |||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420

Qy        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||| |||||| |||||||||| |||||| |||||||||| ||||||||||
Db        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              |||||||||||||||||||| || |||||||||||| |||||||||||||||||||| |||
Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              |||||||||||||||||||||||||| |||||||||||||| |||||||||| ||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              || |||||||||| |||||||||||||| ||||| || |||||||||||||| ||||||
Db        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              |||||||||||||||||||||||||||||| | |||||| || |||||| ||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              || |||||||||||||| ||||||| ||||||||||||||||||||||||||||||||||
Db        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              |||||||||||||||||||||||||||||| |||||||||||||| |||||||||||| ||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900

Qy        967 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026
              |||||||| ||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy       1027 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1086
              |||||||||||||| |||||||| ||  | ||||||||||||||| || || ||||| ||
Db        961 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 1020

Qy       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1146
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 1080

Qy       1147 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1266
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||
Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1200

Qy       1267 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1326
              |||||||||||||| ||||| |||||||||||||| ||||||||||||||| ||||||
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Db       1201 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1260

Qy       1327 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1386
             |||||||||||||||||||| |||| |||||||||||||| |||||||| |||||||||
Db       1261 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1320

Qy       1387 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1446
              || || |||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       1321 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 1380

Qy       1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1506
             |||||||| |||||||||||||||||||||||| |||||| | ||||| |||||||||
Db       1381 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1440

Qy       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1566
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1500

Qy       1567 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
             ||||||||||||||| ||| |||| |||||
Db       1501 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1533


RESULT 8
US-09-917-265A-68/c
; Sequence 68, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-68

  Query Match             85.9%;  Score 1373;  DB 3;  Length 1533;
  Best Local Similarity   93.5%;  Pred. No. 0;
  Matches 1433;  Conservative    0;  Mismatches  100;  Indels    0;  Gaps    0;

Qy          67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
               |||||||||||||||| | ||||||||||||||||||||||||||||||||||||||||
Db        1533 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
               |||||||||||||||||||| |||| |||||||||||||||||| ||||||||
Db        1473 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1414

Qy         187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
               | |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        1413 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
               | |||||||||||||||||||| |||||||||||| |||||||||||   ||   ||||
Db        1353 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1294

Qy         307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
                |||| |||||||| |||||||||||||||||||||||||||||| ||||||||||||
Db        1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

Qy         367 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
               |||||||||||||||||| |||||||||||||||||||||||||||||||||||||| |||
Db        1233 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174
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Qy         427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
               |||||||||||||||||||||||| |||||||||||| |||||||| |||||||||| |
Db        1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy         487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
               |||||||||||| |||||| |||||||||| |||||| |||||||||| ||||||||||
Db        1113 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1054

Qy         547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db        1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 994

Qy         607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
               |||||||||||||||||| || |||||||||| |||||||||||||||||||||| |||
Db         993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy         667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
               |||||||||||||||||||||||| |||||||||||| |||||||||| ||||||
Db         933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 874

Qy         727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
               || |||||||||| |||||||||||||| ||||| || |||||||||||||| ||||||
Db         873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy         787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
               |||||||||||||||||||||||| | |||||| || |||||| ||||||||||||||
Db         813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754

Qy         847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
               || |||||||||||||| ||||||| ||||||||||||||||||||||||||||||||
Db         753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy         907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
               |||||||||||||||||||||||| |||||||||||||| |||||||||||| ||
Db         693 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 634

Qy         967 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026
               |||||||| ||||| |||||||||||||||||||||||||||||||||||||||||||||
Db         633 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        1027 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1086
               |||||||||||||| |||||||| ||  | |||||||||||||| || || ||||| ||
Db         573 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 514

Qy        1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1146
               |||||||||||||||||||||||||||||||||||||||| || ||||||||||||||||
Db         513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 454

Qy        1147 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         453 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy        1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1266
               |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||
Db         393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 334

Qy        1267 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1326
               |||||||||||||  ||||| ||||||||||||  |||||||||||||| ||||||
Db         333 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 274

Qy        1327 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1386
               |||||||||||||||||||| |||| |||||||||||||| |||||||| |||||||||
Db         273 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 214

Qy        1387 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1446
               || || |||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db         213 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 154

Qy        1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1506
               |||||||| |||||||||||||||||||||||| |||||| | ||||| |||||||||
Db         153 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 94

Qy        1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1566
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Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 34

Qy       1567 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
Db         33 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1
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RESULT 9
US-08-751-767A-9
; Sequence 9, Application US/08751767A
; Patent No. 5994104
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, ROBERT J.
; APPLICANT: GRANT, HUGH
; APPLICANT: MACDONALD, IAN D.
; TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,767A
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 117-221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164091
; TELEFAX: 7038164100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1623 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1620
US-08-751-767A-9

Query Match 78.1%; Score 1248.2; DB 2; Length 1623;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 1408; Conservative 0; Mismatches 188; Indels 27; Gaps 2;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
Db          1 ATGGGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
Db         61 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
Db        121 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
Db        181 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
Db        241 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
Db        301 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
Db        361 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
Db        421 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
Db        481 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
Db        541 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 597

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
Db        598 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 657

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
Db        658 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 717

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
Db        718 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 777

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
Db        778 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 837

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
Db        838 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 897

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
Db        898 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 957

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGT---------- 996
Db        958 AGCGAATGGGCATCTGTGCCCTGCAGTGGTGGCGGTGGAAGCGGCGGTGGCGGAAGCGGC 1017

Qy        997 GGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTC 1056
Db       1018 GGTGGCGGCAGCAGAAACCTCCCCCTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTT 1077

Qy       1057 AACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACT 1116
Db       1078 CACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACT 1137

Qy       1117 CTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAA 1176
Db       1138 CTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAA 1197

Qy       1177 ACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCT 1236
Db       1198 ACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAAT 1257

Qy       1237 TCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTT 1296
Db       1258 TCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTT 1317

Qy       1297 ATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTC 1356
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Db       1318 ATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTC 1377

Qy       1357 AAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAAC 1416
                ||| ||||||||||||||| | |||||||||| |||||||||||||| ||||||||||
Db       1378 AAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAAC 1437

Qy       1417 ATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCA 1476
                |||||| ||| |||||||||||| | |||||||||||| ||||||||| ||||||||||
Db       1438 ATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCA 1497

Qy       1477 CAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTT 1536
                || || |||||| | ||||||||||||||||||||||||||||||||||||||||||||
Db       1498 CAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTT 1557

Qy       1537 CTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCT 1596
                |||||||||||||||||| ||||||| ||  | ||| ||| ||||||||||||||||
Db       1558 CTTCATGCTTTCAGAATTCGGGCAGTGACTATTGACAGAGTGACGAGCTATCTGAATGCT 1617

Qy       1597 TCC 1599
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Db       1618 TCC 1620


RESULT 10
US-08-751-767A-7
; Sequence 7, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6139 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3222..4841
US-08-751-767A-7

  Query Match             78.1%;  Score 1248.2;  DB 2;  Length 6139;
  Best Local Similarity   86.8%;  Pred. No. 0;
  Matches 1408;  Conservative    0;  Mismatches  188;  Indels   27;  Gaps    2;
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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              |||  ||  |||||||||||||||| | ||| |||||||||||||| |||||| ||||||||
Db       3222 ATGGGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 3281

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||| ||||| | |||||||| ||||| ||||| ||| | || |||
Db       3282 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 3341

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||| |||||||||||||||||||||| | || |||||||||||||  |||||||||
Db       3342 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 3401

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              |||| |||||||||||||| ||| |||||||||| ||||| ||||||||||||||||||
Db       3402 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 3461

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              || |||| |||||||||||||| |||||||| |||||||||||||||| |||||||||
Db       3462 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 3521

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              |||| ||| | |||||||||||||||||||||||||||||||||| |||| ||| |||
Db       3522 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 3581

Qy        361 AAAGAATCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||| |||||||||||| |||||||| ||| ||||| ||||||||||||||||||||
Db       3582 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 3641

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              |||||||||||||||| |||||||||| ||||||| ||||| ||||||||||||||||
Db       3642 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 3701

Qy        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||| |||||||||||||| |||||| || ||||| || |||||||| |||||||  |||
Db       3702 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 3761

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||| |||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||
Db       3762 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 3818

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              || ||||| |||||||| || |||||||| ||| ||||||| ||  ||||||||||||||
Db       3819 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 3878

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              || |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       3879 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 3938

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||| |||| |||||||||||||| |||||||||| ||||| || |||||||| ||||||
Db       3939 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 3998

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              |||||||||| || |||||||||||||||| | |||||  |||| ||||||||||||
Db       3999 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 4058

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||| ||| |||||||||||||| ||| ||| |  |||||||||||||||| |||| |
Db       4059 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 4118

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              |||| ||| |||||  || |||||  |||  |||||||||||||||||||||||| |||
Db       4119 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 4178

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGT---------------------- 996
              ||| | |||||||| ||| ||||||||||||||||
Db       4179 AGCGAATGGGCATCTGTGCCCTGCAGTGGTGGCGGTGGAAGCGGCGGTGGCGGAAGCGGC 4238

Qy        997 GGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTC 1056
              || |||||    |||||| | ||     | ||||||  ||| || |||||||  |||||
Db       4239 GGTGGCGGCAGCAGAAACCTCCCCCTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTT 4298

Qy       1057 AACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACT 1116
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Db       4299 CACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACT 4358

Qy       1117 CTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAA 1176

Db       4359 CTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAA 4418

Qy       1177 ACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCT 1236

Db       4419 ACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAAT 4478

Qy       1237 TCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTT 1296

Db       4479 TCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTT 4538

Qy       1297 ATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTC 1356

Db       4539 ATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTC 4598

Qy       1357 AAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAAC 1416

Db       4599 AAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAAC 4658

Qy       1417 ATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCA 1476

Db       4659 ATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCA 4718

Qy       1477 CAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTT 1536

Db       4719 CAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTT 4778

Qy       1537 CTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCT 1596

Db       4779 CTTCATGCTTTCAGAATTCGGGCAGTGACTATTGACAGAGTGACGAGCTATCTGAATGCT 4838

Qy       1597 TCC 1599

Db       4839 TCC 4841


RESULT 11
US-08-751-767A-11
; Sequence 11, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100

;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1560 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1557
US-08-751-767A-11

  Query Match             75.1%;  Score 1201.2;  DB 2;  Length 1560;
  Best Local Similarity   86.9%;  Pred. No. 0;
  Matches 1355;  Conservative    0;  Mismatches  178;  Indels   27;  Gaps    2;

Qy         64 GCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCC 123

Db          1 GCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCC 60

Qy        124 CCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACC 183

Db         61 CCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACC 120

Qy        184 TCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAA 243

Db        121 TTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAG 180

Qy        244 TTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTC 303

Db        181 TTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTC 240

Qy        304 CTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAA 363

Db        241 CTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAA 300

Qy        364 GAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACC 423

Db        301 GAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACC 360

Qy        424 TGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGC 483

Db        361 TGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGC 420

Qy        484 TCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGA 543

Db        421 TCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGA 480

Qy        544 GTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCG 603

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Db        538 GCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTAT 597

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAAC 723

Db        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAAC 657

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Db        658 TTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGAC 717

Qy        784 ACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAG 843

Db        718 ACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAG 777

Qy        844 AACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGC 903

Db        778 AGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGC 837

Qy        904 CACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGC 963
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Db        838 CGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGC 897

Qy        964 AACTGGGCATCCGTGTCCTGCAGTGGTGGCGGT----------------------GGC 999

Db        898 GAATGGGCATCTGTGCCCTGCAGTGGTGGCGGTGGAAGCGGCGGTGGCGGAAGCGGCGGT 957

Qy       1000 GGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAAC 1059

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Qy       1060 CACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTA 1119

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Db       1078 GAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACC 1137

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Qy       1240 AGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATG 1299

Db       1198 AGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATG 1257

Qy       1300 ACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAG 1359

Db       1258 ATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAG 1317

Qy       1360 GCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATG 1419

Db       1318 ACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATG 1377

Qy       1420 CTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAG 1479

Db       1378 CTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAA 1437

Qy       1480 AACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTT 1539

Db       1438 AAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTT 1497

Qy       1540 CATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599

Db       1498 CATGCTTTCAGAATTCGGGCAGTGACTATTGACAGAGTGACGAGCTATCTGAATGCTTCC 1557
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RESULT 12
US-09-917-265A-29
; Sequence 29, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(987)
US-09-917-265A-29

Query Match 61.5%; Score 983.8; DB 3; Length 987;
Best Local Similarity 99.8%; Pred. No. 2.8e-304;
Matches 985; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987

Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
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RESULT 13
US-09-917-265A-31/c
; Sequence 31, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-31

  Query Match             61.5%;  Score 983.8;  DB 3;  Length 987;
  Best Local Similarity   99.8%;  Pred. No. 2.8e-304;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGCAGT 1


RESULT 14
US-09-917-265A-55
; Sequence 55, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(984)
US-09-917-265A-55

  Query Match             61.4%;  Score 981.8;  DB 3;  Length 985;
  Best Local Similarity   99.8%;  Pred. No. 1.2e-303;
  Matches  983;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 15
US-09-917-265A-57/c
; Sequence 57, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-57

  Query Match             61.4%;  Score 981.8;  DB 3;  Length 985;
  Best Local Similarity   99.8%;  Pred. No. 1.2e-303;
  Matches  983;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGCA 1


Search completed: June 10, 2006, 18:08:46
Job time : 347.172 secs
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 10, 2006, 07:19:28 ; Search time 1822.98 Seconds
(without alignments)
10777.934 Million cell updates/sec

Title: US-10-821-670A-38
Perfect score: 1599
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	2	1599	100.0	1599	3	US-09-917-265-40	Sequence 40, Appl
	3	1599	100.0	1599	9	US-10-821-670-38	Sequence 38, Appl
c	4	1599	100.0	1599	9	US-10-821-670-40	Sequence 40, Appl
	5	1533	95.9	1533	3	US-09-917-265-43	Sequence 43, Appl
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	7	1533	95.9	1533	9	US-10-821-670-43	Sequence 43, Appl
c	8	1533	95.9	1533	9	US-10-821-670-45	Sequence 45, Appl
	9	1429.4	89.4	1599	3	US-09-917-265-61	Sequence 61, Appl
c	10	1429.4	89.4	1599	3	US-09-917-265-63	Sequence 63, Appl
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	19	1258.8	78.7	8608	3	US-09-828-825-7	Sequence 7, Appli
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ALIGNMENTS

RESULT 1
US-09-917-265-38
; Sequence 38, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1599)
; OTHER INFORMATION:
US-09-917-265-38

Query Match 100.0%; Score 1599; DB 3; Length 1599;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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; Sequence 40, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265-40

Query Match 100.0%; Score 1599; DB 3; Length 1599;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        219 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 160

Qy       1441 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        159 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 100

Qy       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 40

Qy       1561 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
              |||||||||||||||||||||||||||||||||||||||
Db         39 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
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RESULT 3
US-10-821-670-38
; Sequence 38, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1599)
US-10-821-670-38

Query Match 100.0%; Score 1599; DB 9; Length 1599;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Qy        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020

Qy       1021 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 1080

Qy       1081 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 1140

Qy       1141 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200

Qy       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 1260

Qy       1261 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 1320

Qy       1321 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 1380

Qy       1381 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 1440

Qy       1441 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 1500

Qy       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 1560

Qy       1561 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
              |||||||||||||||||||||||||||||||||||||||
Db       1561 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
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RESULT 4
US-10-821-670-40/c
; Sequence 40, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
US-10-821-670-40

Query Match 100.0%; Score 1599; DB 9; Length 1599;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1599 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 1540

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy        121 GCCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 GCCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 1420

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1359 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 1300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1299 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 1240

Qy        361 AAAGAATCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1179 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 1120

Qy        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1119 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 1060

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        999 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 940

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        939 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 880

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        879 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 820

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 760

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        759 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 640

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        639 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 580

Qy       1021 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        579 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 520

Qy       1081 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        519 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 460

Qy       1141 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        459 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 400

Qy       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        399 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 340

Qy       1261 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        339 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 280

Qy       1321 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        279 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 220

Qy       1381 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 160

Qy       1441 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        159 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 100

Qy       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 40

Qy       1561 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
              |||||||||||||||||||||||||||||||||||||||
Db         39 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 5
US-09-917-265-43
; Sequence 43, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
;   OTHER INFORMATION:
US-09-917-265-43

  Query Match             95.9%;  Score 1533;  DB 3;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1533;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
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Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy       1027 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020

Qy       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080

Qy       1147 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200

Qy       1267 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260

Qy       1327 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1386
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320

Qy       1387 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380

Qy       1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1506
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440

Qy       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1566
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500

Qy       1567 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
              |||||||||||||||||||||||||||||||
Db       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533


RESULT 6
US-09-917-265-45/c
; Sequence 45, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-45

  Query Match            95.9%;  Score 1533;  DB 3;  Length 1533;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1533;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        967 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy       1027 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        573 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1146
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy       1147 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1266
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy       1267 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1326
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy       1327 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1386
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy       1387 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1446
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy       1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1506
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1566
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy       1567 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
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Db          33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
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RESULT 7
US-10-821-670-43
; Sequence 43, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)
US-10-821-670-43

Query Match 95.9%; Score 1533; DB 9; Length 1533;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy       1027 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020

Qy       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080

Qy       1147 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1266
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Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200

Qy       1267 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1326
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260

Qy       1327 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1386
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320

Qy       1387 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1446
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380

Qy       1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1506
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Db       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440

Qy       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1566
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500

Qy       1567 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
             |||||||||||||||||||||||||||||||||
Db       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533


RESULT 8
US-10-821-670-45/c
; Sequence 45, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-45

  Query Match             95.9%;  Score 1533;  DB 9;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1533;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy         367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy         427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy         487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy         547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy         607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy         667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy         727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy         787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy         847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy         907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy         967 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        1027 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1086
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy        1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1146
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy        1147 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy        1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1266
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy        1267 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1326
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy        1327 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1386
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy        1387 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1446
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy        1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1506
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1566
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy       1567 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
                |||||||||||||||||||||||||||||||||
Db         33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1


RESULT 9
US-09-917-265-61
; Sequence 61, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
US-09-917-265-61

  Query Match             89.4%;  Score 1429.4;  DB 3;  Length 1599;
  Best Local Similarity   93.4%;  Pred. No. 0;
  Matches 1493;  Conservative    0;  Mismatches  106;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||| |||||||||||||||| ||||| ||||||| |||||||||| ||||||||
Db          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||||||||||||| |||| ||||||||||||||||||| |||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              |||||  |||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||| |||||||||||||||||||| |||||||||||| |||||||||||||   ||
Db        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||  |||| |||||||| |||||||||||||||||||||||||||||| |||||||
Db        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              || |||||||||||||||||||||||| |||||||||| |||||||||| ||||||
Db        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              |||| |||||||||||||| |||||| |||||||||| |||||| |||||||||| ||||
Db        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||  |||||||||||||||||||| || |||||||||| ||||||||||||||||||||
Db        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              || |||||||||||||||||||||||||||||||| |||||||||||| ||||||||||
Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              |||||||| |||||||||| |||||||||||||| ||||| || ||||||||||||||
Db        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              |||||||||||||||||||||||||||||| | |||||| || |||||| |||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||||||| |||||||||||||| |||||| |||||||||||||||||||||||||||||
Db        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              |||||||||||||||||||||||||||||||| |||||||||||||| |||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020
              ||| |||||||||| ||||| ||||||||||||||||||||||||||||||||||||||||
Db        961 AGCGACTGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020

Qy       1021 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 1080
              |||||||||||||||||||| |||||||| ||  | |||||||||||||| || || ||
Db       1021 ACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGA 1080

Qy       1081 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 1140
              ||| |||||||||||||||||||||||||||||||||||||||||| || ||||||||||||
Db       1081 GCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCC 1140

Qy       1141 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1141 GAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200

Qy       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 1260
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACT 1260

Qy       1261 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 1320
              || |||||||||||||||||  ||||| |||||||||||||  ||||||||||||||||
Db       1261 AACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGC 1320

Qy       1321 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 1380
              |||||||||||||||||||||||||||| |||| |||||||||||||| |||||||| |||
Db       1321 ATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTA 1380

Qy       1381 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 1440
              |||||||| || |||||||||||||||||||||||||||||||||||||||| |||||||||
Db       1381 ATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTG 1440

Qy       1441 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 1500
              |||||||||||||| |||||||||||||||||||||||||||| |||||| | ||||| |||
Db       1441 TTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCG 1500

Qy       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 1560
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCG 1560

Qy       1561 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
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Db       1561 GTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1599


RESULT 10
US-09-917-265-63/c
; Sequence 63, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-63

  Query Match             89.4%;  Score 1429.4;  DB 3;  Length 1599;
  Best Local Similarity   93.4%;  Pred. No. 0;
  Matches 1493;  Conservative    0;  Mismatches  106;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
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Db       1599 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 1540

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||||||||||| |||| |||||||||||||||||||| |||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 1420

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||| |  |||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1419 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||| |||||||||||||||||||| |||||||||||| ||||||||||||  ||
Db       1359 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 1300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
               ||||  |||| |||||||| |||||||||||||||||||||||||||||| |||||||
Db       1299 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 1240

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              || |||||||||||||||||||||||||| |||||||||||| |||||||| ||||||
Db       1179 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 1120

Qy        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              |||| |||||||||||||| |||||| |||||||||| |||||| |||||||||| ||||
Db       1119 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 1060

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||  |||||||||||||||||||| || |||||||||| ||||||||||||||||||||
Db        999 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 940

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              || ||||||||||||||||||||||||||||||| |||||||||||||| ||||||||||
Db        939 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 880

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              |||||||| |||||||||| |||||||||||||||| ||||| || ||||||||||||||
Db        879 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 820

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              |||||||||||||||||||||||||||||||| | |||||| || |||||| |||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 760

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||| ||||||||||||| ||||||| |||||||||||||||||||||||||||||
Db        759 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              |||||||||||||||||||||||||||||||| |||||||||||||| |||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 640

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020
              ||| |||||||||| ||||| ||||||||||||||||||||||||||||||||||||||
Db        639 AGCGACTGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 580

Qy       1021 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 1080
              |||||||||||||||||| |||||||| ||  | ||||||||||||| || || ||
Db        579 ACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGA 520

Qy       1081 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 1140
              ||| |||||||||||||||||||||||||||||||||||||||| || ||||||||||||
Db        519 GCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCC 460

Qy       1141 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        459 GAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTA 400

Qy       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 1260
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        399 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACT 340

Qy       1261 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 1320
              || |||||||||||||||  ||||| |||||||||||||  ||||||||||||||||
Db        339 AACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGC 280

Qy       1321 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 1380
              |||||||||||||||||||||||||| |||| |||||||||||||| |||||||| |||
Db        279 ATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTA 220

Qy       1381 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 1440
              |||||||| || |||||||||||||||||||||||||||||||||||||||| |||||||||
Db        219 ATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTG 160

Qy       1441 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 1500
              |||||||||||||| |||||||||||||||||||||||||| |||||| | ||||| |||
Db        159 TTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCG 100

Qy       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          99 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCG 40

Qy       1561 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
              |||||||||||||||||||  |||  ||||  |||||
Db          39 GTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1


RESULT 11
US-10-821-670-61
; Sequence 61, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
```

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;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-10-821-670-61

  Query Match             89.4%;  Score 1429.4;  DB 9;  Length 1599;
  Best Local Similarity   93.4%;  Pred. No. 0;
  Matches 1493;  Conservative    0;  Mismatches  106;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||| |||||||||||||||| ||||| ||||||| |||||||||||   ||||||||
Db          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||| | ||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||||||||||| |||| |||||||||||||||||| |||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||| |  |||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||| |||||||||||||||||||| |||||||||||| ||||||||||||   ||
Db        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||  |||| |||||||| |||||||||||||||||||||||||||||| |||||||
Db        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              || |||||||||||||||||||||||||||| |||||||||||| ||||||||| ||||||
Db        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              |||| |||||||||||||| |||||| |||||||||| |||||| |||||||||| ||||
Db        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||  |||||||||||||||||||| || |||||||||| ||||||||||||||||||||
Db        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              || |||||||||||||||||||||||||||| |||||||||||||| ||||||||||
Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              |||||||| |||||||||| |||||||||||||| ||||| || ||||||||||||||
Db        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||| | |||||| || |||||| |||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||||||| |||||||||||||| ||||||| |||||||||||||||||||||||||||||
Db        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              |||||||||||||||||||||||||||||||||| |||||||||||||| |||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020
              ||| |||||||||| ||||| ||||||||||||||||||||||||||||||||||||||
Db        961 AGCGACTGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020

Qy       1021 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 1080
              |||||||||||||||||| |||||||| ||  | |||||||||||||| || || ||
Db       1021 ACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGA 1080

Qy       1081 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 1140
              ||| |||||||||||||||||||||||||||||||||||||| || ||||||||||||
Db       1081 GCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCC 1140

Qy       1141 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200

Qy       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 1260
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACT 1260

Qy       1261 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 1320
              || |||||||||||||||  ||||| |||||||||||||  ||||||||||||||||
Db       1261 AACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGC 1320

Qy       1321 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 1380
              |||||||||||||||||||||||||||||| |||| |||||||||||||| |||||||| |||
Db       1321 ATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTA 1380

Qy       1381 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 1440
              |||||||| || |||||||||||||||||||||||||||||||||| |||||||||
Db       1381 ATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTG 1440

Qy       1441 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 1500
              |||||||||||||| |||||||||||||||||||||||| |||||| | ||||| |||
Db       1441 TTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCG 1500

Qy       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCG 1560

Qy       1561 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
              |||||||||||||||||||  ||| |||| |||||
Db       1561 GTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1599


RESULT 12
US-10-821-670-63/c
; Sequence 63, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
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; SEQ ID NO 63
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-821-670-63

Query Match 89.4%; Score 1429.4; DB 9; Length 1599;
Best Local Similarity 93.4%; Pred. No. 0;
Matches 1493; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||| |||||||||||||||| ||||| ||||||| ||||||||||  ||||||||
Db       1599 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 1540

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||||||||||| | ||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||||||||||||| |||| |||||||||||||||||||| |||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 1420

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||| |  |||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1419 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||| |||||||||||||||||||| |||||||||||| ||||||||||||  ||
Db       1359 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 1300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||  |||| |||||||| |||||||||||||||||||||||||||||||| |||||||
Db       1299 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 1240

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              || |||||||||||||||||||||||| |||||||||||| ||||||||| ||||||
Db       1179 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 1120

Qy        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              |||| |||||||||||||| |||||| |||||||||| |||||| |||||||||| ||||
Db       1119 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 1060

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||  |||||||||||||||||||| || |||||||||| ||||||||||||||||||||
Db        999 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 940

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              || |||||||||||||||||||||||||||| |||||||||||||| ||||||||||
Db        939 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 880

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              |||||||| |||||||||| |||||||||||||| ||||| || ||||||||||||||
Db        879 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 820

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              |||||||||||||||||||||||||||||| | |||||| || |||||| |||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 760

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||||||| |||||||||||||| ||||||| ||||||||||||||||||||||||||||
Db        759 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              |||||||||||||||||||||||||||||||| |||||||||||||||| |||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 640
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Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020
              ||| |||||||||| ||||| ||||||||||||||||||||||||||||||||||||||
Db        639 AGCGACTGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 580

Qy       1021 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 1080
              |||||||||||||||||||| |||||||| ||  | |||||||||||||| || || ||
Db        579 ACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGA 520

Qy       1081 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 1140
              ||| ||||||||||||||||||||||||||||||||||||||||| || ||||||||||||
Db        519 GCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCC 460

Qy       1141 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        459 GAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTA 400

Qy       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 1260
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        399 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACT 340

Qy       1261 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 1320
              || |||||||||||||||  ||||| ||||||||||||  ||||||||||||||||
Db        339 AACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGC 280

Qy       1321 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 1380
              |||||||||||||||||||||||||| |||| |||||||||||||| |||||||| |||
Db        279 ATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTA 220

Qy       1381 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 1440
              |||||||| || ||||||||||||||||||||||||||||||||||||| |||||||||
Db        219 ATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTG 160

Qy       1441 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 1500
              ||||||||||||||| |||||||||||||||||||||||||||| |||||| | ||||| |||
Db        159 TTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCG 100

Qy       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 1560
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          99 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCG 40

Qy       1561 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
              |||||||||||||||||||  |||  ||||  |||||
Db          39 GTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1
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RESULT 13
US-09-917-265-66
; Sequence 66, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)
; OTHER INFORMATION:
US-09-917-265-66

Query Match 85.9%; Score 1373; DB 3; Length 1533;
Best Local Similarity 93.5%; Pred. No. 0;

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  Matches 1433;  Conservative    0;  Mismatches  100;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              |||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              |||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              | |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              | |||||||||||||||||| |||||||||||| |||||||||||  ||  ||||
Db        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              |||| |||||||| ||||||||||||||||||||||||||||||| ||||||||||||
Db        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||| |||
Db        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              |||||||||||||||||||| |||||||||||| ||||||||| |||||||||| |
Db        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420

Qy        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||| |||||| |||||||||| |||||| |||||||||| ||||||||||
Db        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              |||||||||||||||||| || |||||||||| |||||||||||||||||||| |||
Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              |||||||||||||||||||||||||||||||||||| |||||||||||| ||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              || |||||||||| |||||||||||||| ||||| || |||||||||||||| ||||||
Db        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              |||||||||||||||||||||||| | |||||| || |||||| ||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              || |||||||||||||| ||||||| |||||||||||||||||||||||||||||||||
Db        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              |||||||||||||||||||||||||||| |||||||||||||| |||||||||||| ||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900

Qy        967 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026
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Db        901 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy       1027 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1086
              |||||||||||| |||||||| ||   | |||||||||||||| || || ||||| ||
Db        961 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 1020

Qy       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1146
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Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 1080

Qy       1147 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206
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Db       1081 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1266
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||
Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1200

Qy       1267 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1326
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Db       1201 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1260

Qy       1327 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1386
              |||||||||||||||||||| |||| |||||||||||||| |||||||| |||||||||
Db       1261 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1320

Qy       1387 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1446
              || || |||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db       1321 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 1380

Qy       1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1506
              ||||||||| |||||||||||||||||||||||||||||| |||||| | ||||| |||||||||
Db       1381 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1440

Qy       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1566
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1500

Qy       1567 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
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Db       1501 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1533


RESULT 14
US-09-917-265-68/c
; Sequence 68, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-68

  Query Match             85.9%;  Score 1373;  DB 3;  Length 1533;
  Best Local Similarity   93.5%;  Pred. No. 0;
  Matches 1433;  Conservative    0;  Mismatches  100;  Indels    0;  Gaps    0;

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Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
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Db       1473 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1414

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
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Db       1413 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
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Db       1353 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1294

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Db       1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

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Db       1233 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Db       1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Db       1113 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1054

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 994

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 874

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Db        873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Db        813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Db        753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

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Qy        967 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026

Db        633 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy       1027 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1086

Db        573 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 514

Qy       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1146

Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 454

Qy       1147 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206

Db        453 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1266

Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 334

Qy       1267 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1326

Db        333 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 274

Qy       1327 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1386

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Db        213 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 154

Qy       1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1506

Db        153 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 94

Qy       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1566

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Qy       1567 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599

Db         33 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1
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RESULT 15
US-10-821-670-66
; Sequence 66, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)
US-10-821-670-66

Query Match 85.9%; Score 1373; DB 9; Length 1533;
Best Local Similarity 93.5%; Pred. No. 0;
Matches 1433; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

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Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

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Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

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Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
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Db        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420

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Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
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Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

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Job time : 1825.98 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

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(without alignments)
7321.729 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 253354 seqs, 63461778 residues

Total number of hits satisfying chosen parameters: 506708

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	35	2.2	2487	6	US-10-471-571A-3681	Sequence 3681, Ap
	3	34.8	2.2	3166	7	US-11-293-697-739	Sequence 739, App
c	4	34.4	2.2	1438	6	US-10-953-349-20792	Sequence 20792, A
	5	34.4	2.2	2268	7	US-11-217-529-1612	Sequence 1612, Ap
	6	33.8	2.1	1287	7	US-11-217-529-80999	Sequence 80999, A
	7	33.8	2.1	1948	6	US-10-508-063A-4	Sequence 4, Appli
	8	33.2	2.1	1710	7	US-11-217-529-79541	Sequence 79541, A
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	11	32.4	2.0	2338	7	US-11-293-697-1600	Sequence 1600, Ap
	12	32	2.0	620	6	US-10-953-349-32903	Sequence 32903, A
	13	32	2.0	2024	7	US-11-293-697-1253	Sequence 1253, Ap
	14	31.8	2.0	1404	6	US-10-471-571A-5411	Sequence 5411, Ap
c	15	31.8	2.0	1906	6	US-10-953-349-22720	Sequence 22720, A
c	16	31.4	2.0	654	6	US-10-488-619-2605	Sequence 2605, Ap
c	17	31.4	2.0	1636	6	US-10-953-349-22635	Sequence 22635, A
c	18	31.4	2.0	6051	7	US-11-313-450-9	Sequence 9, Appli
	19	31.2	2.0	1286	7	US-11-145-307A-72	Sequence 72, Appl
c	20	31.2	2.0	1532	6	US-10-196-749-121	Sequence 121, App
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c	25	30.8	1.9	992	6	US-10-953-349-31065	Sequence 31065, A
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c	29	30.8	1.9	2920	7	US-11-293-697-683	Sequence 683, App
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	31	30.6	1.9	979	6	US-10-953-349-34412	Sequence 34412, A
	32	30.6	1.9	1210	6	US-10-953-349-23356	Sequence 23356, A
	33	30.6	1.9	1761	6	US-10-953-349-22246	Sequence 22246, A
	34	30.6	1.9	2619	7	US-11-302-678-18	Sequence 18, Appl
	35	30.6	1.9	3232	7	US-11-302-678-16	Sequence 16, Appl
c	36	30.4	1.9	296	7	US-11-301-554-517	Sequence 517, App
	37	30.4	1.9	444	7	US-11-217-529-79558	Sequence 79558, A
c	38	30.4	1.9	1467	7	US-11-217-529-79610	Sequence 79610, A
c	39	30.4	1.9	2249	7	US-11-293-697-442	Sequence 442, App
c	40	30.4	1.9	3294	7	US-11-293-697-1397	Sequence 1397, Ap
c	41	30.2	1.9	924	7	US-11-217-529-1898	Sequence 1898, Ap
c	42	30.2	1.9	1422	6	US-10-953-349-31587	Sequence 31587, A
	43	30.2	1.9	1491	6	US-10-953-349-10993	Sequence 10993, A
	44	30.2	1.9	1848	6	US-10-519-335-5	Sequence 5, Appli
	45	30.2	1.9	1878	6	US-10-519-335-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-10-196-749-411
; Sequence 411, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 411
; LENGTH: 3401
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-196-749-411

Query Match 2.3%; Score 36.8; DB 6; Length 3401;
Best Local Similarity 46.5%; Pred. No. 0.22;
Matches 119; Conservative 0; Mismatches 137; Indels 0; Gaps 0;

```
Qy        540 CAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTG 599
              ||  ||  || ||  | |  | |  |||| |   ||||| ||    | || || ||   |
Db        130 CACCGTCTACTACGTGCACAACATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAG 189

Qy        600 CCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAA 659
              || | | | | |    | |   | |  ||   |    ||| | |  |   |||| ||
Db        190 CCTGACGGGCTACCGCACCTACCGCTGTGCCCACCCCCTGGCCACACTCTTCAAGATCCT 249

Qy        660 GTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAA 719
              |       ||||| ||||    || || ||   | | |||||     | || |||
Db        250 GGCGTCCTTCTACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCATGTACACACTGTG 309

Qy        720 GAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCC 779
              |    ||| || |    |  | || || |    |  || |    |  |   |||   |
Db        310 GTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTTGAGTCGATCCGTGAGGAGAGCAG 369

Qy        780 TGACACCTGGAGCACC 795
              ||| |   | | ||
Db        370 CTACAGCGACATCCCC 385
```

RESULT 2
US-10-471-571A-3681
; Sequence 3681, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 3681
; LENGTH: 2487
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-471-571A-3681

Query Match 2.2%; Score 35; DB 6; Length 2487;
Best Local Similarity 46.2%; Pred. No. 0.67;
Matches 116; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

```
Qy       1336 AAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGG 1395
              ||  ||  | | | || |   || |    ||||   |||| |  ||| | | | ||  |
Db       2144 AATATAAAACGGTTGAATCACAGGAATCTGAAGCTAAAGATAGTAAGGAAACATACGACA 2203

Qy       1396 CAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAAT 1455
              ||    ||   | ||    ||| | ||  |   ||  ||        |  ||   |  |
Db       2204 CAACCTTTAAAGTATATCCACAAGGTGCAACAAATGTATCGAAACATCAAGATGCACATG 2263

Qy       1456 GTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACT 1515
              | ||| |   ||    | | | || |||      |  ||  |  | ||| |   || |
Db       2264 GGCAAGATGATGCACATTCAATAGTACTAGATGATAAAACGATGGCATTGTACCAAGAAG 2323

Qy       1516 AAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGA 1575
                || ||          | ||| |  | |||  |  || | |  |  ||  ||||| | |
Db       2324 TGAAACAGCAATCAGCAAGTTCATTGTTCTTATATGATGCTTTAATAGATTATCAAAACA 2383

Qy       1576 ATGATGAGCTA 1586
              |  || | |||
Db       2384 AGCATCAACTA 2394
```

RESULT 3
US-11-293-697-739
; Sequence 739, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 739
; LENGTH: 3166
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-739

Query Match 2.2%; Score 34.8; DB 7; Length 3166;
Best Local Similarity 49.5%; Pred. No. 0.91;
Matches 90; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

```
Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              || ||||| || ||  |  || ||||| |    ||      | |    |   ||| |  |
Db       1418 GGACAGAGAGGTCAGAAATGAATATAACATCACCATCACCGTGACCGACTTGGGGACACC 1477

Qy        597 CTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCT 656
              | | | |    ||||| | | | || || |    |||   |  | | |    ||   |
Db       1478 CAGGCTGAAAACCGAGCACAACATAACCGTGCTGGTCTCCGACGTCAATGACAACGCCCC 1537

Qy        657 CAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACC 716
              || | | |   | || || | | ||| || | || | || ||  || | ||  |
Db       1538 CATCTTCACCCAAACCTCCTACACCCTGTTCGTCCGCGAGAACAACAGCCCCGCCCTGCA 1597

Qy        717 CA 718
              ||
Db       1598 CA 1599
```

RESULT 4
US-10-953-349-20792/c
; Sequence 20792, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20792
; LENGTH: 1438
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-20792

Query Match 2.2%; Score 34.4; DB 6; Length 1438;
Best Local Similarity 50.0%; Pred. No. 0.72;
Matches 86; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

```
Qy        243 ATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTT 302
              ||  ||| |||   || | ||  |||      | | |||    |       ||| ||  | |
Db       1331 ATAGGCACATGGAAGCAATTACTCCTTCACCATATGAGAACAACACTGGAGTCAAGCATG 1272

Qy        303 CCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAA 362
              ||||  || ||| |     |||  ||    |    ||| || | || || | | ||   ||
Db       1271 GATCCTAATCCACTAGTTCGAAACTGTGTTAAACTCCTCTCAAATTTTCATGCAATCTAA 1212

Qy        363 AGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGA 414
                ||   |||| |||||| | |     | | | ||    ||| |   ||
Db       1211 CTGTAACACTGATAACATCTTTTTTACCCCTTATGTAATACTTTACTGCTGA 1160
```

```
RESULT 5
US-11-217-529-1612
; Sequence 1612, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1612
;   LENGTH: 2268
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-1612

  Query Match             2.2%;  Score 34.4;  DB 7;  Length 2268;
  Best Local Similarity   59.0%;  Pred. No. 0.97;
  Matches   59;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy        150 CAATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGG 209
              |||||| |||||||| ||||||      |||  | | |    | ||   ||  |   |
Db       1869 CAATACCCCTGAAGAAAATGACACTGAGGGGAAGTATAATACAATCAAGAAAAGCTCGGA 1928

Qy        210 CTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCA 249
              | || | || |||  | ||   |  ||||||||||  ||
Db       1929 TTATGATGAATCTCATATCACGAATATCAAAGAATTACCA 1968


RESULT 6
US-11-217-529-80999
; Sequence 80999, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80999
;   LENGTH: 1287
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-80999

  Query Match             2.1%;  Score 33.8;  DB 7;  Length 1287;
  Best Local Similarity   53.4%;  Pred. No. 1;
  Matches   71;  Conservative    0;  Mismatches   62;  Indels    0;  Gaps    0;

Qy       1446 GGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTT 1505
              | || |||||         ||||  | |  ||    ||| ||| ||  | ||| ||| |||
Db        327 GCCCATGAATAGATCAGATGTGGATTTAACAATATACTACTCTTTTAATGAAACGGTTTT 386

Qy       1506 TTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGAC 1565
              | ||  | || ||     |   |   | || |||| | |  |   || |  ||| | |
Db        387 AGAGAACCCAAATATAGGTCAAAGTGCAGTTTTTCAGGATGGCTACATCCAAGCATTAGC 446

Qy       1566 CATCAATAGAATG 1578
              ||||| |  | ||
Db        447 CATCAGTCCAGTG 459


RESULT 7
US-10-508-063A-4
; Sequence 4, Application US/10508063A
; Publication No. US20060088832A1
; GENERAL INFORMATION:
;  APPLICANT: Deutsches Krebsforschungszentrum
;  APPLICANT:  ANGEL, Peter
;  APPLICANT:  FURSTENBERGER, Gerhard
;  APPLICANT:  BREITENBACH, Ute
;  APPLICANT:  RICHTER, Harmut
;  APPLICANT:  HESS, Jochen
;  APPLICANT:  TUCKERMAN, Jan
;  TITLE OF INVENTION: TAP-70, A NOVEL MARKER FOR EPITHELIAL TUMORS
;  FILE REFERENCE: 31304-701.831
;  CURRENT APPLICATION NUMBER: US/10/508,063A
;  CURRENT FILING DATE:  2004-09-16
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 1948
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-508-063A-4

  Query Match             2.1%;  Score 33.8;  DB 6;  Length 1948;
  Best Local Similarity   52.4%;  Pred. No. 1.4;
  Matches   99;  Conservative    0;  Mismatches   87;  Indels    3;  Gaps    1;

Qy        495 CCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAG 554
              | ||| ||  | | | | ||     ||   |||  |  | |  || || ||      | |
Db       1111 CAAAGTGGCCAATGGGGCAGAGATGAAGATCTTGGGTGTGTGGGACACAGAAATTAGCCT 1170

Qy        555 GGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGA 614
              ||   | |  |||   |  |  |||| || || || ||  ||| ||   || |  ||||
Db       1171 GGGCAAGACAAAGCTGAAGGCCGAGTTTCTGGTGGCCAACGCCAGC---GCAGAAGAGGC 1227

Qy        615 GAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACAC 674
              |   |   ||  || ||| ||  ||||   | |  |  |||  | | |||| ||  |||
Db       1228 TATTATTGGCACAGACGTCTTGCAGGACCACAATGCCGTGCTGGACTTCGAACACCGCAC 1287

Qy        675 CAGCAGCTT 683
              | ||| | |
Db       1288 CTGCACCCT 1296


RESULT 8
US-11-217-529-79541
; Sequence 79541, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
```

```
; SEQ ID NO 79541
;   LENGTH: 1710
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (1692)..(1692)
;   OTHER INFORMATION: a, c, g, t, unknown, or other
US-11-217-529-79541

  Query Match             2.1%;  Score 33.2;  DB 7;  Length 1710;
  Best Local Similarity   55.1%;  Pred. No. 1.9;
  Matches   65;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy       1085 TCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAG 1144
              |||  |||   ||||| ||   ||    | | | ||| |||| ||     ||    |||||
Db        290 TCAAGAACGATCTTCAAAATTTCATGAAGAATGTAGGATTTGACCAACACAAACTCGAAG 349

Qy       1145 AGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACC 1202
              |  | ||  |||| |||||   | ||||    || ||| |    ||  |    ||||
Db        350 ATGTAGACGATGACGATATAGAAGAAGAATCCACTAGCTCCAAAGAATCTAAAATACC 407


RESULT 9
US-11-293-697-145
; Sequence 145, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 145
;   LENGTH: 2513
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-145

  Query Match             2.1%;  Score 33.2;  DB 7;  Length 2513;
  Best Local Similarity   52.1%;  Pred. No. 2.5;
  Matches   74;  Conservative    0;  Mismatches   68;  Indels    0;  Gaps    0;

Qy        627 TGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTT 686
              ||||  |  |   |||| |||     |  |  |  |||| | |||| || | |     || |
Db        973 TGAAATGGCCCTGGATGCTGAGTTCCTGGACGTGTACAAGAACTGCAACGGGGTGGTCAT 1032

Qy        687 CATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAA 746
               ||     ||||| | ||| | |     |   |||  || | |  | | |||    ||||
Db       1033 GATGTTCGACATTACCAAGCAGTGGACCTTCAATTACATTCTCCGGGAGCTTCCAAAAGT 1092

Qy        747 TTCTCGGCATGTGGAAGTGAGC 768
                |    || |||  |||| ||
Db       1093 GCCCACCCACGTGCCAGTGTGC 1114


RESULT 10
US-10-953-349-38921
; Sequence 38921, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38921
;   LENGTH: 2152
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-38921

  Query Match             2.0%;  Score 32.4;  DB 6;  Length 2152;
  Best Local Similarity   47.9%;  Pred. No. 4;
  Matches   93;  Conservative    0;  Mismatches  101;  Indels    0;  Gaps    0;

Qy        524 TCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTC 583
              |||| || ||| || ||||        | |  | |  | | |||| | || |  ||| |
Db        475 TCTCGGCCGAGGAGATCAGCTCCATGATCCTGAACAAGATGAAGGAGACGGCCGAGGCTT 534

Qy        584 AGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACG 643
              |    ||||   ||  |  |   || |  | | | | ||     |  ||   |    |
Db        535 ACCTCGGCACCACCATCAAGAACGCTGTCGTCACCGTCCCGGCCTACTTCAACGACTCCC 594

Qy        644 CTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCA 703
                  ||      |||| |||    |  || |  | || ||  | ||| |  ||||||||
Db        595 AGCGCCAGGCCACCAAGGACGCCGGCGTCATCTCCGGCCTCAACGTCATGCGCATCATCA 654

Qy        704 AACCGGACCCACCC 717
              |   |  | |  ||
Db        655 ACGAGCCCACCGCC 668


RESULT 11
US-11-293-697-1600
; Sequence 1600, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1600
;   LENGTH: 2338
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1600

  Query Match             2.0%;  Score 32.4;  DB 7;  Length 2338;
  Best Local Similarity   49.4%;  Pred. No. 4.3;
  Matches   84;  Conservative    0;  Mismatches   86;  Indels    0;  Gaps    0;

Qy       1312 CTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCA 1371
              || ||  | | | | | | |  | |  |||||||||||  | || |         || | |
Db       1001 CTCAGGCGGAGCAAAGTGTCCATTGAGATGTACCAGTCGCAGGTGGCAAAGCTGGAGGAT 1060

Qy       1372 AAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATT 1431
                | | |  |  ||  |  ||  | ||  | | ||| |  |    | ||  |
Db       1061 GATATCTACAAAGAGGCCGAAGAGAAGGCCCTGCTGAAGGAGGCCCTGGAGCGCATGGAG 1120

Qy       1432 GATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAA 1481
                |  ||||||  ||||    ||  |||||||| |  |    ||  |||||
Db       1121 CACCAGCTGTGCCAGGAGAAGAGGGTCAACAGGGCCATCCGGCAGCAGAA 1170


RESULT 12
US-10-953-349-32903
; Sequence 32903, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
```

```
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32903
;   LENGTH: 620
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-32903

  Query Match             2.0%;  Score 32;  DB 6;  Length 620;
  Best Local Similarity   47.1%;  Pred. No. 2.4;
  Matches   98;  Conservative    0;  Mismatches  110;  Indels    0;  Gaps    0;

Qy        574 GTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTC 633
              |||||||       | |    ||     || |||||| | |  |   |  ||   |   ||
Db         90 GTGGAGTTGGCAAAAGCTCATGAGATCCAGGCTGCTGTGCTGTTGCACCCTTCTTTTGTT 149

Qy        634 GTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGG 693
                || |||| |||  |  || |||||| || ||  |  | |  | |       ||
Db        150 ACCGTTGACGATATCAAAGAGGTCAAGTGCGCAATTTCTATCCTCGGAGCTGAGATTGAC 209

Qy        694 GACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGG 753
               | ||    |  |||||| | |  |||| |  |  | | |    |  |      || ||  ||
Db        210 AAAATGTCCCCACCGGAGCTAATCAAGCAGTTCGAGCAGGTCCTTTCTTTGAACTCAGGG 269

Qy        754 CATGTGGAAGTGAGCTGGGAATACCCTG 781
                ||    |  |   |  |  | |||||
Db        270 GTTGGCCACTTCGTCAAGATCTTCCCTG 297


RESULT 13
US-11-293-697-1253
; Sequence 1253, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1253
;   LENGTH: 2024
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1253

  Query Match             2.0%;  Score 32;  DB 7;  Length 2024;
  Best Local Similarity   50.7%;  Pred. No. 5.2;
  Matches   77;  Conservative    0;  Mismatches   75;  Indels    0;  Gaps    0;

Qy        210 CTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTG 269
              |||||  |  |||  |  ||      |||    | |   | | |   |||       |||| ||
Db        496 CTCTGTTGAAAGTTTGTTTCACCAGCAAATACTTTCTTCTTGTGCCAAAAGCTATAACTT 555

Qy        270 TCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGG 329
              |  ||  ||     |  ||||  | |  |||||  |    | ||  |   ||  || |||||   |
Db        556 TGATCAATATAGGAAGGTCTTTACTCATTCATCATTGCTTAATCAACAAGAGGAAATAGA 615

Qy        330 AATTTGGTCCACTGATATCTTAAGGGAACAGA 361
               ||||||    |    ||  | ||   ||  | |
Db        616 TATTTGGGGAAAACATCACATATATGATAAAA 647


RESULT 14
US-10-471-571A-5411
; Sequence 5411, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 5411
;   LENGTH: 1404
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-5411

  Query Match             2.0%;  Score 31.8;  DB 6;  Length 1404;
  Best Local Similarity   57.6%;  Pred. No. 4.7;
  Matches   57;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy        328 GGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTA 387
              | |||||  |  |   |  | |  | |  || ||  ||| |||   ||   ||||  ||| ||
Db         11 GTAATTTTTTAAATGTAGAGTTAATAGGTACTAAAATAATAACAATGGAAGACTTTTATA 70

Qy        388 AAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              |||||   |   ||||||| ||||  |  | | | || |
Db         71 AAATGAAGGAAGAAGAATTTTTCTTAAAATCTAAGCTAC 109


RESULT 15
US-10-953-349-22720/c
; Sequence 22720, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22720
;   LENGTH: 1906
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-22720

  Query Match             2.0%;  Score 31.8;  DB 6;  Length 1906;
  Best Local Similarity   61.4%;  Pred. No. 5.8;
  Matches   51;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy        226 ACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAG 285
              || ||||||||||  ||  ||||||  | |        ||   | ||||||      | |
Db        918 ACTATCCAAGTCACTGACATTGCAGTTCCCATTATTTAACGCAGTCATATCTATAGAGGA 859

Qy        286 GTTCTGAGCCATTCGTTCCTCCT 308
                || |||||||  |  ||||||||
Db        858 ATTTTGAGCCAATGCTTCCTCCT 836


Search completed: June 10, 2006, 18:18:59
Job time : 28.719 secs
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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 12, 2006, 15:14:42 ; Search time 7227.31 Seconds
(without alignments)
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Title: US-10-821-670A-39
Perfect score: 2799
Sequence: 1 MHPQQLVIAWLSLVLLAPPL.....HAFRIRAVTINRMMSYLNAS 533

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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5: gb_pr:*
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8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		2799	100.0	1599	2	AR595956	AR595956 Sequence
2	c	2799	100.0	1599	2	AR595957	AR595957 Sequence
3		2687	96.0	1533	2	AR595959	AR595959 Sequence
4	c	2687	96.0	1533	2	AR595960	AR595960 Sequence
5		2643	94.4	1599	2	AR595971	AR595971 Sequence
6	c	2643	94.4	1599	2	AR595972	AR595972 Sequence
7		2546	91.0	1533	2	AR595973	AR595973 Sequence
8	c	2546	91.0	1533	2	AR595974	AR595974 Sequence
9		2427	86.7	1626	8	AF401989	AF401989 Synthetic
10		2390.5	85.4	1623	2	AR091394	AR091394 Sequence
11		2390.5	85.4	6139	2	AR091393	AR091393 Sequence
12		2324.5	83.0	1560	2	AR091395	AR091395 Sequence
13		1758	62.8	1006	14	FCIL12P40	Y07762 Felis catus
14		1748	62.5	4522	2	AX076209	AX076209 Sequence
15		1748	62.5	4522	2	AX076476	AX076476 Sequence
16		1747	62.4	987	2	AR595950	AR595950 Sequence
17	c	1747	62.4	987	2	AR595951	AR595951 Sequence
18		1747	62.4	990	2	AX076200	AX076200 Sequence
19		1747	62.4	990	2	AX076482	AX076482 Sequence
20		1743	62.3	985	2	AR595967	AR595967 Sequence
21	c	1743	62.3	985	2	AR595968	AR595968 Sequence
22		1742	62.2	990	14	FCU83184	U83184 Felis catus
23		1741	62.2	2193	2	AR242435	AR242435 Sequence
24		1741	62.2	2193	2	AR280203	AR280203 Sequence
25		1741	62.2	2193	2	AR322418	AR322418 Sequence
26		1741	62.2	5252	2	CQ803341	CQ803341 Sequence
27		1741	62.2	9049	2	CQ803350	CQ803350 Sequence
28		1741	62.2	10633	2	CQ803349	CQ803349 Sequence
29		1741	62.2	11746	2	CQ803348	CQ803348 Sequence
30		1741	62.2	38246	2	CQ803351	CQ803351 Sequence
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32		1669.5	59.6	2438	2	CQ812173	CQ812173 Sequence
33		1646	58.8	921	2	AR595948	AR595948 Sequence
34	c	1646	58.8	921	2	AR595949	AR595949 Sequence
35		1643	58.7	987	2	AR595969	AR595969 Sequence
36	c	1643	58.7	987	2	AR595970	AR595970 Sequence
37		1643	58.7	990	2	AR151071	AR151071 Sequence
38		1643	58.7	990	2	BD014663	BD014663 Process f
39		1643	58.7	990	2	E15017	E15017 Canine mRNA
40		1643	58.7	990	2	AR316470	AR316470 Sequence
41		1643	58.7	2267	2	AR596011	AR596011 Sequence
42	c	1643	58.7	2267	2	AR596012	AR596012 Sequence
43		1639	58.6	921	2	AR242436	AR242436 Sequence
44		1639	58.6	921	2	AR242437	AR242437 Sequence
45		1639	58.6	921	2	AR280204	AR280204 Sequence

ALIGNMENTS

RESULT 1
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LOCUS AR595956 1599 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 38 from patent US 6818444.
ACCESSION AR595956
VERSION AR595956.1 GI:56646937
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1599)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 38 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .1599
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.: 1.84e-297 Length: 1599
Score: 2799.00 Matches: 533
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0

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DB:                    2              Gaps:          0

US-10-821-670A-39 (1-533) x AR595956 (1-1599)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuPro 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020

Qy        341 ThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArg 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 1080

Qy        361 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 1140

Qy        381 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeu 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200

Qy        401 ProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 1260

Qy        421 AsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSer 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 1320

Qy        441 IleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeu 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 1380

Qy        461 MetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 1440

Qy        481 LeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluPro 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        501 AspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAla 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 1560

Qy        521 ValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 533
              |||||||||||||||||||||||||||||||||||||||
Db       1561 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599

RESULT 2
AR595957/c
LOCUS       AR595957               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 40 from patent US 6818444.
ACCESSION   AR595957
VERSION     AR595957.1  GI:56646938
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 40 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

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Pred. No.:              1.84e-297       Length:         1599
Score:                  2799.00         Matches:        533
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-39 (1-533) x AR595957 (1-1599)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1599 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 1540
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Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 1420

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1359 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 1300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1299 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 1240

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1179 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 1120

Qy        161 GlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1119 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 1060

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        999 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 940

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        939 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 880

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        879 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 820

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 760

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        759 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 640

Qy        321 SerAsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuPro 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        639 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 580

Qy        341 ThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArg 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        579 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 520

Qy        361 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        519 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 460
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Qy        381 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeu 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        459 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 400

Qy        401 ProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        399 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 340

Qy        421 AsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSer 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        339 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 280

Qy        441 IleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeu 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        279 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 220

Qy        461 MetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 160

Qy        481 LeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluPro 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        159 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 100

Qy        501 AspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAla 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 40

Qy        521 ValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 533
              ||||||||||||||||||||||||||||||||||||||
Db         39 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
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RESULT 3
AR595959
LOCUS       AR595959                1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 43 from patent US 6818444.
ACCESSION   AR595959
VERSION     AR595959.1  GI:56646940
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 43 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.73e-285       Length:         1533
Score:                  2687.00         Matches:        511
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            96.0%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-39 (1-533) x AR595959 (1-1533)
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Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        163 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        323 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy        343 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020

Qy        363 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080

Qy        383 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy        403 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200

Qy        423 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260

Qy        443 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320

Qy        463 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380

Qy        483 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440

Qy        503 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500

Qy        523 IleAsnArgMetMetSerTyrLeuAsnAlaSer 533
              |||||||||||||||||||||||||||||||||
Db       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
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RESULT 4
AR595960/c

LOCUS	AR595960	1533 bp DNA	linear PAT 15-DEC-2004
DEFINITION	Sequence 45 from patent US 6818444.		
ACCESSION	AR595960		
VERSION	AR595960.1 GI:56646941		
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
	Unclassified.		
REFERENCE	1 (bases 1 to 1533)		
AUTHORS	Wonderling,R.S. and Boroughs,K.L.		
TITLE	Canine and feline proteins, nucleic acid molecules and uses thereof		
JOURNAL	Patent: US 6818444-A 45 16-NOV-2004; Heska Corporation; Fort Collins, CO		

FEATURES Location/Qualifiers
source 1. .1533
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.:	3.73e-285	Length:	1533
Score:	2687.00	Matches:	511
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	96.0%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-39 (1-533) x AR595960 (1-1533)

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Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
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Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
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Db      1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy       143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162

Db      1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy       163 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182

Db      1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy       183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202

Db      1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222

Db       993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242

Db       933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy       243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262

Db       873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy       263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282

Db       813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy       283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302

Db       753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy       303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322

Db       693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy       323 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 342

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Qy       343 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 362

Db       573 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy       363 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 382

Db       513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy       383 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 402

Db       453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy       403 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 422

Db       393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy       423 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 442

Db       333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy       443 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 462

Db       273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy       463 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 482

Db       213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy       483 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 502
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Db       153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy       503 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 522

Db        93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy       523 IleAsnArgMetMetSerTyrLeuAsnAlaSer 533

Db        33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
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RESULT 5
AR595971
LOCUS AR595971 1599 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 61 from patent US 6818444.
ACCESSION AR595971
VERSION AR595971.1 GI:56646952
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1599)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 61 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .1599
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Alignment Scores:

Pred. No.:	2.8e-280	Length:	1599
Score:	2643.00	Matches:	501
Percent Similarity:	96.4%	Conservative:	13
Best Local Similarity:	94.0%	Mismatches:	19
Query Match:	94.4%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-39 (1-533) x AR595971 (1-1599)

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Qy         1 MetHisProGlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeu 20

Db         1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

Qy        21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40

Db        61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60

Db       121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy        61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80

Db       181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100

Db       241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy       101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120

Db       301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360

Qy       121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140

Db       361 AAAGAATCCAAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy       141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160

Db       421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
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Qy       161 GlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
Db       481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540

Qy       181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
Db       541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy       201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
Db       601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Qy       221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
Db       661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy       241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
Db       721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy       261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
Db       781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Qy       281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
Db       841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy       301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
Db       901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960

Qy       321 SerAsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuPro 340
Db       961 AGCGACTGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020

Qy       341 ThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArg 360
Db      1021 ACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGA 1080

Qy       361 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 380
Db      1081 GCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCC 1140

Qy       381 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeu 400
Db      1141 GAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200

Qy       401 ProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThr 420
Db      1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACT 1260

Qy       421 AsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSer 440
Db      1261 AACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGC 1320

Qy       441 IleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeu 460
Db      1321 ATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTA 1380

Qy       461 MetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 480
Db      1381 ATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTG 1440

Qy       481 LeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluPro 500
Db      1441 TTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCG 1500

Qy       501 AspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAla 520
Db      1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCG 1560

Qy       521 ValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 533
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Db      1561 GTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1599

RESULT 6
AR595972/c
LOCUS       AR595972                1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 63 from patent US 6818444.
ACCESSION   AR595972
VERSION     AR595972.1  GI:56646953
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 63 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.8e-280        Length:         1599
Score:                  2643.00         Matches:        501
Percent Similarity:     96.4%           Conservative:   13
Best Local Similarity:  94.0%           Mismatches:     19
Query Match:            94.4%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-39 (1-533) x AR595972 (1-1599)

Qy         1 MetHisProGlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeu 20
Db      1599 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 1540

Qy        21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
Db      1539 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy        41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
Db      1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 1420

Qy        61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
Db      1419 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy        81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
Db      1359 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 1300

Qy       101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
Db      1299 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 1240

Qy       121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
Db      1239 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy       141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
Db      1179 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 1120

Qy       161 GlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
Db      1119 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 1060

Qy       181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
Db      1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000
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Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              |||:::|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        999 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 940

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        939 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 880

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        879 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 820

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              |||||||||||||||||||||||||||||||||||||||||||   :::|||   ||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 760

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        759 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 640

Qy        321 SerAsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuPro 340
              |||:::|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        639 AGCGACTGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 580

Qy        341 ThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArg 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        579 ACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGA 520

Qy        361 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 380
              |||:::|||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        519 GCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCC 460

Qy        381 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeu 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        459 GAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTA 400

Qy        401 ProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        399 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACT 340

Qy        421 AsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSer 440
              ||||||||||||||||||   |||   ||||||||||   ||||||||||||||||||||
Db        339 AACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGC 280

Qy        441 IleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeu 460
              ||||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||
Db        279 ATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTA 220

Qy        461 MetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 ATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTG 160

Qy        481 LeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluPro 500
              ||||||||||||||   ||||||||||||||||||||   ||||||||||||||||||||
Db        159 TTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCG 100

Qy        501 AspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAla 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCG 40

Qy        521 ValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 533
              |||||||||||||||||||||||||||||||:::|||
Db         39 GTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1

RESULT 7
AR595973
LOCUS       AR595973               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 66 from patent US 6818444.
ACCESSION   AR595973
VERSION     AR595973.1  GI:56646954
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 66 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.27e-269       Length:         1533
Score:                  2546.00         Matches:        482
Percent Similarity:     96.7%           Conservative:   12
Best Local Similarity:  94.3%           Mismatches:     17
Query Match:            91.0%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-39 (1-533) x AR595973 (1-1533)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||||:::|||||||||   |||   |||
Db        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||||
Db        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420

Qy        163 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              ||||||||||||   ||||||||||||||||   ||||||||||||||:::|||||||||
Db        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282

Db        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302

Db        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322

Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900

Qy        323 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 342

Db        901 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy        343 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 362

Db        961 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 1020

Qy        363 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 382

Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 1080

Qy        383 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 402

Db       1081 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy        403 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 422

Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1200

Qy        423 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 442

Db       1201 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1260

Qy        443 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 462

Db       1261 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1320

Qy        463 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 482

Db       1321 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 1380

Qy        483 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 502

Db       1381 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1440

Qy        503 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 522

Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1500

Qy        523 IleAsnArgMetMetSerTyrLeuAsnAlaSer 533

Db       1501 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1533

RESULT 8
AR595974/c
LOCUS       AR595974                1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 68 from patent US 6818444.
ACCESSION   AR595974
VERSION     AR595974.1  GI:56646955
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 68 16-NOV-2004;
            Heska Corporation; Fort Collins, CO

FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.27e-269       Length:         1533
Score:                  2546.00         Matches:        482
Percent Similarity:     96.7%           Conservative:   12
Best Local Similarity:  94.3%           Mismatches:     17
Query Match:            91.0%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-39 (1-533) x AR595974 (1-1533)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42

Db       1533 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62

Db       1473 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1414

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82

Db       1413 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102

Db       1353 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1294

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122

Db       1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142

Db       1233 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162

Db       1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy        163 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182

Db       1113 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1054

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202

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Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242

Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 874

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262

Db        873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282

Db        813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302

Db        753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
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Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 634

Qy        323 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 342

Db        633 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        343 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 362

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Qy        363 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 382

Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 454

Qy        383 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 402

Db        453 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy        403 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 422

Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 334

Qy        423 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 442

Db        333 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 274

Qy        443 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 462

Db        273 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 214

Qy        463 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 482

Db        213 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 154

Qy        483 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 502

Db        153 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 94

Qy        503 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 522

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Db         33 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1
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LOCUS       AF401989               1626 bp    mRNA    linear   SYN 14-FEB-2002
DEFINITION  Synthetic construct single chain interleukin-12 mRNA, complete cds.
ACCESSION   AF401989
VERSION     AF401989.1  GI:18656516
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 1626)
  AUTHORS   McMonagle,E.L.J., Taylor,S., van Zuilekom,H., Sanders,L.,
            Scholtes,N., Keanie,L.J., Hopkins,C.A., Logan,N.A., Bain,D.,
            Argyle,D.J., Onions,D.E., Schijns,V.E. and Nicolson,L.
  TITLE     Production of biologically active equine interleukin 12 through
            expression of p35, p40 and single chain IL-12 in mammalian and
            baculovirus expression systems
  JOURNAL   Equine Vet. J. 33 (7), 693-698 (2001)
   PUBMED   11770992
REFERENCE   2  (bases 1 to 1626)
  AUTHORS   McMonagle,L.J., Taylor,S., Keanie,L.J., Hopkins,C.A., Logan,N.A.,
            Argyle,D.J., Onions,D.E. and Nicolson,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUL-2001) Veterinary Pathology, Glasgow Veterinary
            School, Bearsden Rd, Glasgow G61 1QH, UK
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     CDS             1. .1626
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Percent Similarity:     90.6%           Conservative:   31
Best Local Similarity:  84.8%           Mismatches:     43
Query Match:            86.7%           Indels:         8
DB:                     8               Gaps:           1

US-10-821-670A-39 (1-533) x AF401989 (1-1626)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeu 20

Db          1 ATGGGTCACCAGTGGTTGGTCCTCTCCTGGTTTTCCCTGGTTTTGCTGGCGTCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40

Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTGTATGTTGTAGAATTGGATTGGTACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60

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Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80

Db        181 ACCTCGGCCCAGAGCAATGAGGTCTTAGGCTCTGGCAAAACCTTGACCATCCAAGTCAAA 240

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Db        301 CACCTGCTGCTTCACAAGAAGGAAGATGGAATTTGGTCCACTGACATTTTAAAAGACCAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140

Db        361 AAAGAATCCAAAAATAAGACCTTTCTAAAATGTGAGGCAAAGAATTATTCCGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
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Db        421 ACATGCTGGTGGCTGACAGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180

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Db        601 CCGGCCGCCGAGGAGAGCCTGCCCATTGAGATCGTGGTGGATGCTGTTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240

Db        661 TATGAAAACTACACCAGCGGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260

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Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280

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Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300

Db        841 AAGAACAAGAAGGAAAGGAAAGACAGACTCTTCATGGATGAGACTTCAGCCACAGTCACA 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320

Db        901 TGCCACAAGGATGGCCAGATCCGTGTCCAAGCCAGGGACCGCTACTACAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSerGlyGly----------Gly 332

Db        961 AGCGAATGGGCATCCGTATCCTGCAGTGGTGGCGGTGGCTCGGGCGGTGGTGGATCCGGT 1020

Qy        333 GlyGlyGlySerArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeu 352

Db       1021 GGCGGCGGATCTAGGAACCTCCCCACAGCCACACCAGGCCCAGGAATGTTCCAGTGCCTC 1080

Qy        353 AsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThr 372

Db       1081 AACCACTCCCAAAACCTGCTGAGGACCGTCAGCAACACGCTTCAGAAGGCCAGGCAAACC 1140

Qy        373 LeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLys 392

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Qy        393 ThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAla 412

Db       1201 AGCAGCACCGTGGCGGCCTGCCTCCCCCTGGAACTCGCCCCGAACGAGAGTTGCCTGGCT 1260

Qy        413 SerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPhe 432

Db       1261 TCCAGAGAGATCTCTTTCATAACTAATGGGAGTTGCCTGACCCCCGGAAAGGCCTCTTCT 1320

Qy        433 MetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPhe 452

Db       1321 ATGATGACGCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTC 1380

Qy        453 LysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsn 472

Db       1381 AAGGCCATGAATGCCAAGCTGTTGATAGATCCTCAGAGGCAGATCTTTCTGGATGAGAAC 1440

Qy        473 MetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValPro 492

Db       1441 ATGCTGACAGCCATTGACAAGCTGATGCAGGCCCTGAACTTCAACAGTGAGACTGTGCCA 1500

Qy        493 GlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeu 512

Db       1501 CAAAAGCCCTCCCTTGAAGGACTGGATTTTTATAAAACTAAAGTCAAGCTCTGCATCCTT 1560
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Qy        513 LeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAla 532

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Qy        533 Ser 533

Db       1621 TCC 1623
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LOCUS       AR091394               1623 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 9 from patent US 5994104.
ACCESSION   AR091394
VERSION     AR091394.1  GI:10018149
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1623)
  AUTHORS   Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
  TITLE     Interleukin-12 fusion protein
  JOURNAL   Patent: US 5994104-A 9 30-NOV-1999;
FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:              1.86e-252      Length:         1623
Score:                  2390.50        Matches:        456
Percent Similarity:     89.6%          Conservative:   29
Best Local Similarity:  84.3%          Mismatches:     47
Query Match:            85.4%          Indels:         9
DB:                     2              Gaps:           2

US-10-821-670A-39 (1-533) x AR091394 (1-1623)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeu 20

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Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140

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Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160

Db        421 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 480

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Db        598 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 657

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Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280

Db        778 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 837

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Qy        533 Ser 533

Db       1618 TCC 1620
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RESULT 11
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DEFINITION Sequence 7 from patent US 5994104.
ACCESSION AR091393
VERSION AR091393.1 GI:10018148
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 6139)
AUTHORS Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
TITLE Interleukin-12 fusion protein
JOURNAL Patent: US 5994104-A 7 30-NOV-1999;
FEATURES Location/Qualifiers
source 1. .6139
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ORIGIN

Alignment Scores:

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Score:	2390.50	Matches:	456
Percent Similarity:	89.6%	Conservative:	29
Best Local Similarity:	84.3%	Mismatches:	47
Query Match:	85.4%	Indels:	9
DB:	2	Gaps:	2

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Db       3282 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 3341

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60

Db       3342 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 3401

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80

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Db       3462 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 3521

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120

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Db       3762 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 3818

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Db       3819 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 3878

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240

Db       3879 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 3938

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260

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Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300

Db       4059 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 4118

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320

Db       4119 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 4178

Qy        321 SerAsnTrpAlaSerValSerCysSerGlyGly----------------------Gly 332

Db       4179 AGCGAATGGGCATCTGTGCCCTGCAGTGGTGGCGGTGGAAGCGGCGGTGGCGGAAGCGGC 4238

Qy        333 GlyGlyGlySerArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeu 352

Db       4239 GGTGGCGGCAGCAGAAACCTCCCCCTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTT 4298

Qy        353 AsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThr 372

Db       4299 CACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACT 4358

Qy        373 LeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLys 392

Db       4359 CTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAA 4418

Qy        393 ThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAla 412

Db       4419 ACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAAT 4478

Qy        413 SerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPhe 432

Db       4479 TCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTT 4538

Qy        433 MetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPhe 452

Db       4539 ATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTC 4598

Qy        453 LysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsn 472

Db       4599 AAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAAC 4658

Qy        473 MetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValPro 492

Db       4659 ATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCA 4718

Qy        493 GlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeu 512

Db       4719 CAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTT 4778

Qy        513 LeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAla 532

Db       4779 CTTCATGCTTTCAGAATTCGGGCAGTGACTATTGACAGAGTGACGAGCTATCTGAATGCT 4838

Qy        533 Ser 533

Db       4839 TCC 4841
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RESULT 12
AR091395
LOCUS       AR091395               1560 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 11 from patent US 5994104.
ACCESSION   AR091395
VERSION     AR091395.1  GI:10018150
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1560)
  AUTHORS   Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
  TITLE     Interleukin-12 fusion protein
  JOURNAL   Patent: US 5994104-A 11 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .1560
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.24e-245       Length:         1560
Score:                  2324.50         Matches:        442
Percent Similarity:     90.2%           Conservative:   27
Best Local Similarity:  85.0%           Mismatches:     42
Query Match:            83.0%           Indels:         9
DB:                     2               Gaps:           2

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Qy         22 AlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAla 41

Db          1 GCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCC 60

Qy         42 ProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThr 61

Db         61 CCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACC 120

Qy         62 SerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGlu 81

Db        121 TTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAG 180

Qy         82 PheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPhe 101

Db        181 TTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTC 240

Qy        102 LeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLys 121

Db        241 CTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAA 300

Qy        122 GluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThr 141

Db        301 GAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACC 360

Qy        142 CysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGly 161

Db        361 TGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGC 420

Qy        162 SerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArg 181

Db        421 TCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGA 480

Qy        182 ValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysPro 201

Db        481 GGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCA 537

Qy        202 AlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyr 221

Db        538 GCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTAT 597

Qy        222 GluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsn 241
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Db        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAAC 657

Qy        242 LeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAsp 261
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Db        658 TTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGAC 717

Qy        262 ThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLys 281
              ||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        718 ACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAG 777

Qy        282 AsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCys 301
              :::   ||||||||||||||||||:::      ||||||||||||||   |||:::|||
Db        778 AGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGC 837

Qy        302 HisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSer 321
              |||:::|||   |||   |||:::|||:::||||||||||||||||||||||||||||
Db        838 CGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGC 897

Qy        322 AsnTrpAlaSerValSerCysSerGlyGly----------------------GlyGly 333
              ||||||||||||   ||||||||||||                      ||||||
Db        898 GAATGGGCATCTGTGCCCTGCAGTGGTGGCGGTGGAAGCGGCGGTGGCGGAAGCGGCGGT 957

Qy        334 GlyGlySerArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsn 353
              ||||||||||||||||||||      ||||||   ||||||||||||   ||||||:::
Db        958 GGCGGCAGCAGAAACCTCCCCCTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCAC 1017

Qy        354 HisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeu 373
              |||||||||   ||||||||||:::||||||   ||||||||||||||||||||||||
Db       1018 CACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTA 1077

Qy        374 GluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThr 393
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1078 GAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACC 1137

Qy        394 SerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSer 413
              ||||||||||||||||||||||||||||||||||   ||||||||||||||   |||
Db       1138 AGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCC 1197

Qy        414 ArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMet 433
              ||||||   |||   ||||||||||||||||||||||||||||||||||||||||||||
Db       1198 AGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATG 1257

Qy        434 ThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLys 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1258 ATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAG 1317

Qy        454 AlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMet 473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1318 ACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATG 1377

Qy        474 LeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGln 493
              |||      ||||||||||||:::||||||||||||   ||||||   ||||||||||||
Db       1378 CTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAA 1437

Qy        494 AsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeu 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1438 AAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTT 1497

Qy        514 HisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 533
              ||||||||||||||||||||||||||||||:::|||:::   ||||||||||||||||||
Db       1498 CATGCTTTCAGAATTCGGGCAGTGACTATTGACAGAGTGACGAGCTATCTGAATGCTTCC 1557

RESULT 13
FCIL12P40
LOCUS       FCIL12P40               1006 bp    mRNA    linear   MAM 18-APR-2005
DEFINITION  Felis catus mRNA for interleukin-12 p40 chain.
ACCESSION   Y07762
VERSION     Y07762.1  GI:2102664
KEYWORDS    interleukin-12 p40.
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1
  AUTHORS   Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
  TITLE     Molecular cloning of cat interleukin-12
  JOURNAL   Immunogenetics 45 (6), 462-463 (1997)
   PUBMED   9089110
REFERENCE   2  (bases 1 to 1006)
  AUTHORS   Schijns,V.E.C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
            Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
            Utrecht, NETHERLANDS
FEATURES             Location/Qualifiers
     source          1. .1006
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                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
                     /cell_type="lymphocyte"
                     /tissue_type="peripheral blood"
     gene            1. .1006
                     /gene="IL-12.p40"
     CDS             1. .990
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                     /product="interleukin-12 p40 chain"
                     /protein_id="CAA69068.1"
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                     GSSDPQEVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPAAEESLPIEVVVDAIHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFGV
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ORIGIN

Alignment Scores:
Pred. No.:                4.03e-183       Length:          1006
Score:                    1758.00         Matches:         329
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              62.8%           Indels:          0
DB:                       14              Gaps:            0

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Qy          1 MetHisProGlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
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Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
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Db        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987

RESULT 14
AX076209
LOCUS       AX076209               4522 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 10 from Patent WO0104155.
ACCESSION   AX076209
VERSION     AX076209.1  GI:12710834
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 10 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .4522
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Plasmid pMol-fil12p40"
ORIGIN
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Alignment Scores:
Pred. No.:              5.45e-181       Length:         4522
Score:                  1748.00         Matches:        333
Percent Similarity:     94.1%           Conservative:   2
Best Local Similarity:  93.5%           Mismatches:     11
Query Match:            62.5%           Indels:         11
DB:                     2               Gaps:           1

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Qy          1 MetHisProGlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||    ||||||||||||||||||||||||||
Db       3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
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Db       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
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Db       3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy        161 GlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db       3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
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Db       3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
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Db       3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
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Db       3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
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Db       3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006
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Qy        321 SerAsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlySerArgAsnLeu--- 339
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Db       4007 AGCAACTGGGCATCCGTGTCCTGCAGTTA-GGAGCTCATAATCAGCCATACCACATTTGT 4065

Qy        340 ---------------------------ProThrProThrProSerPro 346
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Db       4066 AGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCT 4113

RESULT 15
AX076476
LOCUS       AX076476               4522 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 2 from Patent WO0104280.
ACCESSION   AX076476
VERSION     AX076476.1  GI:12711028
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 2 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="IL-12p40"
ORIGIN

Alignment Scores:
Pred. No.:              5.45e-181      Length:         4522
Score:                  1748.00        Matches:        333
Percent Similarity:     94.1%          Conservative:   2
Best Local Similarity:  93.5%          Mismatches:     11
Query Match:            62.5%          Indels:         11
DB:                     2              Gaps:           1

US-10-821-670A-39 (1-533) x AX076476 (1-4522)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db       3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
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Db       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
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Db       3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
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Db       3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
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Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
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Qy        161 GlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
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Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
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Db       3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
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Db       3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

Qy        321 SerAsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlySerArgAsnLeu--- 339
              ||||||||||||||||||||||||||   |||                  ::::::
Db       4007 AGCAACTGGGCATCCGTGTCCTGCAGTTA-GGAGCTCATAATCAGCCATACCACATTTGT 4065

Qy        340 ---------------------------ProThrProThrProSerPro 346
                                          |||||||||   |||   |||
Db       4066 AGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCT 4113


Search completed: June 13, 2006, 03:27:05
Job time : 7259.31 secs
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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 9, 2006, 23:43:41 ; Search time 1137.77 Seconds
(without alignments)
4899.317 Million cell updates/sec

Title: US-10-821-670A-39
Perfect score: 2799
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Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/abss/ABSSWEB_spool/US10821670/runat_07062006_110100_26141/app_query.fasta_1
-DB=N_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05h
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	2	2799	100.0	1599	6	ABK98951	Abk98951 Feline in
	3	2799	100.0	1599	14	ADV34691	Adv34691 Feline si
c	4	2799	100.0	1599	14	ADV34693	Adv34693 Feline si
c	5	2687	96.0	1533	6	ABK98954	Abk98954 Feline in
	6	2687	96.0	1533	6	ABK98953	Abk98953 Feline in
c	7	2687	96.0	1533	14	ADV34697	Adv34697 Feline si
	8	2687	96.0	1533	14	ADV34695	Adv34695 Feline si
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c	11	2643	94.4	1599	14	ADV34715	Adv34715 Canine si
	12	2643	94.4	1599	14	ADV34713	Adv34713 Canine si
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c	15	2546	91.0	1533	14	ADV34718	Adv34718 Canine si
	16	2546	91.0	1533	14	ADV34716	Adv34716 Canine si
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	18	2400.5	85.8	11453	10	ADG25152	Adg25152 Vector pS
	19	2390.5	85.4	6139	3	AAZ40023	Aaz40023 Interleuk
	20	2383	85.1	8608	6	AAD31548	Aad31548 pIRES-hB7
	21	2383	85.1	8629	6	AAD31552	Aad31552 pIRES-IL1
	22	2380.5	85.0	8623	6	AAD31547	Aad31547 pIRES-hB7
	23	2380.5	85.0	8644	6	AAD31551	Aad31551 pIRES-IL1
	24	2378	85.0	8638	6	AAD31549	Aad31549 pIRES-hB7
	25	2378	85.0	8659	6	AAD31550	Aad31550 pIRES-IL1
	26	2349	83.9	8578	6	AAD31546	Aad31546 pIRES-hB7
	27	2349	83.9	8578	6	AAD31545	Aad31545 pIRES-hB7
	28	1748	62.5	4522	4	AAF26076	Aaf26076 Feline IL
	29	1748	62.5	4522	4	AAF26094	Aaf26094 Plasmid p
	30	1747	62.4	987	6	ABK98944	Abk98944 Feline in
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	32	1747	62.4	987	14	ADV34682	Adv34682 Feline si
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	34	1747	62.4	990	4	AAF26082	Aaf26082 Feline IL
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c	36	1743	62.3	985	6	ABK98962	Abk98962 Feline in
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	38	1743	62.3	985	14	ADV34707	Adv34707 Feline N-
c	39	1743	62.3	985	14	ADV34709	Adv34709 Feline N-
	40	1741	62.2	2193	2	AAV56625	Aav56625 Feline FL
	41	1741	62.2	5252	12	ADO07652	Ado07652 Tricistro
	42	1741	62.2	9049	12	ADO07661	Ado07661 Viral vec
	43	1741	62.2	10633	12	ADO07660	Ado07660 Viral vec
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ALIGNMENTS

RESULT 1
ABK98950
ID ABK98950 standard; cDNA; 1599 BP.
XX
AC ABK98950;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12-1599 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX

```
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69306.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 58-60; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              7.84e-232       Length:         1599
Score:                  2799.00         Matches:        533
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-39 (1-533) x ABK98950 (1-1599)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
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Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
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Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
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Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
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Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
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Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
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Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
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Qy        321 SerAsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuPro 340
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Db        961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020

Qy        341 ThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArg 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 1080

Qy        361 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 1140

Qy        381 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeu 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        401 ProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThr 420
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Qy        421 AsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSer 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 1320

Qy        441 IleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeu 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 1380

Qy        461 MetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 1440

Qy        481 LeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluPro 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 1500

Qy        501 AspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAla 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 1560

Qy        521 ValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 533
              |||||||||||||||||||||||||||||||||||||||
Db       1561 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599

RESULT 2
```

```
ABK98951/c
ID   ABK98951 standard; cDNA; 1599 BP.
XX
AC   ABK98951;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1599 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 61-62; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              7.84e-232      Length:          1599
Score:                  2799.00        Matches:         533
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            100.0%         Indels:          0
DB:                     6              Gaps:            0

US-10-821-670A-39 (1-533) x ABK98951 (1-1599)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1599 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 1540

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 1420

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1359 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 1300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1299 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 1240

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1179 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 1120

Qy        161 GlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1119 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 1060

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        999 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 940

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        939 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 880

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        879 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 820

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 760

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        759 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 640

Qy        321 SerAsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuPro 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        639 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 580

Qy        341 ThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArg 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        579 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 520

Qy        361 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        519 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 460

Qy        381 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeu 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        459 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 400

Qy        401 ProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        399 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 340
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Qy        421 AsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSer 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        339 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 280

Qy        441 IleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeu 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        279 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 220

Qy        461 MetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 160

Qy        481 LeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluPro 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        159 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 100

Qy        501 AspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAla 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 40

Qy        521 ValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 533
              |||||||||||||||||||||||||||||||||||||||
Db         39 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
```

RESULT 3
ADV34691

```
ID   ADV34691 standard; cDNA; 1599 BP.
XX
AC   ADV34691;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1599
FT                   /*tag=  a
FT                   /product= "PFeIL-12p533 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34692.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 38; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;
```

Alignment Scores:

Pred. No.:	7.84e-232	Length:	1599
Score:	2799.00	Matches:	533
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-39 (1-533) x ADV34691 (1-1599)

```
Qy          1 MetHisProGlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuPro 340
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020

Qy        341 ThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArg 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 1080

Qy        361 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 380
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 1140

Qy        381 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeu 400
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200

Qy        401 ProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThr 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 1260

Qy        421 AsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSer 440
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 1320

Qy        441 IleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeu 460
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 1380

Qy        461 MetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 1440

Qy        481 LeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluPro 500
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 1500

Qy        501 AspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAla 520
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 1560

Qy        521 ValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 533
                |||||||||||||||||||||||||||||||||||||
Db       1561 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599

RESULT 4
ADV34693/c
ID   ADV34693 standard; DNA; 1599 BP.
XX
AC   ADV34693;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 complementary DNA, nFeIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 40; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 complementary DNA.
XX
SQ   Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              7.84e-232       Length:         1599
Score:                  2799.00         Matches:        533
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-39 (1-533) x ADV34693 (1-1599)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeu 20
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1599 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 1540

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 1420

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1359 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 1300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1299 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 1240

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1179 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 1120

Qy        161 GlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1119 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 1060

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        999 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 940

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        939 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 880

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        879 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 820

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 760

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        759 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 640

Qy        321 SerAsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuPro 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        639 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 580

Qy        341 ThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArg 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        579 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 520

Qy        361 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        519 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 460

Qy        381 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeu 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        459 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 400

Qy        401 ProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        399 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 340

Qy        421 AsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSer 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        339 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 280

Qy        441 IleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeu 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        279 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 220

Qy        461 MetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 160

Qy        481 LeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluPro 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        159 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 100

Qy        501 AspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAla 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 40

Qy        521 ValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 533
              |||||||||||||||||||||||||||||||||||||||
Db         39 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 5
ABK98954/c
ID   ABK98954 standard; cDNA; 1533 BP.
XX
AC   ABK98954;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1533 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 66-67; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              3.53e-222       Length:         1533
Score:                  2687.00         Matches:        511
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            96.0%           Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-39 (1-533) x ABK98954 (1-1533)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
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Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122

Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142

Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162

Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        163 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182

Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202

Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222

Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242

Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262

Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282

Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302

Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322

Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        323 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 342

Db        633 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        343 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 362

Db        573 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy        363 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 382

Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy        383 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 402

Db        453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy        403 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 422

Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy        423 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 442

Db        333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy        443 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 462
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Db        273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy        463 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 482

Db        213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy        483 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 502

Db        153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy        503 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 522

Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy        523 IleAsnArgMetMetSerTyrLeuAsnAlaSer 533

Db         33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
```

RESULT 6
ABK98953
ID ABK98953 standard; cDNA; 1533 BP.
XX
AC ABK98953;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12-1533 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69307.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 63-64; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	3.53e-222	Length:	1533
Score:	2687.00	Matches:	511
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	96.0%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-39 (1-533) x ABK98953 (1-1533)

```
Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        163 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        323 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 342
Db        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy        343 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 362
Db        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020

Qy        363 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 382
Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080

Qy        383 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 402
Db       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy        403 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 422
Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200

Qy        423 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 442
Db       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260

Qy        443 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 462
Db       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320

Qy        463 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 482
Db       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380

Qy        483 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 502
Db       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440

Qy        503 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 522
Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500

Qy        523 IleAsnArgMetMetSerTyrLeuAsnAlaSer 533
Db       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
```

RESULT 7
ADV34697/c
ID ADV34697 standard; DNA; 1533 BP.
XX
AC ADV34697;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain IL-12 complementary DNA, nFeIL-12 1533.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Felis catus.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a

```
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 45; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 complementary DNA.
XX
SQ   Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              3.53e-222       Length:         1533
Score:                  2687.00         Matches:        511
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            96.0%           Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-39 (1-533) x ADV34697 (1-1533)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        163 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        323 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        343 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy        363 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy        383 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy        403 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy        423 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy        443 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy        463 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy        483 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy        503 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy        523 IleAsnArgMetMetSerTyrLeuAsnAlaSer 533
              |||||||||||||||||||||||||||||||||
Db         33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 8
ADV34695
ID   ADV34695 standard; cDNA; 1533 BP.
XX
AC   ADV34695;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1533
FT                   /*tag=  a
```

```
FT                   /product= "PFeIL-12 511 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34696.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 43; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              3.53e-222       Length:         1533
Score:                  2687.00         Matches:        511
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            96.0%           Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-39 (1-533) x ADV34695 (1-1533)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        163 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        323 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy        343 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020

Qy        363 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080

Qy        383 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy        403 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200

Qy        423 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260

Qy        443 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320

Qy        463 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380

Qy        483 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440

Qy        503 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
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Qy        523 IleAsnArgMetMetSerTyrLeuAsnAlaSer 533
              ||||||||||||||||||||||||||||||||
Db       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533

RESULT 9
ABK98965
ID   ABK98965 standard; cDNA; 1599 BP.
XX
AC   ABK98965;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1599 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69313.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 79-80; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 452 A; 392 C; 383 G; 372 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.37e-218      Length:         1599
Score:                  2643.00        Matches:        501
Percent Similarity:     96.4%          Conservative:   13
Best Local Similarity:  94.0%          Mismatches:     19
Query Match:            94.4%          Indels:         0
DB:                     6              Gaps:           0

US-10-821-670A-39 (1-533) x ABK98965 (1-1599)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpLeuSerLeuValLeuAlaProProLeu 20
              ||||||||||||||||||||||||:::|||   ||||||||||||||||||   ||||||
Db          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||:::||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||  ||||||||||||||||||||||||||||||:::|||||||||   |||
Db        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              |||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||:::||||||||||||||||
Db        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Qy        161 GlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              |||  ||||||||||||  ||||||||||||||  ||||||||||||||:::|||
Db        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              |||||||||||||||||||||||||||||||||||||||||||   :::|||   ||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuPro 340
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGCGACTGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020

Qy        341 ThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArg 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGA 1080

Qy        361 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 380
              |||:::|||||||||||||||||||||||||||||||||   ||||||||||||||||
Db       1081 GCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCC 1140

Qy        381 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeu 400
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Db       1141 GAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200

Qy        401 ProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThr 420

Db       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACT 1260

Qy        421 AsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSer 440

Db       1261 AACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGC 1320

Qy        441 IleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeu 460

Db       1321 ATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTA 1380

Qy        461 MetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 480

Db       1381 ATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTG 1440

Qy        481 LeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluPro 500

Db       1441 TTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCG 1500

Qy        501 AspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAla 520

Db       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCG 1560

Qy        521 ValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 533

Db       1561 GTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1599

RESULT 10
ABK98966/c
ID   ABK98966 standard; cDNA; 1599 BP.
XX
AC   ABK98966;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1599 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 82-83; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 372 A; 383 C; 392 G; 452 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.37e-218      Length:          1599
Score:                  2643.00        Matches:         501
Percent Similarity:     96.4%          Conservative:    13
Best Local Similarity:  94.0%          Mismatches:      19
Query Match:            94.4%          Indels:          0
DB:                     6              Gaps:            0

US-10-821-670A-39 (1-533) x ABK98966 (1-1599)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeu 20

Db       1599 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 1540

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40

Db       1539 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60

Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 1420

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80

Db       1419 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100

Db       1359 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 1300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120

Db       1299 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 1240

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140

Db       1239 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160

Db       1179 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 1120

Qy        161 GlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180

Db       1119 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 1060

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200

Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220

Db        999 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 940

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240

Db        939 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 880

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260

Db        879 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 820
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Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||   :::|||   ||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 760

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        759 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 640

Qy        321 SerAsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuPro 340
              |||:::|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        639 AGCGACTGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 580

Qy        341 ThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArg 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        579 ACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGA 520

Qy        361 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 380
              |||:::|||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        519 GCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCC 460

Qy        381 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeu 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        459 GAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTA 400

Qy        401 ProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        399 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACT 340

Qy        421 AsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSer 440
              ||||||||||||||||||||   |||   ||||||||||||   ||||||||||||||||
Db        339 AACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGC 280

Qy        441 IleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeu 460
              ||||||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||
Db        279 ATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTA 220

Qy        461 MetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 ATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTG 160

Qy        481 LeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluPro 500
              ||||||||||||||   ||||||||||||||||||||   ||||||||||||||||||||
Db        159 TTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCG 100

Qy        501 AspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAla 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCG 40

Qy        521 ValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 533
              |||||||||||||||||||||||||||||:::|||
Db         39 GTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1

RESULT 11
ADV34715/c
ID   ADV34715 standard; DNA; 1599 BP.
XX
AC   ADV34715;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12 complementary DNA, nCaIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 63; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 complementary DNA.
XX
SQ   Sequence 1599 BP; 372 A; 383 C; 392 G; 452 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                2.37e-218       Length:          1599
Score:                    2643.00         Matches:         501
Percent Similarity:       96.4%           Conservative:    13
Best Local Similarity:    94.0%           Mismatches:      19
Query Match:              94.4%           Indels:          0
DB:                       14              Gaps:            0

US-10-821-670A-39 (1-533) x ADV34715 (1-1599)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||:::|||   |||||||||||||||||||   ||||||
Db       1599 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 1540

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||:::|||||||||||||||||||||||||||||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 1420

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||   ||||||||||||||||||||||||||||:::|||||||||   |||
Db       1359 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 1300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||
Db       1299 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 1240

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||
Db       1179 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 1120

Qy        161 GlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
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Db       1119 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 1060

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200

Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220

Db        999 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 940

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240

Db        939 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 880

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260

Db        879 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 820

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280

Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 760

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300

Db        759 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320

Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 640

Qy        321 SerAsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlySerArgAsnLeuPro 340

Db        639 AGCGACTGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 580

Qy        341 ThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArg 360

Db        579 ACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGA 520

Qy        361 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 380

Db        519 GCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCC 460

Qy        381 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeu 400

Db        459 GAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTA 400

Qy        401 ProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThr 420

Db        399 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACT 340

Qy        421 AsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSer 440

Db        339 AACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGC 280

Qy        441 IleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeu 460

Db        279 ATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTA 220

Qy        461 MetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 480

Db        219 ATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTG 160

Qy        481 LeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluPro 500

Db        159 TTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCG 100

Qy        501 AspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAla 520

Db         99 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCG 40

Qy        521 ValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 533
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Db         39 GTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1

RESULT 12
ADV34713
ID   ADV34713 standard; cDNA; 1599 BP.
XX
AC   ADV34713;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12 protein cDNA, nCaIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1599
FT                   /*tag=  a
FT                   /product= "PCaIL-12 533 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34714.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 61; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1599 BP; 452 A; 392 C; 383 G; 372 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                2.37e-218       Length:          1599
Score:                    2643.00         Matches:         501
Percent Similarity:       96.4%           Conservative:    13
Best Local Similarity:    94.0%           Mismatches:      19
Query Match:              94.4%           Indels:          0
DB:                       14              Gaps:            0

US-10-821-670A-39 (1-533) x ADV34713 (1-1599)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeu 20

Db          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
```

```
Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60

Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80

Db        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100

Db        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120

Db        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140

Db        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160

Db        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Qy        161 GlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180

Db        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200

Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220

Db        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240

Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260

Db        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280

Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300

Db        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320

Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuPro 340

Db        961 AGCGACTGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020

Qy        341 ThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArg 360

Db       1021 ACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGA 1080

Qy        361 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 380

Db       1081 GCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCC 1140

Qy        381 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeu 400

Db       1141 GAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200

Qy        401 ProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThr 420

Db       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACT 1260

Qy        421 AsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSer 440

Db       1261 AACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGC 1320

Qy        441 IleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeu 460

Db       1321 ATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTA 1380

Qy        461 MetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 480

Db       1381 ATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTG 1440

Qy        481 LeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluPro 500

Db       1441 TTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCG 1500

Qy        501 AspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAla 520

Db       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCG 1560

Qy        521 ValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 533

Db       1561 GTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1599
```

RESULT 13
ABK98967
ID ABK98967 standard; cDNA; 1533 BP.
XX
AC ABK98967;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12-1533 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69314.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 83-85; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,

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CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 446 A; 368 C; 369 G; 350 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                5.4e-210      Length:          1533
Score:                    2546.00       Matches:         482
Percent Similarity:       96.7%         Conservative:    12
Best Local Similarity:    94.3%         Mismatches:      17
Query Match:              91.0%         Indels:          0
DB:                       6             Gaps:            0

US-10-821-670A-39 (1-533) x ABK98967 (1-1533)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||:::|||||||||   |||   |||
Db        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420

Qy        163 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              |||||||||||   ||||||||||||||   |||||||||||||:::|||||||||||
Db        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              |||||||||||||||||||||||||||||||||   :::|||   ||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900

Qy        323 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy        343 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        961 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 1020

Qy        363 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 382
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 1080

Qy        383 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy        403 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1200

Qy        423 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 442
              ||||||||||||||   |||   ||||||||||||   ||||||||||||||||||||
Db       1201 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1260

Qy        443 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 462
              ||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||
Db       1261 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1320

Qy        463 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 1380

Qy        483 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 502
              |||||||||   ||||||||||||||||||||   ||||||||||||||||||||||||
Db       1381 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1440

Qy        503 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1500

Qy        523 IleAsnArgMetMetSerTyrLeuAsnAlaSer 533
              |||||||||||||||||||||||||:::|||
Db       1501 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1533

RESULT 14
ABK98968/c
ID   ABK98968 standard; cDNA; 1533 BP.
XX
AC   ABK98968;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1533 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
```

PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 86-87; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	5.4e-210	Length:	1533
Score:	2546.00	Matches:	482
Percent Similarity:	96.7%	Conservative:	12
Best Local Similarity:	94.3%	Mismatches:	17
Query Match:	91.0%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-39 (1-533) x ABK98968 (1-1533)

```
Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1414

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
                 ||||||||||||||||||||||||||||||||:::|||||||||   |||   |||
Db       1353 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1294

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||
Db       1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy        163 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              ||||||||||||   ||||||||||||||   ||||||||||||:::|||||||||
Db       1113 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1054

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 994

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 874

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||   :::|||   ||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db        753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 634

Qy        323 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        343 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        573 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 514

Qy        363 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 382
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 454

Qy        383 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy        403 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 334

Qy        423 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 442
              ||||||||||||||   |||   ||||||||||||   ||||||||||||||||||||||
Db        333 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 274

Qy        443 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 462
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        273 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 214

Qy        463 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 154

Qy        483 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 502
              |||||||||   ||||||||||||||||||||   ||||||||||||||||||||||||
Db        153 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 94

Qy        503 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 34

Qy        523 IleAsnArgMetMetSerTyrLeuAsnAlaSer 533
              ||||||||||||||||||||||||||:::|||
Db         33 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1

RESULT 15
```

```
ADV34718/c
ID   ADV34718 standard; DNA; 1533 BP.
XX
AC   ADV34718;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12 complementary DNA, nCaIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 68; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 complementary DNA.
XX
SQ   Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                5.4e-210      Length:          1533
Score:                    2546.00       Matches:         482
Percent Similarity:       96.7%         Conservative:    12
Best Local Similarity:    94.3%         Mismatches:      17
Query Match:              91.0%         Indels:          0
DB:                       14            Gaps:            0

US-10-821-670A-39 (1-533) x ADV34718 (1-1533)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1414

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
                ||||||||||||||||||||||||||||||:::|||||||||   |||   |||
Db       1353 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1294

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
                                                                  |||||||||||||
Db       1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
                ||||||||||||||||||||||||||||||||||:::|||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy        163 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
                ||||||||||||   ||||||||||||||||   ||||||||||||||:::|||||||||
Db       1113 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1054

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 994

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
                ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db       933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 874

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
                ||||||||||||||||||||||||||||||||||||   :::|||   ||||||||||||
Db       813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
                ||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db       753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db       693 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 634

Qy        323 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 342
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       633 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        343 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 362
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db       573 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 514

Qy        363 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 382
                ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db       513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 454

Qy        383 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 402
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       453 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy        403 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 422
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 334

Qy        423 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 442
                ||||||||||||||   |||   ||||||||||||   ||||||||||||||||||||||
Db       333 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 274

Qy        443 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 462
                ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db       273 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 214

Qy        463 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 482
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        213 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 154

Qy        483 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 502
              |||||||||   ||||||||||||||||||||   ||||||||||||||||||||||||
Db        153 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 94

Qy        503 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 34

Qy        523 IleAsnArgMetMetSerTyrLeuAsnAlaSer 533
              |||||||||||||||||||||||:::|||
Db         33 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1
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Search completed: June 10, 2006, 01:17:50
Job time : 1163.77 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 10, 2006, 00:20:47 ; Search time 6532.82 Seconds
(without alignments)
6843.525 Million cell updates/sec

Title: US-10-821-670A-39
Perfect score: 2799
Sequence: 1 MHPQQLVIAWLSLVLLAPPL.....HAFRIRAVTINRMMSYLNAS 533

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10821670/runat_07062006_110104_26172/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
-USER=US10821670_@CGN_1_1_27300_@runat_07062006_110104_26172 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1169.5	41.8	1839	6	AK162981	AK162981 Mus muscu
	2	1156.5	41.3	2908	6	AK155593	AK155593 Mus muscu
	3	1097.5	39.2	735	5	CD559605	CD559605 AGENCOURT
	4	1097.5	39.2	756	5	CK130264	CK130264 AGENCOURT
	5	1084.5	38.7	747	5	CD559607	CD559607 AGENCOURT
	6	1070	38.2	772	5	CD559604	CD559604 AGENCOURT
	7	967.5	34.6	745	5	CD559602	CD559602 AGENCOURT
c	8	957	34.2	785	5	CD559448	CD559448 AGENCOURT
c	9	955.5	34.1	736	5	CD559453	CD559453 AGENCOURT
c	10	952.5	34.0	772	5	CD559450	CD559450 AGENCOURT
c	11	947.5	33.9	762	5	CD559451	CD559451 AGENCOURT
c	12	898.5	32.1	766	5	CD559449	CD559449 AGENCOURT
c	13	890.5	31.8	754	5	CD559452	CD559452 AGENCOURT
	14	890	31.8	762	14	DQ033872	DQ033872 Homo sapi
	15	877	31.3	762	14	DQ033873	DQ033873 Pan trogl
	16	862.5	30.8	1136	4	CD013915	CD013915 90138132
c	17	816	29.2	725	5	CD559454	CD559454 AGENCOURT
	18	816	29.2	935	4	CD013914	CD013914 90138124
	19	769	27.5	724	5	CD559603	CD559603 AGENCOURT
	20	765	27.3	1042	5	CD559606	CD559606 AGENCOURT
	21	755.5	27.0	1938	6	BC035571	BC035571 Homo sapi
	22	752.5	26.9	649	5	CJ134671	CJ134671 CJ134671
	23	670	23.9	863	4	CD013916	CD013916 90138296
	24	574.5	20.5	475	7	BF704417	BF704417 MI-P-E6-a
	25	500.5	17.9	417	8	CO949904	CO949904 UMC-pd12c
	26	460	16.4	1299	6	AK153729	AK153729 Mus muscu
	27	455	16.3	387	4	BY167742	BY167742 BY167742
	28	446	15.9	432	4	BY154173	BY154173 BY154173
	29	419.5	15.0	812	2	BG702253	BG702253 602683459
	30	419	15.0	423	4	BY218447	BY218447 BY218447
	31	418.5	15.0	563	3	BU698113	BU698113 LL2in1206
	32	406	14.5	375	4	BY222535	BY222535 BY222535
	33	404	14.4	589	1	AI050362	AI050362 ub30a07.r
	34	400	14.3	346	4	BY164658	BY164658 BY164658
	35	388	13.9	355	4	BY221814	BY221814 BY221814
	36	378	13.5	535	11	AZ441303	AZ441303 1M0232M24
c	37	374.5	13.4	1099	2	BI523344	BI523344 603175938
	38	357	12.8	700	12	CE093997	CE093997 tigr-gss-
c	39	355	12.7	778	1	AJ820622	AJ820622 AJ820622
c	40	351	12.5	569	11	AZ853726	AZ853726 2M0157M01
	41	349.5	12.5	561	3	BU699383	BU699383 LL2in1157
	42	345	12.3	373	7	BF552757	BF552757 UI-R-C0-i
	43	344	12.3	692	5	CJ137697	CJ137697 CJ137697
	44	338.5	12.1	252	10	DV799576	DV799576 est_t_tru
	45	324	11.6	832	2	BI523569	BI523569 603175938

ALIGNMENTS

RESULT 1
AK162981
LOCUS AK162981 1839 bp mRNA linear HTC 21-SEP-2005
DEFINITION Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430014H12 product:interleukin 12b, full insert sequence.
ACCESSION AK162981
VERSION AK162981.1 GI:74188061
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,

Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

PUBMED 11076861

REFERENCE 4

AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

CONSRTM RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409 (6821), 685-690 (2001)

PUBMED 11217851

REFERENCE 5

AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420 (6915), 563-573 (2002)

PUBMED 12466851

REFERENCE 6

AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE The transcriptional landscape of the mammalian genome

JOURNAL Science 309 (5740), 1559-1563 (2005)

PUBMED 16141072

REFERENCE 7

AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.

CONSRTM RIKEN Genome Exploration Research Group

TITLE Antisense transcription in the mammalian transcriptome

JOURNAL Science 309 (5740), 1564-1566 (2005)

PUBMED 16141073

REFERENCE 8 (bases 1 to 1839)

AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

```
     source          1. .1839
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM_DB:A430014H12"
                     /db_xref="taxon:10090"
                     /clone="A430014H12"
                     /tissue_type="thymus"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="0 day neonate"
     CDS             58. .1065
                     /note="unnamed protein product; interleukin 12b
                     (MGD|MGI:96540 GB|M86671, evidence: BLASTN, 100%,
                     match=1816)
                     putative"
                     /codon_start=1
                     /protein_id="BAE37146.1"
                     /db_xref="GI:74188062"
                     /translation="MCPQKLTISWFAIVLLVSPLMAMWELEKDVYVVEVDWTPDAPGE
                     TVNLTCDTPEEDDITWTSDQRHGVIGSGKTLTITVKEFLDAGQYTCHKGGETLSHSHL
                     LLHKKENGIWSTEILKNFKNKTFLKCEAPNYSGRFTCSWLVQRNMDLKFNIKSSSSSP
                     DSRAVTCGMASLSAEKVTLDQRDYEKYSVSCQEDVTCPTAEETLPIELALEARQQNKY
                     ENYSTSFFIRDIIKPDPPKNLQMKPLKNSQVEVSWEYPDSWSTPHSYFSLKFFVRIQR
                     KKEKMKETEEGCNQKGAFLVEKTSTEVQCKGGNVCVQAQDRYYNSSCSKWACVPCRVR
                     S"
ORIGIN

Alignment Scores:
Pred. No.:              1.1e-109        Length:         1839
Score:                  1169.50         Matches:        224
Percent Similarity:     77.7%           Conservative:   37
Best Local Similarity:  66.7%           Mismatches:     62
Query Match:            41.8%           Indels:         13
DB:                     6               Gaps:           4

US-10-821-670A-39 (1-533) x AK162981 (1-1839)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeu 20
              |||   ||||||:::|||   |||:::|||   ::::::|||||||||       ||||||
Db         58 ATGTGTCCTCAGAAGCTAACCATCTCCTGGTTTGCCATCGTTTTGCTGGTGTCTCCACTC 117

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||:::|||||||||||||||:::|||||||||||||||:::||||||   ||||||
Db        118 ATGGCCATGTGGGAGCTGGAGAAAGACGTTTATGTTGTAGAGGTGGACTGGACTCCCGAT 177

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||   |||   |||||||||:::||||||||||||||||||||||||||||
Db        178 GCCCCTGGAGAAACAGTGAACCTCACCTGTGACACGCCTGAAGAAGATGACATCACCTGG 237

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||          |||:::|||||||||||||||||||||||   ||||||
Db        238 ACCTCAGACCAGAGACATGGAGTCATAGGCTCTGGAAAGACCCTGACCATCACTGTCAAA 297

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||   ||||||||||||||||||||||||||||||||||   ||||||||||||
Db        298 GAGTTTCTAGATGCTGGCCAGTACACCTGCCACAAAGGAGGCGAGACTCTGAGCCACTCA 357

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
                ||||||:::|||||||||||||:::||||||||||||||:::||||||
Db        358 CATCTGCTGCTCCACAAGAAGGAAAATGGAATTTGGTCCACTGAAATTTTA--------- 408

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              |||      |||||||||   ||||||||||||||||||   ||||||||||||||||||
Db        409 AAAAATTTCAAAAACAAGACTTTCCTGAAGTGTGAAGCACCAAATTACTCCGGACGGTTC 468

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||   ||||||         :::   ||||||||||||   :::|||||||||
Db        469 ACGTGCTCATGGCTGGTGCAAAGAAACATGGACTTGAAGTTCAACATCAAGAGCAGTAGC 528

Qy        161 GlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
                 |||   |||   :::   ||||||||||||   |||:::||||||||||||||||||
Db        529 AGTTCCCCTGACTCTCGGGCAGTGACATGTGGAATGGCGTCTCTGTCTGCAGAGAAGGTC 588

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
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Db        589 ACACTGGACCAAAGGGACTATGAGAAGTATTCAGTGTCCTGCCAGGAGGATGTCACCTGC 648

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              |||   |||||||||:::||||||||||||:::   :::::::|||       :::   |||
Db        649 CCAACTGCCGAGGAGACCCTGCCCATTGAACTGGCGTTGGAAGCACGGCAGCAGAATAAA 708

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||::::::||||||||||||||||||||||||||||||||||||||||||
Db        709 TATGAGAACTACAGCACCAGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAG 768

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              |||||||||:::||||||||||||||||:::   |||||||||||||||||||||||||
Db        769 AACTTGCAGATGAAGCCTTTGAAGAACTCACAG---GTGGAGGTCAGCTGGGAGTACCCT 825

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              |||:::||||||||||||||||||||||||||||||||   |||   |||::::::|||
Db        826 GACTCCTGGAGCACTCCCCATTCCTACTTCTCCCTCAAGTTCTTTGTTCGAATCCAGCGC 885

Qy        281 LysAsnAsnArgGluLys----------------------LysAspArgLeuSerVal 292
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Db        886 AAGAAAGAAAAGATGAAGGAGACAGAGGAGGGGGTGTAACCAGAAAGGTGCGTTCCTCGTA 945

Qy        293 AspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaArg 312
              :::|||||||||   :::|||   |||   |||          :::   |||||||||:::
Db        946 GAGAAGACATCTACCGAAGTCCAATGC---AAAGGCGGGAATGTCTGCGTGCAAGCTCAG 1002

Qy        313 AspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 328
              ||||||||||||:::||||||   |||   ||||||   |||   |||
Db       1003 GATCGCTATTACAATTCCTCATGCAGCAAGTGGGCATGTGTTCCCTGC 1050

RESULT 2
AK155593
LOCUS       AK155593               2908 bp    mRNA    linear   HTC 21-SEP-2005
DEFINITION  Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN
            full-length enriched library, clone:F730005O03 product:interleukin
            12b, full insert sequence.
ACCESSION   AK155593
VERSION     AK155593.1  GI:74212721
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
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Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

CONSRTM RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409 (6821), 685-690 (2001)

PUBMED 11217851

REFERENCE 5

AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420 (6915), 563-573 (2002)

PUBMED 12466851

REFERENCE 6

AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE The transcriptional landscape of the mammalian genome

JOURNAL Science 309 (5740), 1559-1563 (2005)

PUBMED 16141072

REFERENCE 7

AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.

CONSRTM RIKEN Genome Exploration Research Group

TITLE Antisense transcription in the mammalian transcriptome

JOURNAL Science 309 (5740), 1564-1566 (2005)

PUBMED 16141073

REFERENCE 8 (bases 1 to 2908)

AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

source 1. .2908
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/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:F730005O03"
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/clone="F730005O03"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"

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ORIGIN

Alignment Scores:
Pred. No.:              5.06e-108       Length:         2908
Score:                  1156.50         Matches:        224
Percent Similarity:     77.4%           Conservative:   37
Best Local Similarity:  66.5%           Mismatches:     62
Query Match:            41.3%           Indels:         14
DB:                     6               Gaps:           4

US-10-821-670A-39 (1-533) x AK155593 (1-2908)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeu 20
              |||   ||||||:::|||   |||:::|||   ::::::|||||||||       ||||||
Db        461 ATGTGTCCTCAGAAGCTAACCATCTCCTGGTTTGCCATCGTTTTGCTGGTGTCTCCACTC 520

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
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Db        521 ATGGCCATGTGGGAGCTGGAGAAAGACGTTTATGTTGTAGAGGTGGACTGGACTCCCGAT 580

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||   |||   ||||||||:::||||||||||||||||||||||||||||
Db        581 GCCCCTGGAGAAACAGTGAACCTCACCTGTGACACGCCTGAAGAAGATGACATCACCTGG 640

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||          |||:::|||||||||||||||||||||||   ||||||
Db        641 ACCTCAGACCAGAGACATGGAGTCATAGGCTCTGGAAAGACCCTGACCATCACTGTCAAA 700

Qy         81 GluPheAlaAspAlaGlyGln-TyrThrCysHisLysGlyGlyGluValLeuSerHisSe 100
              ||||||   |||||||||||| ||||||||||||||||||||||   ||||||||||||
Db        701 GAGTTTCTAGATGCTGGCCAGCTACACCTGCCACAAAGGAGGCGAGACTCTGAGCCACTC 760

Qy        100 rPheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGl 120
              |   ||||||:::|||||||||||:::|||||||||||||||:::||||||
Db        761 ACATCTGCTGCTCCACAAGAAGGAAAATGGAATTTGGTCCACTGAAATTTTA-------- 812

Qy        120 nLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPh 140
              |||      ||||||||   ||||||||||||||||||   ||||||||||||||||
Db        813 -AAAAATTTCAAAAACAAGACTTTCCTGAAGTGTGAAGCACCAAATTACTCCGGACGGTT 871

Qy        140 eThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerAr 160
              |||||||   ||||||       :::   ||||||||||||   :::|||||||||
Db        872 CACGTGCTCATGGCTGGTGCAAAGAAACATGGACTTGAAGTTCAACATCAAGAGCAGTAG 931

Qy        160 gGlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysVa 180
              |||   |||   :::   ||||||||||||   |||:::||||||||||||||||||
Db        932 CAGTTCCCCTGACTCTCGGGCAGTGACATGTGGAATGGCGTCTCTGTCTGCAGAGAAGGT 991

Qy        180 lArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCy 200
              |   :::|||   |||||||||:::||||||:::|||   |||||||||         ||
Db        992 CACACTGGACCAAAGGGACTATGAGAAGTATTCAGTGTCCTGCCAGGAGGATGTCACCTG 1051

Qy        200 sProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLy 220
              ||||   |||||||||:::|||||||||||:::   ::::::|||      :::   ||
Db       1052 CCCAACTGCCGAGGAGACCCTGCCCATTGAACTGGCGTTGGAAGCACGGCAGCAGAATAA 1111

Qy        220 sTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLy 240
              ||||||||||||||::::::||||||||||||||||||||||||||||||||||||||||
Db       1112 ATATGAGAACTACAGCACCAGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAA 1171

Qy        240 sAsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPr 260
              ||||||||||:::|||||||||||||||||::::   ||||||||||||||||||||||
Db       1172 GAACTTGCAGATGAAGCCTTTGAAGAACTCACAG---GTGGAGGTCAGCTGGGAGTACCC 1228

Qy        260 oAspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGl 280
              ||||:::|||||||||||||||||||||||||||||||   |||   |||::::::|||
Db       1229 TGACTCCTGGAGCACTCCCCATTCCTACTTCTCCCTCAAGTTCTTTGTTCGAATCCAGCG 1288

Qy        280 yLysAsnAsnArgGluLys----------------------LysAspArgLeuSerVa 292
                 |||       :::   |||                                 |||           ||
Db       1289 CAAGAAAGAAAAGATGAAGGAGACAGAGGAGGGGTGTAACCAGAAAGGTGCGTTCCTCGT 1348

Qy        292 lAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaAr 312
              |:::|||||||||   :::|||   |||   |||          :::   |||||||||::
Db       1349 AGAGAAGACATCTACCGAAGTCCAATGC---AAAGGCGGGAATGTCTGCGTGCAAGCTCA 1405

Qy        312 gAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 328
              :||||||||||||:::||||||   |||   ||||||   |||   |||
Db       1406 GGATCGCTATTACAATTCCTCATGCAGCAAGTGGGCATGTGTTCCCTGC 1454

RESULT 3
CD559605
LOCUS       CD559605                735 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496534 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971870 5', mRNA sequence.
ACCESSION   CD559605
VERSION     CD559605.2  GI:38558937
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 735)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585673.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 01
            High quality sequence stop: 709.
FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              7.77e-103       Length:         735
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Score:                 1097.50       Matches:       204
Percent Similarity:    93.7%         Conservative:  18
Best Local Similarity: 86.1%         Mismatches:    14
Query Match:           39.2%         Indels:        1
DB:                    5             Gaps:          1

US-10-821-670A-39 (1-533) x CD559605 (1-735)

Qy          4 GlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeuMetAlaIle 23
              |||||||||||||||:::|||   |||||||||   ||||||   ||||||:::||||||
Db         26 CAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTCGTGGCCATA 85

Qy         24 TrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaProGly 43
              |||||||||:::|||:::|||||||||||||||||||||||:::|||||||||||||||
Db         86 TGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCTGGA 145

Qy         44 GluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSerAsp 63
              ||||||||||||||||||||:::|||||||||||||||   ||||||||||||   |||
Db        146 GAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTGGAC 205

Qy         64 GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheAla 83
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 CAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTTGGA 265

Qy         84 AspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeuLeu 103
              |||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        266 GATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTGCTG 325

Qy        104 IleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGluSer 123
              :::|||||||||||||||||||||||||||||||||||||:::::|||||||||
Db        326 CTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAACCC 385

Qy        124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrp 143
              |||||||||   ||||||:::|||||||||||||||||||||||||||||||||||||
Db        386 AAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGG 445

Qy        144 TrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSer 163
              |||||||||   |||||||||||||||   |||:::|||||||||||||||||||||||||
Db        446 TGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAGAGCAGCAGAGGCTCTTCT 505

Qy        164 AspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAsp 183
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Db        506 GACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGAC 565

Qy        184 AsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAla 203
              |||::::::|||   :::|||:::|||||||||||||||   ||||||||||||||||||
Db        566 AACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCT 622

Qy        204 GluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsn 223
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Db        623 GAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAAC 682

Qy        224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
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Db        683 TACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 733

RESULT 4
CK130264
LOCUS       CK130264                 756 bp    mRNA    linear   EST 02-DEC-2003
DEFINITION  AGENCOURT_14496566 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971871 5', mRNA sequence.
ACCESSION   CK130264
VERSION     CK130264.1  GI:38622200
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 756)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 02
            High quality sequence start: 5
            High quality sequence stop: 731.
FEATURES              Location/Qualifiers
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                      loxP-HindIII; Clones from this library have been
                      PCR-amplified using gene-specific primers to contain the
                      complete open reading frame (based on known gene sequences
                      available from NCBI's RefSeq). Template for PCR is cDNA
                      derived from either pooled cytoplasmic polyA RNA from 30
                      cells lines or pooled total RNA from 10 different tissues
                      (from BD Biosciences/Clontech and Washington University).
                      PCR products are directionally cloned into the loxP sites
                      of the pDNR-Dual vector. Library constructed by Dr.
                      Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                      Expression Laboratory, Research Technology Program, SAIC
                      Frederick, NCI-Frederick, Frederick, MD 21702). For
                      information on which gene each clone represents, please
                      visit our anonymous ftp site at
                      ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                      a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:             8.12e-103     Length:        756
Score:                 1097.50       Matches:       204
Percent Similarity:    93.3%         Conservative:  18
Best Local Similarity: 85.7%         Mismatches:    15
Query Match:           39.2%         Indels:        1
DB:                    5             Gaps:          1

US-10-821-670A-39 (1-533) x CK130264 (1-756)

Qy          4 GlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeuMetAlaIle 23
              |||||||||||||||:::|||   |||||||||   ||||||   ||||||:::||||||
Db         43 CAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTCGTGGCCATA 102

Qy         24 TrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaProGly 43
              |||||||||:::|||:::|||||||||||||||||||||||:::|||||||||||||||
Db        103 TGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCTGGA 162

Qy         44 GluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSerAsp 63
              ||||||||||||||||||||:::|||||||||||||||   ||||||||||||   |||
Db        163 GAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTGGAC 222

Qy         64 GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheAla 83
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        223 CAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTTGGA 282

Qy         84 AspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeuLeu 103
              |||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        283 GATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTGCTG 342
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Qy        104 IleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGluSer 123
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Db        343 CTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAACCC 402

Qy        124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrp 143
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Db        403 AAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGG 462

Qy        144 TrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSer 163
              |||||||||   ||||||||||||||   |||:::|||||||||||||||||||||||||
Db        463 TGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCT 522

Qy        164 AspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAsp 183
              |||||||||   ||||||||||||||||||||||||||||||:::||||||   |||
Db        523 GACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGAC 582

Qy        184 AsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAla 203
              |||::::::|||   :::|||:::|||||||||||||||   ||||||||||||||||||
Db        583 AACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCT 639

Qy        204 GluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsn 223
              ||||||||||||||||||||||:::||||||||||:::|||||||||||||||||||||
Db        640 GAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAAC 699

Qy        224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsn 241
              ||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        700 TACACCAGCAGCTTCTTCATCAGGGACATCATCNAACCTGACCCACCCAAGAAC 753

RESULT 5
CD559607
LOCUS       CD559607                747 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14497061 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971868 5', mRNA sequence.
ACCESSION   CD559607
VERSION     CD559607.2  GI:38558941
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 747)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585675.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: g  column: 11
            High quality sequence start: 14
            High quality sequence stop: 671.
FEATURES             Location/Qualifiers
     source          1. .747
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971868"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              1.78e-101      Length:          747
Score:                  1084.50        Matches:         201
Percent Similarity:     92.8%          Conservative:    19
Best Local Similarity:  84.8%          Mismatches:      16
Query Match:            38.7%          Indels:          1
DB:                     5              Gaps:            1

US-10-821-670A-39 (1-533) x CD559607 (1-747)

Qy          4 GlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeuMetAlaIle 23
              ||||||||||||||:::|||   |||||||||   ||||||   ||||||:::||||||
Db         38 CAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTCGTGGCCATA 97

Qy         24 TrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaProGly 43
              ||||||||||:::|||:::||||||||||||||||||||||||:::||||||||||||||
Db         98 TGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCTGGA 157

Qy         44 GluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSerAsp 63
              ||||||||||||||||||||:::|||||||||||||||   ||||||||||||   |||
Db        158 GAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTGGAC 217

Qy         64 GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheAla 83
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 CAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTTGGA 277

Qy         84 AspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeuLeu 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        278 GATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTGCTG 337

Qy        104 IleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGluSer 123
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Db        338 CTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAACCC 397

Qy        124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrp 143
              |||||||||   ||||||:::||||||||||||||||||||||||||||||||||||||
Db        398 AAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGG 457

Qy        144 TrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSer 163
              |||||||||   ||||||||||||||   |||:::|||||||||||||||||||||||||
Db        458 TGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCT 517

Qy        164 AspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAsp 183
              |||||||||   ||||||||||||||||||||||||||||||||:::||||||   |||
Db        518 GACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGAC 577

Qy        184 AsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAla 203
              |||::::::|||   :::|||:::|||||||||||||||   ||||||||||||||||||
Db        578 AACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCT 634

Qy        204 GluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsn 223
              ||||||||||||||||||||||:::||||||   :::||||||||||:::|||||||||
Db        635 GAGGAGAGTCTGCCCATTGAGGTCATGGTGGATTGCGTTCACAAGCTCCAGTATGAAAAC 694

Qy        224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
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Db        695 TACACCCGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAA 745
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RESULT 6
CD559604
LOCUS       CD559604                772 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496598 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971872 5', mRNA sequence.
ACCESSION   CD559604
VERSION     CD559604.2  GI:38558934
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 772)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585672.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 03
            High quality sequence start: 13
            High quality sequence stop: 750.
FEATURES             Location/Qualifiers
     source          1. .772
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971872"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              6.01e-100      Length:         772
Score:                  1070.00        Matches:        202
Percent Similarity:     92.8%          Conservative:   18
Best Local Similarity:  85.2%          Mismatches:     16
Query Match:            38.2%          Indels:         2
DB:                     5              Gaps:           1

US-10-821-670A-39 (1-533) x CD559604 (1-772)

Qy          4 GlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeuMetAlaIle 23
              ||||||||||||||:::|||   ||||||||   ||||||   ||||||:::||||||
Db         47 CAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTCGTGGCCATA 106

Qy         24 TrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaProGly 43
              ||||||||:::|||:::||||||||||||||||||||||:::|||||||||||||||
Db        107 TGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCTGGA 166

Qy         44 GluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSerAsp 63
              ||||||||||||||||||:::|||||||||||||||   ||||||||||||   |||
Db        167 GAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTGGAC 226

Qy         64 GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheAla 83
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        227 CAGAGCAGTGAGGTCCTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTTGGA 286

Qy         84 AspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeuLeu 103
              ||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        287 GATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTGCTG 346

Qy        104 IleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGluSer 123
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Db        347 CTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAACCC 406

Qy        124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrp 143
              ||||||||   ||||||:::||||||||||||||||||||||||||||||||||||
Db        407 AAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGG 466

Qy        144 TrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSer 163
              ||||||||   ||||||||||||||   |||:::||||||||||||||||||||||||
Db        467 TGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCT 526

Qy        164 AspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAsp 183
              ||||||||   ||||||||||||||||||||||||||||||:::||||||   |||
Db        527 GACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGAC 586

Qy        184 AsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAla 203
              |||::::::|||   :::|||:::||||||||||||||   ||||||||||||||||||
Db        587 AACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCT 643

Qy        204 GluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsn 223
              ||||||||||||||||||||:::||||||||:::||||||||||||||||||||||||
Db        644 GAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAAC 703

Qy        224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||   ||||||   ||||||
Db        704 TACACCAGCAGCTTCTTCATCAGGGACATCATCAA-CCTGACCAACCCAAA 753

RESULT 7
CD559602
LOCUS       CD559602                745 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496684 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971874 5', mRNA sequence.
ACCESSION   CD559602
VERSION     CD559602.2  GI:38558930
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 745)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585670.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: IRBK2  row: h  column: 05
          High quality sequence start: 2
          High quality sequence stop: 644.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971874"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              2.49e-89        Length:         745
Score:                  967.50          Matches:        187
Percent Similarity:     89.4%           Conservative:   23
Best Local Similarity:  79.6%           Mismatches:     22
Query Match:            34.6%           Indels:         4
DB:                     5               Gaps:           3

US-10-821-670A-39 (1-533) x CD559602 (1-745)

Qy          4 GlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeuMetAlaIle 23
              ||||||||||||||||:::|||   |||||||||   ||||||   ||||||:::||||||
Db         15 CAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTCGTGGCCATA 74

Qy         24 TrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaProGly 43
              |||||||||:::|||:::|||||||||||||||||||||||:::|||||||||||||||
Db         75 TGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCTGGA 134

Qy         44 GluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSerAsp 63
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Db        135 GAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTGGAC 194

Qy         64 GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheAla 83
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        195 CAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTTGGA 254

Qy         84 AspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeuLeu 103
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Db        255 GATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTGCTG 314

Qy        104 IleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGluSer 123
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Db        315 CTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAACCC 374

Qy        124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrp 143
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Db        375 AAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGG 434

Qy        144 TrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSer 163
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Db        435 TGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCT 494

Qy        164 AspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAsp 183
              ||||||||   ||||||||||||||||||||||||||||||:::||||||   |||
Db        495 GACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGAC 554

Qy        184 AsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAla 203
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Db        555 AACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCT 611

Qy        204 GluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsn 223
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Qy        224 TyrThrSerSerProPheIleArgAspIleIleLysProAspPro 238
              :::         ||||||:::   :::   ::::::   ||||||
Db        671 CAC---CACGGCTTCTTTCTCTGAAAT---CTTCAATCTGACCCA 709

RESULT 8
CD559448/c
LOCUS       CD559448                785 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496712 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971874 5', mRNA sequence.
ACCESSION   CD559448
VERSION     CD559448.2  GI:38453466
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 785)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585516.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 05
            High quality sequence stop: 696.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971874"
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                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
```

Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	3.33e-88	Length:	785
Score:	957.00	Matches:	186
Percent Similarity:	89.5%	Conservative:	18
Best Local Similarity:	81.6%	Mismatches:	23
Query Match:	34.2%	Indels:	3
DB:	5	Gaps:	1

US-10-821-670A-39 (1-533) x CD559448 (1-785)

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Qy        102 LeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLys 121
              |||         :::||||||||||||   ||||||||||||   |||::::::||||||
Db        771 CTCTGCTGCTCACAAAAGGAAGATGGAAT-TGGTCCACTGATAT-TTAAAGGACCAGAAA 714

Qy        122 GluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThr 141
              |||   ||||||||   ||||||:::||||||||||||||||||||||||||||||||||
Db        713 GAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACC 654

Qy        142 CysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGly 161
              ||||||||||||||   ||||||||||||||   |||:::||||||||||||||||||
Db        653 TGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGC 594

Qy        162 SerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArg 181
              ||||||||||||||   ||||||||||||||||||||||||||||||:::||||||
Db        593 TCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGA 534

Qy        182 ValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysPro 201
              ||||||::::::|||   :::|||:::|||||||||||||||   ||||||||||||
Db        533 GGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCA 477

Qy        202 AlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyr 221
              ||||||||||||||||||||||||||||:::||||||||:::||||||||||||||||
Db        476 GCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTAT 417

Qy        222 GluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsn 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        416 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAAC 357

Qy        242 LeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAsp 261
              ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        356 TTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGAC 297

Qy        262 ThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLys 281
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        296 ACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAG 237

Qy        282 AsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCys 301
              :::   ||||||||||||||||||:::      ||||||||||||||   |||:::|||
Db        236 AGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGC 177

Qy        302 HisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSer 321
              |||:::|||   |||   |||:::|||:::||||||||||||||||||||||||||||
Db        176 CGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGC 117

Qy        322 AsnTrpAlaSerValSerCysSer 329
              ||||||||||||   ||||||
Db        116 GAATGGGCATCTGTGCCCTGCAGT 93
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RESULT 9
CD559453/c

LOCUS	CD559453 736 bp mRNA linear EST 19-NOV-2003
DEFINITION	AGENCOURT_14497154 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971869 5', mRNA sequence.
ACCESSION	CD559453
VERSION	CD559453.2 GI:38453475
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 736)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	On Jun 10, 2003 this sequence version replaced gi:31585521. Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cgapbs-r@mail.nih.gov Tissue Procurement: Narayan Bhat cDNA Library Preparation: Bhat Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: IRBK2 row: g column: 12 High quality sequence stop: 683.

FEATURES Location/Qualifiers

source	1. .736 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6971869" /tissue_type="mixed" /lab_host="DH5A (T1 phage-resistant)" /clone_lib="NIH_MGC_195" /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	4.31e-88	Length:	736
Score:	955.50	Matches:	181
Percent Similarity:	90.8%	Conservative:	17
Best Local Similarity:	83.0%	Mismatches:	19
Query Match:	34.1%	Indels:	2
DB:	5	Gaps:	1

US-10-821-670A-39 (1-533) x CD559453 (1-736)

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Qy        112 TrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCys 131
              ||||||||||||   |||::::::|||||||||   |||||||||   ||||||:::|||
Db        727 TGGTCCACTGATAT-TTAAAGGACCAGAAAGAACCCAAAAATAAGACCTTTCTAAGATGC 669

Qy        132 GluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAsp 151
              ||||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db        668 GAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGACAATCAGTACTGAT 609

Qy        152 LeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGluValThrCysGly 171
              |||   |||:::|||||||||||||||||||||||||||||||||   ||||||||||||
Db        608 TTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGA 549
```

```
Qy        172 AlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThr 191
              ||||||||||||||||||||:::||||||   ||||||:::::::|||   :::|||:::
Db        548 GCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAACAAGGAGTAT---GAGTACTCA 492

Qy        192 ValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluVal 211
              ||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        491 GTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTC 432

Qy        212 ValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArg 231
              :::|||||||||:::||||||||||||||||||||||||||||||||||||||||||||
Db        431 ATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGG 372

Qy        232 AspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 GACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 312

Qy        252 HisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSer 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 CAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACATTCCTACTTCTCC 252

Qy        272 LeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSer 291
              |||||||||   |||||||||||||||||:::   |||||||||||||||||:::
Db        251 CTGACATTCTGCGTTCAGGTCCAGGGCAAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTC 192

Qy        292 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 311
              ||||||||||||||   |||:::|||   |||:::|||   |||   |||:::|||
Db        191 ACGGACAAGACCTCAGCCACGGTCATCTGCCGCAAAAATGCCAGCATTAGCGTGCGGGCC 132

Qy        312 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSer 329
              :::||||||||||||||||||||||||||   ||||||||||||   ||||||
Db        131 CAGGACCGCTACTATAGCTCATCTTGGAGCGAATGGGCATCTGTGCCCTGCAGT 78

RESULT 10
CD559450/c
LOCUS       CD559450                772 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496612 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971872 5', mRNA sequence.
ACCESSION   CD559450
VERSION     CD559450.2  GI:38453469
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 772)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585518.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 03
            High quality sequence start: 2
            High quality sequence stop: 753.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971872"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:                9.51e-88        Length:          772
Score:                    952.50          Matches:         184
Percent Similarity:       90.2%           Conservative:    18
Best Local Similarity:    82.1%           Mismatches:      21
Query Match:              34.0%           Indels:          3
DB:                       5               Gaps:            1

US-10-821-670A-39 (1-533) x CD559450 (1-772)

Qy        106 LysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsn 125
              :::|||||||||   |||   |||||||||   |||:::::|||||||||   ||||||
Db        768 CAAAAGGAAGATGA-ATTNGGTCCACTGATAT-TTAAAGGACCAGAAAGAACCCAAAAAT 711

Qy        126 LysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeu 145
              |||   ||||||:::||||||||||||||||||||||||||||||||||||||||||||
Db        710 AAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTG 651

Qy        146 ThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSerAspPro 165
              |||   ||||||||||||||   |||:::||||||||||||||||||||||||||||||
Db        650 ACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCTGACCCC 591

Qy        166 GlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArg 185
              |||   |||||||||||||||||||||||||||||:::||||||   ||||||:::
Db        590 CAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAACAAG 531

Qy        186 AspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGlu 205
              :::|||   :::|||:::||||||||||||||   ||||||||||||||||||||||
Db        530 GAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCTGAGGAG 474

Qy        206 SerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThr 225
              ||||||||||||||||||:::||||||||:::|||||||||||||||||||||||||||
Db        473 AGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACC 414

Qy        226 SerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGlnLeuLys 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 AGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAG 354

Qy        246 ProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThrTrpSerThr 265
              ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        353 CCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACT 294

Qy        266 ProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGlu 285
              ||||||||||||||||||||   ||||||||||||||||||:::   ||||||
Db        293 CCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGCAAGAGAGAA 234

Qy        286 LysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHisLysAspAla 305
              ||||||||||:::      ||||||||||||||   |||:::|||   |||:::|||
Db        233 AAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGCAAAAATGCC 174

Qy        306 LysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSer 325
              |||   |||:::|||:::|||||||||||||||||||||||||||   |||||||||
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Db        173 AGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAATGGGCATCT 114

Qy        326 ValSerCysSer 329
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Db        113 GTGCCCTGCAGT 102

RESULT 11
CD559451/c
LOCUS       CD559451                762 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496580 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971871 5', mRNA sequence.
ACCESSION   CD559451
VERSION     CD559451.2  GI:38453471
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585519.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 02
            High quality sequence start: 38
            High quality sequence stop: 761.
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                     /db_xref="taxon:9606"
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                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              3.08e-87        Length:         762
Score:                  947.50          Matches:        183
Percent Similarity:     90.1%           Conservative:   17
Best Local Similarity:  82.4%           Mismatches:     21
Query Match:            33.9%           Indels:         3

DB:                     5               Gaps:           1

US-10-821-670A-39 (1-533) x CD559451 (1-762)

Qy        108 GluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIle 127
              |||||||||   ||||||||||||   |||::::::|||||||||    |||||||||
Db        759 GAAGATGGAAT-TGGTCCACTGATAT-TTAAAGGACCAGAAAGAACCCAAAAATAAGACC 702

Qy        128 PheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAla 147
                 |||:::|||||||||||||||||||||||||||||||||||||||||||||||||||
Db        701 TCTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGACA 642

Qy        148 IleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlu 167
              |||||||||||||||    |||:::|||||||||||||||||||||||||||||||||||
Db        641 ATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGG 582

Qy        168 ValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyr 187
              |||||||||||||||||||||||||||||:::|||||    ||||||::::::|||
Db        581 GTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAACAAGGAGTAT 522

Qy        188 LysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeu 207
                 :::|||:::|||||||||||||||    ||||||||||||||||||||||||||||
Db        521 ---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCTGAGGAGAGTCTG 465

Qy        208 ProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSer 227
              |||||||||||:::|||||||||:::|||||||||||||||||||||||||||||||||||
Db        464 CCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACCAGCAGC 405

Qy        228 PhePheIleArgAspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeu 247
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        404 TTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTA 345

Qy        248 LysAsnSerArgHisValGluValSerTrpGluTyrProAspThrTrpSerThrProHis 267
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Db        344 AAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACAT 285

Qy        268 SerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLys 287
              ||||||||||||||||||||    ||||||||||||||||:::    ||||||||||||
Db        284 TCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGCAAGAGAGAAAAGAAA 225

Qy        288 AspArgLeuSerValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIle 307
              ||||||:::      ||||||||||||||    |||:::|||    |||:::|||    |||
Db        224 GATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGCAAAAATGCCAGCATT 165

Qy        308 ArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSer 327
                 |||:::|||:::|||||||||||||||||||||||||||    ||||||||||||
Db        164 AGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAATGGGCATCTGTGCCC 105

Qy        328 CysSer 329
              ||||||
Db        104 TGCAGT 99

RESULT 12
CD559449/c
LOCUS       CD559449                766 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496649 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971873 5', mRNA sequence.
ACCESSION   CD559449
VERSION     CD559449.2  GI:38453467
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 766)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585517.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
```

```
           Bldg. 31 Rm10A07 Bethesda, MD 20892
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: IRBK2  row: h  column: 04
           High quality sequence stop: 641.
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                     /clone="IMAGE:6971873"
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                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              3.8e-82        Length:         766
Score:                  898.50         Matches:        168
Percent Similarity:     90.6%          Conservative:   15
Best Local Similarity:  83.2%          Mismatches:     18
Query Match:            32.1%          Indels:         1
DB:                     5              Gaps:           1

US-10-821-670A-39 (1-533) x CD559449 (1-766)

Qy        128 PheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAla 147
              ||||||:::|||||||||||||   ||||||||||||||||||   ||||||||||||
Db        693 TTTCTAAGATGCGAGGCCAAGAAGTATTCTGGACGTTTCACCTGGTGGTGGCTGACGACA 634

Qy        148 IleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlu 167
              ||||||||||||||   |||:::||||||||||||||||||||||||||||||||||||
Db        633 ATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGG 574

Qy        168 ValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyr 187
              ||||||||||||||||||||||||||||||||:::||||||   ||||||::::::|||
Db        573 GTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAACAAGGAGTAT 514

Qy        188 LysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeu 207
                 :::|||:::|||||||||||||||   ||||||||||||||||||||||||||||||
Db        513 ---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCTGAGGAGAGTCTG 457

Qy        208 ProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSer 227
              ||||||||||||:::|||||||||:::||||||||||||||||||||||||||||||||
Db        456 CCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACCAGCAGC 397

Qy        228 PhePheIleArgAspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeu 247
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Db        396 TTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTA 337

Qy        248 LysAsnSerArgHisValGluValSerTrpGluTyrProAspThrTrpSerThrProHis 267
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db        336 AAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACAT 277

Qy        268 SerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLys 287
              ||||||||||||||||||||   ||||||||||||||||||:::   ||||||||||||
Db        276 TCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGCAAGAGAGAAAAGAAA 217

Qy        288 AspArgLeuSerValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIle 307
              ||||||:::      ||||||||||||||   |||:::|||   |||:::|||   |||
Db        216 GATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGCAAAAATGCCAGCATT 157

Qy        308 ArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSer 327
                 |||:::|||:::||||||||||||||||||||||||||   ||||||||||||
Db        156 AGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAATGGGCATCTGTGCCC 97

Qy        328 CysSer 329
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Db         96 TGCAGT 91

RESULT 13
CD559452/c
LOCUS       CD559452                754 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496548 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971870 5', mRNA sequence.
ACCESSION   CD559452
VERSION     CD559452.2  GI:38453473
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 754)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585520.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 01
            High quality sequence start: 130
            High quality sequence stop: 572.
FEATURES             Location/Qualifiers
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                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
```

Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	2.51e-81	Length:	754
Score:	890.50	Matches:	171
Percent Similarity:	85.8%	Conservative:	17
Best Local Similarity:	78.1%	Mismatches:	30
Query Match:	31.8%	Indels:	2
DB:	5	Gaps:	1

US-10-821-670A-39 (1-533) x CD559452 (1-754)

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Db        750 ATTTGGTCCAATGATAT-TTAAAGGACCAGAAAGAACCCAAAAATAAGACCTTTCTAAGA 692

Qy        131 CysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThr 150
              ||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db        691 TGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGACAATCAGTACT 632

Qy        151 AspLeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGluValThrCys 170
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Db        631 GATTTGACATTCAGTGTCAAGAGCAGCAGAGGCTTTTTTGACCCCCAAGGGGTGACGTGC 572

Qy        171 GlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyr 190
              ||||||||||||||   ||||||:::||||||   ||||||:::::|||   :::|||
Db        571 GGAGCTGCTACACTCTTTGCAGAGAGAGTCAGAGGGGACAACAAGGAGTAT---GAGTAC 515

Qy        191 ThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGlu 210
              :::||||||||||||||   ||||||||||||||   ||||||||||||||||||||||
Db        514 TCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGGTGAGGAGAGTTTGCCCATTGAG 455

Qy        211 ValValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIle 230
              |||:::|||||||||:::|||||||||||||||||||||||||||||||   |||||||||
Db        454 GTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACCAGCAGGTTTTTCATC 395

Qy        231 ArgAspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSer 250
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Db        394 AGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCT 335

Qy        251 ArgHisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPhe 270
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Db        334 TGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACATTCCTAATTT 275

Qy        271 SerLeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeu 290
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Db        274 TCCCTGACATTTTGCGTTCAGGTTCAGGGCAAGAGCAAGAGAGAAAAGAAAGATAGAGTT 215

Qy        291 SerValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGln 310
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Db        214 TTCACGGACAAGACCTTAGCCACGGTCATTTGCCGCAAAAATGCCAGCATTAGCGTGCGG 155

Qy        311 AlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSer 329
              |||:::||||||||||||||||||   ||||||   ||||||   |||   ||||||
Db        154 GCCCAGGACCGGTACTATAGCTCATTTTGGAGCGAATGGGCATTTGTGCCCTGCAGT 98
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RESULT 14
DQ033872
LOCUS DQ033872 762 bp DNA linear GSS 02-JUN-2005
DEFINITION Homo sapiens IL12A gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION DQ033872
VERSION DQ033872.1 GI:66885081
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 762)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 762)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.
FEATURES Location/Qualifiers
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gene <1. .>762
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ORIGIN

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Best Local Similarity:	76.3%	Mismatches:	34
Query Match:	31.8%	Indels:	15
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US-10-821-670A-39 (1-533) x DQ033872 (1-762)

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Qy        289 ArgLeuSerValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArg 308
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Db         68 CGGCTCGCCCTGTGTCCCTGCAGTGCCGGCTCAGCATGT---------------------- 106

Qy        309 ValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 328
              ||||||         |||      ||||||   |||       ||:::|||   :::
Db        107 GTCCAG---------CGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCTCCTGGACCACC 157

Qy        329 SerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrProThrProSerProGlyMet 348
              |||                 :::||||||||||||      ||||||   |||||||||
Db        158 TCA-----------GTTTG-GCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATG 204

Qy        349 PheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLys 368
              |||   ||||||:::|||||||||   ||||||||||:::||||||   |||||||||
Db        205 TTCCCATGCCTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAG 264

Qy        369 AlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIle 388
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        265 GCCAGACAAACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATC 324

Qy        389 ThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGlu 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        325 ACAAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAG 384

Qy        409 SerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArg 428
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Db        385 AGTTGCCTAAATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGA 444

Qy        429 LysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyr 448
              ||||||||||||||      ||||||||||||||||||||||||||||||||||||||||
Db        445 AAGACCTCTTTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTAC 504
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Qy        449 GlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePhe 468
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Db        505 CAGGTGGAGTTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTT 564

Qy        469 LeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSer 488
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Db        565 CTAGATCAAAACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGT 624

Qy        489 ValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLys 508
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Db        625 GAGACTGTGCCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAG 684

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Db        685 CTCTGCATACTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGC 744

Qy        529 TyrLeuAsnAlaSer 533
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RESULT 15
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DEFINITION  Pan troglodytes IL12A gene, VIRTUAL TRANSCRIPT, partial sequence,
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ACCESSION   DQ033873
VERSION     DQ033873.1  GI:66885082
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     A Scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
  JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
   PUBMED   15869325
REFERENCE   2  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.  Translation starts at the beginning of
            alignment.
FEATURES             Location/Qualifiers
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     gene            <1. .>762
                     /gene="IL12A"
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ORIGIN

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Score:                  877.00          Matches:        176
Percent Similarity:     86.0%           Conservative:   8
Best Local Similarity:  82.2%           Mismatches:     23
Query Match:            31.3%           Indels:         8
DB:                     14              Gaps:           1

US-10-821-670A-39 (1-533) x DQ033873 (1-762)

Qy        320 TrpSerAsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeu 339
              |||||||:::|||      :::|||                          :::||||||||||

Db        140 TGGTCCTCCTGGACCAC-CTCAGTTTG--------------------GCCAGAAACCTC 177

Qy        340 ProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeu 359
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Db        178 CCCGTGGCCACCCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCCAAAACCTGCTG 237

Qy        360 ArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThr 379
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Db        238 AGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTTTACCCTTGCACT 297

Qy        380 SerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCys 399
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Db        298 TCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGT 357

Qy        400 LeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIle 419
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Db        358 TTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGAGAGACCTCTTTCATA 417

Qy        420 ThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSer 439
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Db        418 ACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATGGCCCTGTGCCTTAGT 477

Qy        440 SerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeu 459
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Db        478 AGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAATGCAAAGCTT 537

Qy        460 LeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGlu 479
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Qy        500 ProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArg 519
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Qy        520 AlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 533
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 10, 2006, 01:16:39 ; Search time 275.268 Seconds
(without alignments)
5434.532 Million cell updates/sec

Title: US-10-821-670A-39
Perfect score: 2799
Sequence: 1 MHPQQLVIAWLSLVLLAPPL.....HAFRIRAVTINRMMSYLNAS 533

Scoring table: BLOSUM62
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Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	2	2799	100.0	1599	3	US-09-917-265A-40	Sequence 40, Appl
	3	2687	96.0	1533	3	US-09-917-265A-43	Sequence 43, Appl
c	4	2687	96.0	1533	3	US-09-917-265A-45	Sequence 45, Appl
	5	2643	94.4	1599	3	US-09-917-265A-61	Sequence 61, Appl
c	6	2643	94.4	1599	3	US-09-917-265A-63	Sequence 63, Appl
	7	2546	91.0	1533	3	US-09-917-265A-66	Sequence 66, Appl
c	8	2546	91.0	1533	3	US-09-917-265A-68	Sequence 68, Appl
	9	2390.5	85.4	1623	2	US-08-751-767A-9	Sequence 9, Appli
	10	2390.5	85.4	6139	2	US-08-751-767A-7	Sequence 7, Appli
	11	2324.5	83.0	1560	2	US-08-751-767A-11	Sequence 11, Appl
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c	13	1747	62.4	987	3	US-09-917-265A-31	Sequence 31, Appl
	14	1743	62.3	985	3	US-09-917-265A-55	Sequence 55, Appl
c	15	1743	62.3	985	3	US-09-917-265A-57	Sequence 57, Appl
	16	1741	62.2	2193	3	US-09-011-143-5	Sequence 5, Appli
	17	1741	62.2	2193	3	US-09-302-495-5	Sequence 5, Appli
	18	1741	62.2	2193	3	US-10-079-616-5	Sequence 5, Appli
	19	1646	58.8	921	3	US-09-917-265A-26	Sequence 26, Appl
c	20	1646	58.8	921	3	US-09-917-265A-28	Sequence 28, Appl
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ALIGNMENTS

RESULT 1
US-09-917-265A-38
; Sequence 38, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1599)
US-09-917-265A-38

Alignment Scores:

Pred. No.:	2.98e-302	Length:	1599
Score:	2799.00	Matches:	533
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
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RESULT 2
US-09-917-265A-40/c
; Sequence 40, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-40

Alignment Scores:
Pred. No.:              2.98e-302       Length:         1599
Score:                  2799.00         Matches:        533
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 160

Qy        481 LeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluPro 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        159 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 100

Qy        501 AspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAla 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 40

Qy        521 ValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 533
              |||||||||||||||||||||||||||||||||||||||
Db         39 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 3
US-09-917-265A-43
; Sequence 43, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-09-917-265A-43

Alignment Scores:
Pred. No.:              9.08e-290       Length:         1533
Score:                  2687.00         Matches:        511
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            96.0%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-39 (1-533) x US-09-917-265A-43 (1-1533)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        163 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        323 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy        343 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020

Qy        363 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080

Qy        383 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy        403 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200

Qy        423 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260

Qy        443 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320

Qy        463 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380

Qy        483 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440

Qy        503 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500

Qy        523 IleAsnArgMetMetSerTyrLeuAsnAlaSer 533
              |||||||||||||||||||||||||||||||||
Db       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533

RESULT 4
US-09-917-265A-45/c
; Sequence 45, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-45

Alignment Scores:
Pred. No.:              9.08e-290       Length:         1533
Score:                  2687.00         Matches:        511
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            96.0%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-39 (1-533) x US-09-917-265A-45 (1-1533)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294
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Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        163 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        323 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        343 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy        363 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy        383 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy        403 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy        423 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy        443 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy        463 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 482
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy        483 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy        503 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy        523 IleAsnArgMetMetSerTyrLeuAsnAlaSer 533
              |||||||||||||||||||||||||||||||||
Db         33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 5
US-09-917-265A-61
; Sequence 61, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-09-917-265A-61

Alignment Scores:
Pred. No.:              8.03e-285       Length:         1599
Score:                  2643.00         Matches:        501
Percent Similarity:     96.4%           Conservative:   13
Best Local Similarity:  94.0%           Mismatches:     19
Query Match:            94.4%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-39 (1-533) x US-09-917-265A-61 (1-1599)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||:::|||   |||||||||||||||||   ||||||
Db          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||:::|||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||   ||||||||||||||||||||||||||||||||||:::|||||||||   |||
Db        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
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Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||
Db        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Qy        161 GlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              |||   ||||||||||||   ||||||||||||||||   ||||||||||||||:::|||
Db        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||   :::|||   ||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||    ||||||||||||||||||||||||
Db        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuPro 340
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGCGACTGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020

Qy        341 ThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArg 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGA 1080

Qy        361 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 380
              |||:::|||||||||||||||||||||||||||||||||    ||||||||||||||||
Db       1081 GCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCC 1140

Qy        381 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeu 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200

Qy        401 ProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACT 1260

Qy        421 AsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSer 440
              ||||||||||||||||||   |||   ||||||||||||   ||||||||||||||||
Db       1261 AACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGC 1320

Qy        441 IleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeu 460
              ||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||
Db       1321 ATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTA 1380

Qy        461 MetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 ATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTG 1440

Qy        481 LeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluPro 500
              ||||||||||||||||   ||||||||||||||||||||   ||||||||||||||||||
Db       1441 TTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCG 1500

Qy        501 AspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAla 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCG 1560

Qy        521 ValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 533
              ||||||||||||||||||||||||||||||:::|||
Db       1561 GTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1599

RESULT 6
US-09-917-265A-63/c
; Sequence 63, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-63

Alignment Scores:
Pred. No.:              8.03e-285       Length:         1599
Score:                  2643.00         Matches:        501
Percent Similarity:     96.4%           Conservative:   13
Best Local Similarity:  94.0%           Mismatches:     19
Query Match:            94.4%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-39 (1-533) x US-09-917-265A-63 (1-1599)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||:::|||   |||||||||||||||||   ||||||
Db       1599 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 1540

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||:::||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||:::||||||||||||||||||||||||||||||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 1420

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              |||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||   ||||||||||||||||||||||||||||||:::|||||||||   |||
Db       1359 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 1300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||
Db       1299 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 1240

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
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Db       1179 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 1120

Qy        161 GlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180

Db       1119 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 1060

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200

Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220

Db        999 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 940

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240

Db        939 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 880

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260

Db        879 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 820

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280

Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTGCATACAGGCCCAGGGC 760

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300

Db        759 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320

Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 640

Qy        321 SerAsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlySerArgAsnLeuPro 340

Db        639 AGCGACTGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 580

Qy        341 ThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArg 360

Db        579 ACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGA 520

Qy        361 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 380

Db        519 GCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCC 460

Qy        381 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeu 400

Db        459 GAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTA 400

Qy        401 ProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThr 420

Db        399 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACT 340

Qy        421 AsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSer 440

Db        339 AACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGC 280

Qy        441 IleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeu 460

Db        279 ATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTA 220

Qy        461 MetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 480

Db        219 ATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTG 160

Qy        481 LeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluPro 500

Db        159 TTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCG 100

Qy        501 AspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAla 520

Db         99 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCG 40

Qy        521 ValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 533

Db         39 GTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1
```

RESULT 7
US-09-917-265A-66
; Sequence 66, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)
US-09-917-265A-66

Alignment Scores:

Pred. No.:	5.16e-274	Length:	1533
Score:	2546.00	Matches:	482
Percent Similarity:	96.7%	Conservative:	12
Best Local Similarity:	94.3%	Mismatches:	17
Query Match:	91.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-39 (1-533) x US-09-917-265A-66 (1-1533)

```
Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42

Db          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62

Db         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82

Db        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102

Db        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122

Db        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142

Db        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162

Db        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420

Qy        163 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182

Db        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
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Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900

Qy        323 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy        343 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        961 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 1020

Qy        363 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 1080

Qy        383 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy        403 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1200

Qy        423 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 442
              ||||||||||||||   |||  ||||||||||||  ||||||||||||||||||||||||
Db       1201 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1260

Qy        443 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 462
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1320

Qy        463 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 1380

Qy        483 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 502
              |||||||||   ||||||||||||||||||||   ||||||||||||||||||||||||||
Db       1381 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1440

Qy        503 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1500

Qy        523 IleAsnArgMetMetSerTyrLeuAsnAlaSer 533
              |||||||||||||||||||||||||:::|||
Db       1501 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1533

RESULT 8

US-09-917-265A-68/c
; Sequence 68, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-68

Alignment Scores:
Pred. No.:              5.16e-274       Length:         1533
Score:                  2546.00         Matches:        482
Percent Similarity:     96.7%           Conservative:   12
Best Local Similarity:  94.3%           Mismatches:     17
Query Match:            91.0%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-39 (1-533) x US-09-917-265A-68 (1-1533)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1414

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||:::|||||||||   |||   |||
Db       1353 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1294

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||
Db       1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||:::|||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy        163 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              ||||||||||||   ||||||||||||||   ||||||||||||||:::|||||||||
Db       1113 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1054

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 994

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 874

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              |||||||||||||||||||||||||||||||||||||   :::|||   ||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||   |||||||||||||||||||||||||||||||||||
Db        753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 634

Qy        323 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        343 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        573 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 514

Qy        363 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 382
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 454

Qy        383 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy        403 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 334

Qy        423 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 442
              ||||||||||||||   |||   ||||||||||||   ||||||||||||||||||||||
Db        333 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 274

Qy        443 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 462
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        273 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 214

Qy        463 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 154

Qy        483 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 502
              |||||||||   ||||||||||||||||||||   ||||||||||||||||||||||||
Db        153 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 94

Qy        503 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 34

Qy        523 IleAsnArgMetMetSerTyrLeuAsnAlaSer 533
              |||||||||||||||||||||||||:::|||
Db         33 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1

RESULT 9
US-08-751-767A-9
; Sequence 9, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1623 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1620
US-08-751-767A-9

Alignment Scores:
Pred. No.:              1.34e-256     Length:          1623
Score:                  2390.50       Matches:         456
Percent Similarity:     89.6%         Conservative:    29
Best Local Similarity:  84.3%         Mismatches:      47
Query Match:            85.4%         Indels:          9
DB:                     2             Gaps:            2

US-10-821-670A-39 (1-533) x US-08-751-767A-9 (1-1623)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeu 20
              |||   ||||||||||||||:::|||   |||||||||   ||||||   ||||||
Db          1 ATGGGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              :::||||||||||||||:::|||:::|||||||||||||||||||||:::||||||
Db         61 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||:::|||||||||||||   |||||||||
Db        121 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||:::||||||||||||||||||||||||||||||||||||||:::::::|||
Db        301 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||   |||||||||   |||||||:::|||||||||||||||||||||||||||||
Db        361 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
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Db        421 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180

Db        481 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200

Db        541 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 597

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220

Db        598 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 657

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240

Db        658 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 717

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260

Db        718 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 777

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280

Db        778 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 837

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300

Db        838 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 897

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320

Db        898 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 957

Qy        321 SerAsnTrpAlaSerValSerCysSerGlyGly----------------------Gly 332

Db        958 AGCGAATGGGCATCTGTGCCCTGCAGTGGTGGCGGTGGAAGCGGCGGTGGCGGAAGCGGC 1017

Qy        333 GlyGlyGlySerArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeu 352

Db       1018 GGTGGCGGCAGCAGAAACCTCCCCCTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTT 1077

Qy        353 AsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThr 372

Db       1078 CACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACT 1137

Qy        373 LeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLys 392

Db       1138 CTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAA 1197

Qy        393 ThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAla 412

Db       1198 ACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAAT 1257

Qy        413 SerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPhe 432

Db       1258 TCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTT 1317

Qy        433 MetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPhe 452

Db       1318 ATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTC 1377

Qy        453 LysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsn 472

Db       1378 AAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAAC 1437

Qy        473 MetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValPro 492

Db       1438 ATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCA 1497

Qy        493 GlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeu 512

Db       1498 CAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTT 1557

Qy        513 LeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAla 532

Db       1558 CTTCATGCTTTCAGAATTCGGGCAGTGACTATTGACAGAGTGACGAGCTATCTGAATGCT 1617

Qy        533 Ser 533

Db       1618 TCC 1620
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RESULT 10
US-08-751-767A-7
; Sequence 7, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6139 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3222..4841
US-08-751-767A-7

Alignment Scores:
Pred. No.:              1.23e-255      Length:          6139
Score:                  2390.50        Matches:         456
Percent Similarity:     89.6%          Conservative:    29
Best Local Similarity:  84.3%          Mismatches:      47
Query Match:            85.4%          Indels:          9
DB:                     2              Gaps:            2

US-10-821-670A-39 (1-533) x US-08-751-767A-7 (1-6139)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeu 20

Db       3222 ATGGGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 3281

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40

Db       3282 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 3341
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Qy        41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
Db      3342 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 3401

Qy        61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
Db      3402 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 3461

Qy        81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
Db      3462 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 3521

Qy       101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
Db      3522 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 3581

Qy       121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
Db      3582 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 3641

Qy       141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
Db      3642 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 3701

Qy       161 GlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
Db      3702 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 3761

Qy       181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
Db      3762 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 3818

Qy       201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
Db      3819 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 3878

Qy       221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
Db      3879 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 3938

Qy       241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
Db      3939 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 3998

Qy       261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
Db      3999 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 4058

Qy       281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
Db      4059 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 4118

Qy       301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
Db      4119 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 4178

Qy       321 SerAsnTrpAlaSerValSerCysSerGlyGly----------------------Gly 332
Db      4179 AGCGAATGGGCATCTGTGCCCTGCAGTGGTGGCGGTGGAAGCGGCGGTGGCGGAAGCGGC 4238

Qy       333 GlyGlyGlySerArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeu 352
Db      4239 GGTGGCGGCAGCAGAAACCTCCCCCTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTT 4298

Qy       353 AsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThr 372
Db      4299 CACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACT 4358

Qy       373 LeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLys 392
Db      4359 CTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAA 4418

Qy       393 ThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAla 412
Db      4419 ACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAAT 4478

Qy       413 SerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPhe 432
Db      4479 TCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTT 4538

Qy       433 MetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPhe 452
Db      4539 ATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTC 4598

Qy       453 LysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsn 472
Db      4599 AAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAAC 4658

Qy       473 MetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValPro 492
Db      4659 ATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCA 4718

Qy       493 GlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeu 512
Db      4719 CAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTT 4778

Qy       513 LeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAla 532
Db      4779 CTTCATGCTTTCAGAATTCGGGCAGTGACTATTGACAGAGTGACGAGCTATCTGAATGCT 4838

Qy       533 Ser 533
Db      4839 TCC 4841
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RESULT 11
US-08-751-767A-11
; Sequence 11, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1560 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
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;      LOCATION:  1..1557
US-08-751-767A-11

Alignment Scores:
Pred. No.:              2.98e-249       Length:         1560
Score:                  2324.50         Matches:        442
Percent Similarity:     90.2%           Conservative:   27
Best Local Similarity:  85.0%           Mismatches:     42
Query Match:            83.0%           Indels:         9
DB:                     2               Gaps:           2

US-10-821-670A-39 (1-533) x US-08-751-767A-11 (1-1560)

Qy         22 AlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAla 41
              ||||||||||||||||:::|||:::|||||||||||||||||||||||:::|||||||||
Db          1 GCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCC 60

Qy         42 ProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThr 61
              ||||||||||||||||||||||||:::|||||||||||||||   ||||||||||||
Db         61 CCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACC 120

Qy         62 SerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGlu 81
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAG 180

Qy         82 PheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPhe 101
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTC 240

Qy        102 LeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLys 121
              ||||||:::||||||||||||||||||||||||||||||||||||:::::::||||||
Db        241 CTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAA 300

Qy        122 GluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThr 141
              |||   |||||||||   |||||||:::|||||||||||||||||||||||||||||||
Db        301 GAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACC 360

Qy        142 CysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGly 161
              ||||||||||||||   ||||||||||||||   |||:::||||||||||||||||||
Db        361 TGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGC 420

Qy        162 SerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArg 181
              ||||||||||||||   ||||||||||||||||||||||||||||||:::||||||
Db        421 TCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGA 480

Qy        182 ValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysPro 201
              ||||||:::::|||   :::|||:::|||||||||||||   ||||||||||||
Db        481 GGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCA 537

Qy        202 AlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyr 221
              ||||||||||||||||||||||||||||:::||||||||:::|||||||||||||||||
Db        538 GCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTAT 597

Qy        222 GluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsn 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAAC 657

Qy        242 LeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAsp 261
              ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        658 TTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGAC 717

Qy        262 ThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLys 281
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        718 ACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAG 777

Qy        282 AsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCys 301
              :::   ||||||||||||||||||:::      ||||||||||||||   |||:::|||
Db        778 AGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGC 837

Qy        302 HisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSer 321
              |||:::|||   |||   |||:::|||:::|||||||||||||||||||||||||||||
Db        838 CGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGC 897

Qy        322 AsnTrpAlaSerValSerCysSerGlyGly----------------------GlyGly 333
              ||||||||||||   ||||||||||||                        ||||||
Db        898 GAATGGGCATCTGTGCCCTGCAGTGGTGGCGGTGGAAGCGGCGGTGGCGGAAGCGGCGGT 957

Qy        334 GlyGlySerArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsn 353
              ||||||||||||||||||||      ||||||   ||||||||||   ||||||:::
Db        958 GGCGGCAGCAGAAACCTCCCCCTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCAC 1017

Qy        354 HisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeu 373
              |||||||||   ||||||||||||:::||||||   ||||||||||||||||||||||
Db       1018 CACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTA 1077

Qy        374 GluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThr 393
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db       1078 GAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACC 1137

Qy        394 SerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSer 413
              ||||||||||||||||||||||||||||||||||   ||||||||||||||   |||
Db       1138 AGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCC 1197

Qy        414 ArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMet 433
              ||||||   |||   ||||||||||||||||||||||||||||||||||||||||||||
Db       1198 AGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATG 1257

Qy        434 ThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLys 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1258 ATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAG 1317

Qy        454 AlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMet 473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1318 ACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATG 1377

Qy        474 LeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGln 493
              |||      ||||||||||||:::||||||||||||   ||||||   ||||||||||||
Db       1378 CTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAA 1437

Qy        494 AsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeu 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1438 AATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTT 1497

Qy        514 HisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 533
              ||||||||||||||||||||||||||||:::|||:::   ||||||||||||||||||
Db       1498 CATGCTTTCAGAATTCGGGCAGTGACTATTGACAGAGTGACGAGCTATCTGAATGCTTCC 1557

RESULT 12
US-09-917-265A-29
; Sequence 29, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
US-09-917-265A-29

Alignment Scores:
Pred. No.:              4.67e-185       Length:         987
Score:                  1747.00         Matches:        327
Percent Similarity:     99.4%           Conservative:   0
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Best Local Similarity:  99.4%          Mismatches:    2
Query Match:            62.4%          Indels:        0
DB:                     3              Gaps:          0

US-10-821-670A-39 (1-533) x US-09-917-265A-29 (1-987)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
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RESULT 13
US-09-917-265A-31/c
; Sequence 31, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-31

Alignment Scores:
Pred. No.:              4.67e-185      Length:         987
Score:                  1747.00        Matches:        327
Percent Similarity:     99.4%          Conservative:   0
Best Local Similarity:  99.4%          Mismatches:     2
Query Match:            62.4%          Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-39 (1-533) x US-09-917-265A-31 (1-987)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        161 GlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388
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Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGCAGT 1
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RESULT 14
US-09-917-265A-55
; Sequence 55, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
; LENGTH: 985
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(984)
US-09-917-265A-55

Alignment Scores:

Pred. No.:	1.3e-184	Length:	985
Score:	1743.00	Matches:	326
Percent Similarity:	99.4%	Conservative:	0
Best Local Similarity:	99.4%	Mismatches:	2
Query Match:	62.3%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-39 (1-533) x US-09-917-265A-55 (1-985)

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Qy          1 MetHisProGlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

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Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
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Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
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Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
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Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
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Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
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Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
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RESULT 15
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; Sequence 57, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111

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;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-57

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Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
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Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
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Searched: 18892170 seqs, 6143817638 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	3	2799	100.0	1599	9	US-10-821-670-38	Sequence 38, Appl
c	4	2799	100.0	1599	9	US-10-821-670-40	Sequence 40, Appl
	5	2687	96.0	1533	3	US-09-917-265-43	Sequence 43, Appl
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c	43	1646	58.8	921	9	US-10-821-670-28	Sequence 28, Appl
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c	45	1643	58.7	987	3	US-09-917-265-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1
US-09-917-265-38
; Sequence 38, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1599)
; OTHER INFORMATION:
US-09-917-265-38

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Pred. No.:              0           Length:         1599
Score:                  2799.00     Matches:        533
Percent Similarity:     100.0%      Conservative:   0
Best Local Similarity:  100.0%      Mismatches:     0
Query Match:            100.0%      Indels:         0
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US-10-821-670A-39 (1-533) x US-09-917-265-38 (1-1599)

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Qy        321 SerAsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuPro 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020

Qy        341 ThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArg 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 1080

Qy        361 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 1140

Qy        381 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeu 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200

Qy        401 ProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 1260

Qy        421 AsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSer 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 1320

Qy        441 IleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeu 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 1380

Qy        461 MetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 1440

Qy        481 LeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluPro 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 1500

Qy        501 AspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAla 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 1560

Qy        521 ValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 533
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Db       1561 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599

RESULT 2
US-09-917-265-40/c
; Sequence 40, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-40

Alignment Scores:
Pred. No.:              0           Length:         1599
Score:                  2799.00     Matches:        533
Percent Similarity:     100.0%      Conservative:   0
Best Local Similarity:  100.0%      Mismatches:     0
Query Match:            100.0%      Indels:         0
DB:                     3           Gaps:           0
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US-10-821-670A-39 (1-533) x US-09-917-265-40 (1-1599)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1599 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 1540

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 1420

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1359 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 1300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
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Db       1299 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 1240

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1179 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 1120

Qy        161 GlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1119 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 1060

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        999 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 940

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        939 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 880

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        879 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 820

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 760

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        759 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 640

Qy        321 SerAsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuPro 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        639 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 580

Qy        341 ThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArg 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        579 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 520

Qy        361 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        519 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 460

Qy        381 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeu 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        459 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 400

Qy        401 ProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        399 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 340

Qy        421 AsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSer 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        339 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 280

Qy        441 IleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeu 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        279 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 220

Qy        461 MetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 160

Qy        481 LeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluPro 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        159 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 100

Qy        501 AspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAla 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 40

Qy        521 ValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 533
              |||||||||||||||||||||||||||||||||||||||
Db         39 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 3
US-10-821-670-38
; Sequence 38, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-10-821-670-38

Alignment Scores:
Pred. No.:              0               Length:         1599
Score:                  2799.00         Matches:        533
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-39 (1-533) x US-10-821-670-38 (1-1599)
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Qy          1 MetHisProGlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeu 20
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Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
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Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
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Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
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Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
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Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
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Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
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Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
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Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuPro 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020

Qy        341 ThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArg 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 1080

Qy        361 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 1140

Qy        381 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeu 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200

Qy        401 ProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 1260

Qy        421 AsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSer 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 1320

Qy        441 IleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeu 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 1380

Qy        461 MetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 1440

Qy        481 LeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluPro 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 1500

Qy        501 AspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAla 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 1560

Qy        521 ValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 533
              |||||||||||||||||||||||||||||||||||||||
Db       1561 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
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RESULT 4
US-10-821-670-40/c
; Sequence 40, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
US-10-821-670-40

Alignment Scores:

Pred. No.:	0	Length:	1599
Score:	2799.00	Matches:	533
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	9	Gaps:	0

US-10-821-670A-39 (1-533) x US-10-821-670-40 (1-1599)

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Qy          1 MetHisProGlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1599 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 1540

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       1539 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60

Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 1420

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80

Db       1419 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100

Db       1359 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 1300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120

Db       1299 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 1240

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140

Db       1239 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160

Db       1179 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 1120

Qy        161 GlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180

Db       1119 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 1060

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200

Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220

Db        999 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 940

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240

Db        939 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 880

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260

Db        879 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 820

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280

Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 760

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300

Db        759 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320

Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 640

Qy        321 SerAsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuPro 340

Db        639 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 580

Qy        341 ThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArg 360

Db        579 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 520

Qy        361 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 380

Db        519 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 460

Qy        381 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeu 400

Db        459 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 400

Qy        401 ProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThr 420

Db        399 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 340

Qy        421 AsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSer 440

Db        339 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 280

Qy        441 IleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeu 460

Db        279 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 220

Qy        461 MetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 480

Db        219 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 160

Qy        481 LeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluPro 500

Db        159 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 100

Qy        501 AspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAla 520

Db         99 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 40

Qy        521 ValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 533

Db         39 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
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RESULT 5
US-09-917-265-43
; Sequence 43, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)
; OTHER INFORMATION:
US-09-917-265-43

Alignment Scores:

Pred. No.:	7.04e-314	Length:	1533
Score:	2687.00	Matches:	511
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	96.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-39 (1-533) x US-09-917-265-43 (1-1533)

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Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42

Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62

Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
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Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102

Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122

Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142

Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162

Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        163 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182

Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202

Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222

Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242

Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262

Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282

Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302

Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322

Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        323 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 342

Db        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy        343 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 362

Db        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020

Qy        363 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 382

Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080

Qy        383 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 402

Db       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy        403 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 422

Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200

Qy        423 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 442

Db       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260

Qy        443 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 462

Db       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320

Qy        463 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 482

Db       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380

Qy        483 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 502

Db       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440

Qy        503 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 522

Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500

Qy        523 IleAsnArgMetMetSerTyrLeuAsnAlaSer 533

Db       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533

RESULT 6
US-09-917-265-45/c
; Sequence 45, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-45

Alignment Scores:
Pred. No.:              7.04e-314       Length:         1533
Score:                  2687.00         Matches:        511
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            96.0%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-39 (1-533) x US-09-917-265-45 (1-1533)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42

Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62

Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82

Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102

Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122

Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234
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Qy       123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
Db      1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy       143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
Db      1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy       163 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
Db      1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy       183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
Db      1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy       203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
Db       993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy       223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
Db       933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy       243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
Db       873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy       263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
Db       813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy       283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
Db       753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy       303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
Db       693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy       323 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 342
Db       633 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy       343 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 362
Db       573 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy       363 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 382
Db       513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy       383 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 402
Db       453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy       403 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 422
Db       393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy       423 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 442
Db       333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy       443 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 462
Db       273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy       463 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 482
Db       213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy       483 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 502
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Db       153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy       503 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 522
Db        93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy       523 IleAsnArgMetMetSerTyrLeuAsnAlaSer 533
Db        33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
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RESULT 7
US-10-821-670-43
; Sequence 43, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)
US-10-821-670-43

Alignment Scores:

Pred. No.:	7.04e-314	Length:	1533
Score:	2687.00	Matches:	511
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	96.0%	Indels:	0
DB:	9	Gaps:	0

US-10-821-670A-39 (1-533) x US-10-821-670-43 (1-1533)

```
Qy        23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
Db         1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
Db        61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
Db       121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
Db       181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy       103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
Db       241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy       123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
Db       301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy       143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
Db       361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
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Qy        163 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        323 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy        343 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020

Qy        363 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080

Qy        383 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy        403 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200

Qy        423 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260

Qy        443 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320

Qy        463 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380

Qy        483 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440

Qy        503 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500

Qy        523 IleAsnArgMetMetSerTyrLeuAsnAlaSer 533
              |||||||||||||||||||||||||||||||||
Db       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
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RESULT 8
US-10-821-670-45/c
; Sequence 45, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
US-10-821-670-45

Alignment Scores:

Pred. No.:	7.04e-314	Length:	1533
Score:	2687.00	Matches:	511
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	96.0%	Indels:	0
DB:	9	Gaps:	0

US-10-821-670A-39 (1-533) x US-10-821-670-45 (1-1533)

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Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        163 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        323 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 342
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        343 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 362
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy        363 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 382
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy        383 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 402
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy        403 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 422
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy        423 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 442
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy        443 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 462
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy        463 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 482
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy        483 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 502
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy        503 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 522
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy        523 IleAsnArgMetMetSerTyrLeuAsnAlaSer 533
                 ||||||||||||||||||||||||||||||||
Db         33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 9
US-09-917-265-61
; Sequence 61, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
US-09-917-265-61

Alignment Scores:
Pred. No.:              1.62e-308       Length:         1599
Score:                  2643.00         Matches:        501
Percent Similarity:     96.4%           Conservative:   13
Best Local Similarity:  94.0%           Mismatches:     19
Query Match:            94.4%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-39 (1-533) x US-09-917-265-61 (1-1599)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||:::|||   |||||||||||||||||   ||||||
Db          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||:::|||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||   ||||||||||||||||||||||||||||||||:::|||||||||   |||
Db        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||
Db        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Qy        161 GlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              |||   ||||||||||||   ||||||||||||||||   ||||||||||||||:::|||
Db        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
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Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||   :::|||   ||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTGCATACAGGCCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||    ||||||||||||||||||||||||||||||
Db        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuPro 340
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGCGACTGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020

Qy        341 ThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArg 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGA 1080

Qy        361 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 380
              |||:::|||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db       1081 GCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCC 1140

Qy        381 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeu 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200

Qy        401 ProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACT 1260

Qy        421 AsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSer 440
              ||||||||||||||||||||   |||   ||||||||||||   ||||||||||||||||
Db       1261 AACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGC 1320

Qy        441 IleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeu 460
              ||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db       1321 ATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTA 1380

Qy        461 MetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 ATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTG 1440

Qy        481 LeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluPro 500
              ||||||||||||||   ||||||||||||||||||||   ||||||||||||||||||||
Db       1441 TTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCG 1500

Qy        501 AspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAla 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCG 1560

Qy        521 ValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 533
              |||||||||||||||||||||||||||||||:::|||
Db       1561 GTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1599

RESULT 10
US-09-917-265-63/c
; Sequence 63, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-63

Alignment Scores:
Pred. No.:              1.62e-308       Length:         1599
Score:                  2643.00         Matches:        501
Percent Similarity:     96.4%           Conservative:   13
Best Local Similarity:  94.0%           Mismatches:     19
Query Match:            94.4%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-39 (1-533) x US-09-917-265-63 (1-1599)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||:::|||   ||||||||||||||||||   ||||||
Db       1599 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 1540

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||:::|||||||||||||||||||||||||||||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 1420

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||   ||||||||||||||||||||||||||||||:::|||||||||   |||
Db       1359 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 1300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db       1299 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 1240

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||||
Db       1179 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 1120

Qy        161 GlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              |||   ||||||||||||   ||||||||||||||||   ||||||||||||||:::|||
Db       1119 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 1060

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        999 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 940

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        939 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 880

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        879 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 820
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Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||   :::|||   ||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 760

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db        759 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 640

Qy        321 SerAsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuPro 340
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        639 AGCGACTGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 580

Qy        341 ThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArg 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        579 ACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGA 520

Qy        361 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 380
              |||:::||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        519 GCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCC 460

Qy        381 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeu 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        459 GAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTA 400

Qy        401 ProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        399 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACT 340

Qy        421 AsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSer 440
              ||||||||||||||||||   |||   ||||||||||||   ||||||||||||||||
Db        339 AACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGC 280

Qy        441 IleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeu 460
              ||||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||
Db        279 ATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTA 220

Qy        461 MetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 ATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTG 160

Qy        481 LeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluPro 500
              ||||||||||||||||   ||||||||||||||||||||   ||||||||||||||||||||
Db        159 TTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCG 100

Qy        501 AspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAla 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCG 40

Qy        521 ValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 533
              ||||||||||||||||||||||||||||||||:::|||
Db         39 GTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1

RESULT 11
US-10-821-670-61
; Sequence 61, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2

; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-10-821-670-61

Alignment Scores:
Pred. No.:              1.62e-308       Length:         1599
Score:                  2643.00         Matches:        501
Percent Similarity:     96.4%           Conservative:   13
Best Local Similarity:  94.0%           Mismatches:     19
Query Match:            94.4%           Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-39 (1-533) x US-10-821-670-61 (1-1599)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||:::|||   |||||||||||||||||   ||||||
Db          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||:::|||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||   ||||||||||||||||||||||||||||||||:::|||||||||   |||
Db        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Qy        161 GlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              |||   ||||||||||||   ||||||||||||||||   ||||||||||||||:::|||
Db        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||   :::|||   ||||||
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Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||    ||||||||||||||||||||||||||
Db        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuPro 340
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGCGACTGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020

Qy        341 ThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArg 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGA 1080

Qy        361 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 380
              |||:::||||||||||||||||||||||||||||||||    ||||||||||||||||||
Db       1081 GCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCC 1140

Qy        381 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeu 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200

Qy        401 ProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACT 1260

Qy        421 AsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSer 440
              ||||||||||||||||||    |||   ||||||||||    ||||||||||||||||
Db       1261 AACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGC 1320

Qy        441 IleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeu 460
              ||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||
Db       1321 ATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTA 1380

Qy        461 MetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 ATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTG 1440

Qy        481 LeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluPro 500
              ||||||||||||||||    ||||||||||||||||||||    ||||||||||||||||
Db       1441 TTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCG 1500

Qy        501 AspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAla 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCG 1560

Qy        521 ValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 533
              |||||||||||||||||||||||||||||:::|||
Db       1561 GTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1599

RESULT 12
US-10-821-670-63/c
; Sequence 63, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-63

Alignment Scores:
Pred. No.:                1.62e-308       Length:          1599
Score:                    2643.00         Matches:         501
Percent Similarity:       96.4%           Conservative:    13
Best Local Similarity:    94.0%           Mismatches:      19
Query Match:              94.4%           Indels:          0
DB:                       9               Gaps:            0

US-10-821-670A-39 (1-533) x US-10-821-670-63 (1-1599)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpLeuSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||:::|||   ||||||||||||||||||    ||||||
Db       1599 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 1540

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||:::|||||||||||||||||||||||||||||||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 1420

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||   ||||||||||||||||||||||||||||||:::|||||||||   |||
Db       1359 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 1300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db       1299 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 1240

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||:::||||||||||||||||
Db       1179 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 1120

Qy        161 GlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              |||   ||||||||||||   ||||||||||||||||||||:::|||
Db       1119 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 1060

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        999 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 940

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        939 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 880

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        879 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 820

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||   :::|||   ||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 760

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||    ||||||||||||||||||||||||||
Db        759 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 700
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Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 640

Qy        321 SerAsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuPro 340
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        639 AGCGACTGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 580

Qy        341 ThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArg 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        579 ACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGA 520

Qy        361 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 380
              |||:::|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        519 GCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCC 460

Qy        381 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeu 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        459 GAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTA 400

Qy        401 ProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        399 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACT 340

Qy        421 AsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSer 440
              ||||||||||||||||||||   |||   ||||||||||   ||||||||||||||||||
Db        339 AACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGC 280

Qy        441 IleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeu 460
              ||||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||
Db        279 ATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTA 220

Qy        461 MetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 ATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTG 160

Qy        481 LeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluPro 500
              ||||||||||||||||   ||||||||||||||||||   ||||||||||||||||||||
Db        159 TTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCG 100

Qy        501 AspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAla 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCG 40

Qy        521 ValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 533
              ||||||||||||||||||||||||||||||||:::|||
Db         39 GTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1

RESULT 13
US-09-917-265-66
; Sequence 66, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
;   OTHER INFORMATION:
US-09-917-265-66
```

```
Alignment Scores:
Pred. No.:              8.6e-297        Length:         1533
Score:                  2546.00         Matches:        482
Percent Similarity:     96.7%           Conservative:   12
Best Local Similarity:  94.3%           Mismatches:     17
Query Match:            91.0%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-39 (1-533) x US-09-917-265-66 (1-1533)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
              ||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
              ||||||||||||||||||||||||||||||||||:::|||||||||   |||   |||
Db        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
              ||||||||||||||||||||||||||||||||||||||||||:::||||||||||||||||
Db        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
              ||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420

Qy        163 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              ||||||||||||   ||||||||||||||||   ||||||||||||||:::|||||||||
Db        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
              ||||||||||||||||||||||||||||||||||||   :::|||   ||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900

Qy        323 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
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Qy        343 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 362
Db        961 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 1020

Qy        363 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 382
Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 1080

Qy        383 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 402
Db       1081 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy        403 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 422
Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1200

Qy        423 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 442
Db       1201 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1260

Qy        443 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 462
Db       1261 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1320

Qy        463 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 482
Db       1321 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 1380

Qy        483 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 502
Db       1381 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1440

Qy        503 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 522
Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1500

Qy        523 IleAsnArgMetMetSerTyrLeuAsnAlaSer 533
Db       1501 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1533

RESULT 14
US-09-917-265-68/c
; Sequence 68, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-68

Alignment Scores:
Pred. No.:              8.6e-297      Length:          1533
Score:                  2546.00       Matches:         482
Percent Similarity:     96.7%         Conservative:    12
Best Local Similarity:  94.3%         Mismatches:      17
Query Match:            91.0%         Indels:          0
DB:                     3             Gaps:            0

US-10-821-670A-39 (1-533) x US-09-917-265-68 (1-1533)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42

Db       1533 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62
Db       1473 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1414

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
Db       1413 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
Db       1353 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1294

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122
Db       1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142
Db       1233 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162
Db       1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy        163 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
Db       1113 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1054

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 994

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 874

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262
Db        873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282
Db        813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302
Db        753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 634

Qy        323 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 342
Db        633 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        343 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 362
Db        573 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 514

Qy        363 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 382
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 454

Qy        383 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 402
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Db        453 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy        403 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 422

Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 334

Qy        423 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 442

Db        333 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 274

Qy        443 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 462

Db        273 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 214

Qy        463 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 482

Db        213 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 154

Qy        483 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 502

Db        153 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 94

Qy        503 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 522

Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 34

Qy        523 IleAsnArgMetMetSerTyrLeuAsnAlaSer 533

Db         33 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1

RESULT 15
US-10-821-670-66
; Sequence 66, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-10-821-670-66

Alignment Scores:
Pred. No.:              8.6e-297      Length:         1533
Score:                  2546.00       Matches:        482
Percent Similarity:     96.7%         Conservative:   12
Best Local Similarity:  94.3%         Mismatches:     17
Query Match:            91.0%         Indels:         0
DB:                     9             Gaps:           0

US-10-821-670A-39 (1-533) x US-10-821-670-66 (1-1533)

Qy         23 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 42

Db          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 62

Db         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82

Db        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102

Db        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240

Qy        103 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 122

Db        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300

Qy        123 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 142

Db        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360

Qy        143 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 162

Db        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420

Qy        163 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182

Db        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 202

Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540

Qy        203 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 222

Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        223 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 242

Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660

Qy        243 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 262

Db        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720

Qy        263 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 282

Db        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780

Qy        283 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 302

Db        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        303 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 322

Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900

Qy        323 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 342

Db        901 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy        343 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 362

Db        961 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 1020

Qy        363 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 382

Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 1080

Qy        383 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 402

Db       1081 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy        403 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 422

Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1200

Qy        423 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 442
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                ||||||||||||||||   |||   ||||||||||||   ||||||||||||||||||||
Db       1201 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1260

Qy        443 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 462
                ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db       1261 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1320

Qy        463 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 482
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 1380

Qy        483 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 502
                |||||||||   ||||||||||||||||||||   ||||||||||||||||||||||||
Db       1381 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1440

Qy        503 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 522
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1500

Qy        523 IleAsnArgMetMetSerTyrLeuAsnAlaSer 533
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Db       1501 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1533


Search completed: June 10, 2006, 04:33:49
Job time : 2112.51 secs
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 10, 2006, 01:18:36 ; Search time 27.7307 Seconds
(without alignments)
3659.318 Million cell updates/sec

Title: US-10-821-670A-39
Perfect score: 2799
Sequence: 1 MHPQQLVIAWLSLVLLAPPL.....HAFRIRAVTINRMMSYLNAS 533

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 253354 seqs, 63461778 residues

Total number of hits satisfying chosen parameters: 506708

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
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-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	189.5	6.8	1363	6	US-10-827-684B-6	Sequence 6, Appli
2	189.5	6.8	1369	6	US-10-827-684B-5	Sequence 5, Appli
3	176	6.3	1923	7	US-11-145-307A-52	Sequence 52, Appl
4	134.5	4.8	1161	7	US-11-297-134-9	Sequence 9, Appli
5	115.5	4.1	2582	7	US-11-293-697-2331	Sequence 2331, Ap
6	114	4.1	2341	6	US-10-511-937-349	Sequence 349, App
7	112.5	4.0	3123	7	US-11-217-529-76356	Sequence 76356, A
8	107.5	3.8	3646	6	US-10-511-937-358	Sequence 358, App
9	105.5	3.8	1614	7	US-11-217-529-409	Sequence 409, App
10	105.5	3.8	2534	7	US-11-293-697-1946	Sequence 1946, Ap
11	104.5	3.7	2123	7	US-11-274-375-5	Sequence 5, Appli
12	104	3.7	3117	7	US-11-217-529-774	Sequence 774, App
13	103.5	3.7	3084	6	US-10-511-937-448	Sequence 448, App
14	103	3.7	3510	7	US-11-217-529-191047	Sequence 191047,
15	102.5	3.7	2832	7	US-11-145-307A-22	Sequence 22, Appl
16	99.5	3.6	1416	6	US-10-953-349-864	Sequence 864, App
17	99.5	3.6	1875	7	US-11-217-529-174200	Sequence 174200,
18	99.5	3.6	1910	7	US-11-274-375-9	Sequence 9, Appli
19	99	3.5	6327	7	US-11-217-529-75787	Sequence 75787, A
20	98.5	3.5	4761	7	US-11-217-529-1821	Sequence 1821, Ap
21	98.5	3.5	5997	7	US-11-313-450-1	Sequence 1, Appli
22	98.5	3.5	8370	7	US-11-263-326-90	Sequence 90, Appl
23	98.5	3.5	8377	7	US-11-263-326-95	Sequence 95, Appl
24	98.5	3.5	8380	7	US-11-263-326-89	Sequence 89, Appl
25	98.5	3.5	8381	7	US-11-263-326-1	Sequence 1, Appli
26	98.5	3.5	8381	7	US-11-263-326-3	Sequence 3, Appli
27	98.5	3.5	8381	7	US-11-263-326-5	Sequence 5, Appli
28	98.5	3.5	8381	7	US-11-263-326-7	Sequence 7, Appli
29	98.5	3.5	8381	7	US-11-263-326-8	Sequence 8, Appli
30	98.5	3.5	8381	7	US-11-263-326-11	Sequence 11, Appl
31	98.5	3.5	8381	7	US-11-263-326-91	Sequence 91, Appl
32	98.5	3.5	8381	7	US-11-263-326-92	Sequence 92, Appl
33	98.5	3.5	8381	7	US-11-263-326-93	Sequence 93, Appl
34	98.5	3.5	8381	7	US-11-263-326-96	Sequence 96, Appl
35	98.5	3.5	8381	7	US-11-263-326-97	Sequence 97, Appl
36	98.5	3.5	8381	7	US-11-263-326-108	Sequence 108, App
37	98.5	3.5	8381	7	US-11-263-326-136	Sequence 136, App
38	98.5	3.5	8381	7	US-11-263-326-137	Sequence 137, App
39	98.5	3.5	8381	7	US-11-263-326-138	Sequence 138, App
40	98.5	3.5	8381	7	US-11-263-326-139	Sequence 139, App
41	98.5	3.5	8381	7	US-11-263-326-140	Sequence 140, App
42	98.5	3.5	8381	7	US-11-263-326-141	Sequence 141, App
43	98.5	3.5	8381	7	US-11-263-326-142	Sequence 142, App
44	98.5	3.5	8381	7	US-11-263-326-143	Sequence 143, App
45	98.5	3.5	8381	7	US-11-263-326-144	Sequence 144, App

ALIGNMENTS

RESULT 1
US-10-827-684B-6
; Sequence 6, Application US/10827684B
; Publication No. US20060115807A1
; GENERAL INFORMATION:
; APPLICANT: Chambers, Ian P
; TITLE OF INVENTION: Improved episomal expression system
; FILE REFERENCE: 78870/00003
; CURRENT APPLICATION NUMBER: US/10/827,684B
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 09/359,672
; PRIOR FILING DATE: 1999-07-23
; PRIOR APPLICATION NUMBER: GB 9701492.2
; PRIOR FILING DATE: 1997-01-24
; PRIOR APPLICATION NUMBER: PCT/GB98/00216
; PRIOR FILING DATE: 1998-01-26
; PRIOR APPLICATION NUMBER: GB 0407043.9
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1363
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-827-684B-6

Alignment Scores:

Pred. No.:	2.15e-09	Length:	1363
Score:	189.50	Matches:	96
Percent Similarity:	37.4%	Conservative:	63
Best Local Similarity:	22.6%	Mismatches:	169

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Query Match:           6.8%          Indels:        98
DB:                    6             Gaps:          18

US-10-821-670A-39 (1-533) x US-10-827-684B-6 (1-1363)

Qy         37 TrpHisProAsp-Ala---ProGlyGluMetValValLeuThrCysAsnThrProGlu-- 54
Db         76 TGGCACAGTGACAAGCCTGCCAGGGGCCACCGTTACCCTGATTTGCCCCGGGAAGGAAGC 135

Qy         55 -GluAspAspIleThr------------TrpThrSerAspGlnSerSerGluValLeuGl 70
Db        136 AGCAGGCAATGTTACCATTCACTGGGTGTACTCTGGCTCACAAAACAGAGAATGGACTAC 195

Qy         70 ySerGlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCy 90
Db        196 CACAGGAAACACACTGGTTCTGAGGGACGTGCAGCTCAGCGACACTGGGGACTATTTATG 255

Qy         90 sHisLysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGl 110
Db        256 CTCCCTGAATGATCACCTGGTGGGGACTGTGCCCTTGCTGGTG---------------- 298

Qy        110 yIleTrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLy 130
Db        299 ------------GATGTTCCCCCAGAGGAGCCCAAG-----------------CTCTC 327

Qy        130 sCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerTh 150
Db        328 CTGCTTCCGGAAGAACCCCCTTGTCAACGCCATCTGTGAGTGG---------------- 370

Qy        150 rAspLeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGluValThrCy 170
Db        371 --------------------------CGTCCGAGCAGCACCCCCTCTCCAACCACG-- 400

Qy        170 sGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTy 190
Db        401 ----AAGGCTGTGCTGTTTGCAAAGAAAATCAACACCACCAAC---GGGAAGAGTGACTT 453

Qy        190 rThrValGluCysGlnGluGlySerAlaCys--------------------------Pr 201
Db        454 CCAGGTGCCCTGCCAGTATTC-TCAGCAGCTGAAAAGCTTCTCCTGCCAGGTGGAGATCC 512

Qy        201 oAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTy 221
Db        513 TGGAGGGTGACAAAGTATACCACATAGTGTCACTGTGCGTTGCAAACAGTGTGGGAAGCA 572

Qy        221 r-GluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysA 241
Db        573 AGTCCAGCCACAACGAAGCGTTTCACAGCTTAAAAATGGTGCAGCCGGATCCACCTGCCA 632

Qy        241 snLeuGlnLeuLysProLeuLys---AsnSerArgHisValGluValSerTrpGluTyrP 260
Db        633 ACCTTGTGGTATCAGCCATACCTGGAAGGCCGCGCTGGCTCAAAGTCAGCTGGCAGCACC 692

Qy        260 roAspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnG 280
Db        693 CTGAGACCTGGGACCCG------AGTTACTACTTGCTGCAGTTCCAGCTTCGATACCGAC 746

Qy        280 lyLysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValV 300
Db        747 CTGTATGGTCAAAGGAG---TTCACGGTGTTGCTGCTCCCGGTGGCCCAGTACCAATGCG 803

Qy        300 alCysHisLysAspAlaLys--------------IleArgValGlnAlaArgAspArgT 315
Db        804 TCATCCATGATGCCTTGCGAGGAGTGAAGCACGTGGTCCAGGTCCGTGGGAAGGAGGAGC 863

Qy        315 yrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlyG 335
Db        864 TTGACCTTGGCCAGTGGAGTGAATGGTCC---------------------------- 892

Qy        335 lySerArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisS 355
Db        893 -------------CCAGAGGTCACGGGCACTCCTTGGATAGCAGAG---------CCCA 929

Qy        355 erGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluP 375
Db        930 GGACCACCCCGGCAGGAATCCTCTGGAACCCCACACAGGTCTCT---------------- 973

Qy        375 heTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerT 395
Db        974 -----------GTTGAAGACTCTGCCAACCACGAGGATCAGTACGAAAGTTCTACAGAAG 1022

Qy        395 hrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgG 415
Db       1023 CAACGAGTGTCCTCGCCCCAGTGCAA-----------GAATCCTCGTCCATGTCCCTGC 1070

Qy        415 luIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrT 435
Db       1071 CCACATTCCTGGTAGCTGGAGGAAGC----------------TTGGCGTTTGGGTTGC 1112

Qy        435 hrLeuCysLeu 438
Db       1113 TTCTCTGTGTC 1123

RESULT 2
US-10-827-684B-5
; Sequence 5, Application US/10827684B
; Publication No. US20060115807A1
; GENERAL INFORMATION:
;  APPLICANT: Chambers, Ian P
;  TITLE OF INVENTION: Improved episomal expression system
;  FILE REFERENCE: 78870/00003
;  CURRENT APPLICATION NUMBER: US/10/827,684B
;  CURRENT FILING DATE:  2004-04-19
;  PRIOR APPLICATION NUMBER: US 09/359,672
;  PRIOR FILING DATE: 1999-07-23
;  PRIOR APPLICATION NUMBER: GB 9701492.2
;  PRIOR FILING DATE: 1997-01-24
;  PRIOR APPLICATION NUMBER: PCT/GB98/00216
;  PRIOR FILING DATE: 1998-01-26
;  PRIOR APPLICATION NUMBER: GB 0407043.9
;  PRIOR FILING DATE: 2004-03-29
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 1369
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-827-684B-5

Alignment Scores:
Pred. No.:             2.16e-09      Length:        1369
Score:                 189.50        Matches:       96
Percent Similarity:    37.4%         Conservative:  63
Best Local Similarity: 22.6%         Mismatches:    169
Query Match:           6.8%          Indels:        98
DB:                    6             Gaps:          18

US-10-821-670A-39 (1-533) x US-10-827-684B-5 (1-1369)

Qy         37 TrpHisProAsp-Ala---ProGlyGluMetValValLeuThrCysAsnThrProGlu-- 54
Db         82 TGGCACAGTGACAAGCCTGCCAGGGGCCACCGTTACCCTGATTTGCCCCGGGAAGGAAGC 141

Qy         55 -GluAspAspIleThr------------TrpThrSerAspGlnSerSerGluValLeuGl 70
Db        142 AGCAGGCAATGTTACCATTCACTGGGTGTACTCTGGCTCACAAAACAGAGAATGGACTAC 201

Qy         70 ySerGlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCy 90
Db        202 CACAGGAAACACACTGGTTCTGAGGGACGTGCAGCTCAGCGACACTGGGGACTATTTATG 261

Qy         90 sHisLysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGl 110
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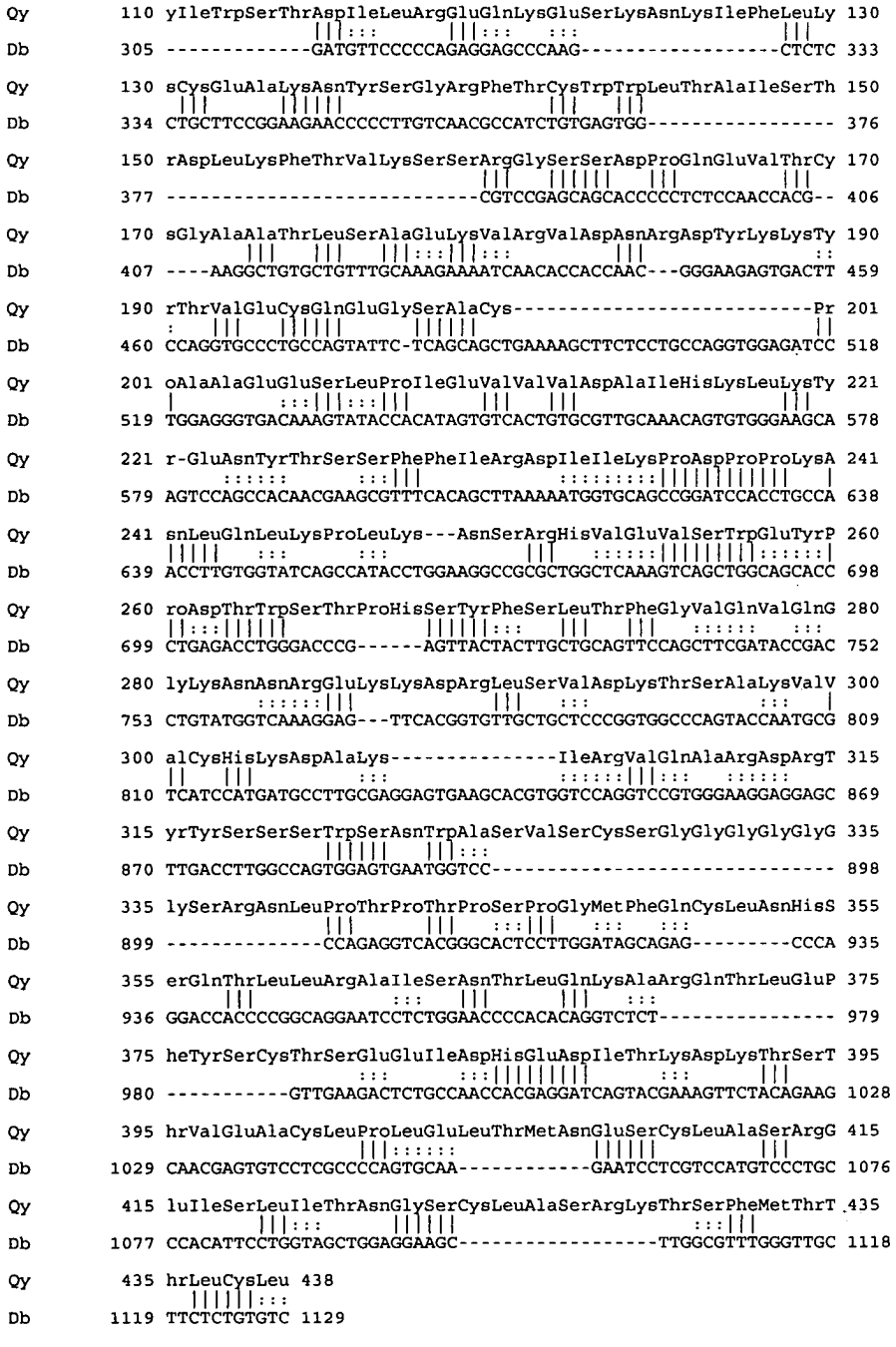

RESULT 3
US-11-145-307A-52
; Sequence 52, Application US/11145307A
; Publication No. US20060094035A1
; GENERAL INFORMATION:
; APPLICANT: Arcturus Bioscience, Inc.
; APPLICANT: Erlander, Mark G.
; APPLICANT: Ma, Xiao-Jun
; TITLE OF INVENTION: Identification of Tumors
; FILE REFERENCE: 022041-002020US
; CURRENT APPLICATION NUMBER: US/11/145,307A
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 60/577,084
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 1923
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-145-307A-52

Alignment Scores:

Pred. No.:	7.47e-08	Length:	1923
Score:	176.00	Matches:	79
Percent Similarity:	37.8%	Conservative:	40
Best Local Similarity:	25.1%	Mismatches:	105
Query Match:	6.3%	Indels:	93
DB:	7	Gaps:	17

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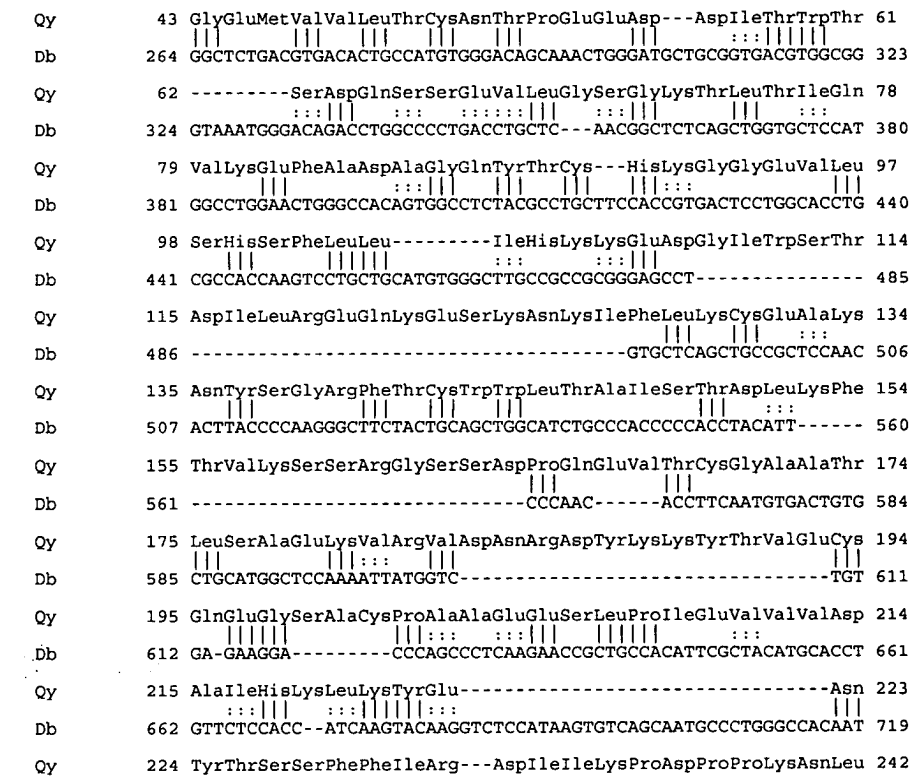

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Qy        243 GlnLeuLysProLeu---LysAsnSerArgHisValGluValSerTrpGluTyrProAsp 261

Db        780 GTAGCCCGGCCAGTGCCCAGCAACCCTCGCCGGCTGGAGGTGACGTGGCAGACCCCCTCG 839

Qy        262 ThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLys 281

Db        840 ACCTGGCCTGACCCTGAGTCT---TTTCCTCTCAAGTTCTTTCTGCGCTACCGA------ 890

Qy        282 AsnAsnArgGluLysLysAspArgLeuSerValAspLys---------------------- 294

Db        891 ----------------------CCCCTCATCCTGGACCAGTGGCAGCATGTGGAGCTGTCC 929

Qy        295 ---------------ThrSerAlaLysValValCysHisLysAspAlaLysIleArgVal 309

Db        930 GACGGCACAGCACACACCATCACAGATGCCTACGCCGGGAAGGAGTACATTATCCAGGTG 989

Qy        310 GlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAla 324

Db        990 GCAGCCAAGGACAATGAGATT---GGGACATGGAGTGACTGGAGC 1031
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RESULT 4
US-11-297-134-9
; Sequence 9, Application US/11297134
; Publication No. US20060111297A1
; GENERAL INFORMATION:
; APPLICANT: Genzyme Corporation
; APPLICANT: Roberts, Bruce
; TITLE OF INVENTION: BLOOD FACTOR DOMAINS
; FILE REFERENCE: 5270C
; CURRENT APPLICATION NUMBER: US/11/297,134
; CURRENT FILING DATE: 2005-12-08
; PRIOR APPLICATION NUMBER: PCT/US2005/018461
; PRIOR FILING DATE: 2004-06-09
; PRIOR APPLICATION NUMBER: US 60/477,291
; PRIOR FILING DATE: 2003-06-09
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 1161
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-297-134-9

Alignment Scores:

Pred. No.:	0.000386	Length:	1161
Score:	134.50	Matches:	53
Percent Similarity:	39.0%	Conservative:	36
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Query Match:	4.8%	Indels:	57
DB:	7	Gaps:	9

US-10-821-670A-39 (1-533) x US-11-297-134-9 (1-1161)

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Qy        129 LeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIle 148

Db        110 GTGCAATGCCGAGCCTCTCGGTACCCGATCGCCGTGGATTGCTCCTGGACCCTGCCGCCT 169

Qy        149 SerThrAspLeuLysPheThrValLys---------------------------SerSer 159

Db        170 GCTCCAAACTCCACCAGCCCCGTGTCCTTCATTGCCACGTACAGGCTCGGCATGGCTGCC 229

Qy        160 ArgGlySerSerAspPro---------GlnGluValThrCysGlyAlaAlaThrLeuSer 176

Db        230 CGGGGCCACAGCTGGCCCTGCCTGCAGCAGACGCCAACGTCCACCAGCTGCACCATCACG 289

Qy        177 AlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGlu 196

Db        290 --------------------------GATGTCCAGCTGTTCTCCATG------------ 310

Qy        197 GlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIle 216

Db        311 ----------------------------GCTCCCTACGTGCTCAATGTCACCGCCGTC 340

Qy        217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236

Db        341 CACCCCTGGGGCTCCAGCAGCAGCTTCGTGCCTTTCATAACAGAGCACATCATCAAGCCC 400

Qy        237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSer 256

Db        401 GACCCTCCAGAAGGCGTGCGCCTAAGCCCCCTCGCT---GAGCGCCACGTACAGGTGCAG 457

Qy        257 TrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyVal 276

Db        458 TGGGAGCCTCCCGGGTCCTGGCCCTTCCCA---GAGATCTTCTCACTGAAGTACTGGATC 514

Qy        277 GlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSer 296

Db        515 CGTTACAAG---CGTCAGGGAGCTGCGCGCTTCCACCGGGTGGGGCCCATTGAAGCCACG 571

Qy        297 AlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyr 316

Db        572 TCCTTCATCCTC-----------------AGGGCTGTGCGGCCCCGAGCCAGGTACTAC 613

Qy        317 -------------------------------------SerSerSerTrpSerAsnTrp 323

Db        614 GTCCAAGTGGCGGCTCAGGACCTCACAGACTACGGGGAACTGAGTGACTGGAGTCTCCCC 673

Qy        324 AlaSerValSerCysSerGlyGly 331

Db        674 GCCACTGCCACAATGAGCCTGGGC 697
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RESULT 5
US-11-293-697-2331
; Sequence 2331, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2331
; LENGTH: 2582
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-2331

Alignment Scores:

Pred. No.:	0.0915	Length:	2582
Score:	115.50	Matches:	116
Percent Similarity:	29.6%	Conservative:	71
Best Local Similarity:	18.4%	Mismatches:	196
Query Match:	4.1%	Indels:	249
DB:	7	Gaps:	30

US-10-821-670A-39 (1-533) x US-11-293-697-2331 (1-2582)

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Db        223 ATGCTTCTGTGGCTGCTGCTGCTGATCCTGACTCCTGGAAGAGAACAATCAGGGGTGGCC 282

Qy         27 GluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaProGlyGluMetVal 46

Db        283 CCAAAAGCTGTACTTCTCCTCAATCCTCCATGGTCCACAGCCTTCAAAGGAGAAAAAGTG 342

Qy         47 ValLeuThrCysAsnThrProGlu-----------GluAspAspIleThrTrpThrSer 62

Db        343 GCTCTCATATGCAGCAGCATATCACATTCCCTAGCCCAGGGAGACACATATTGGTATCAC 402
```

```
Qy        63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
             |||:::          :::         |||         ||||||:::   |||
Db       403 GATGAGAAGTTGTTGAAAATAAAACATGACAAG---------ATCCAAATTACAGAG--- 450

Qy        83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
                 |||  |||  |||         |||      ||||||  :::
Db       451 ------CCTGGAAATTACCAATGTAAGACCCGAGGATCCTCCCTCAGTGATGCC------ 498

Qy       103 LeuIleHisLysLysGluAspGlyIleTrp---SerThrAspIleLeuArgGluGlnLys 121
               :::|||  :::         |||                |||
Db       499 ---GTGCATGTGGAATTTTCACCTGACTGGCTGATCCTGCAGGCTTTACATCCTGTCTTT 555

Qy       122 GluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThr 141
             |||      |||  :::   |||:::|||:::   |||:::
Db       556 GAAGGAGACAAT---GTCATTCTGAGATGTCAGGGGAAAGACAACAAA------------ 600

Qy       142 CysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGly 161
                         :::|||      |||         |||         |||
Db       601 --------------------AACACTCATCAAAAGGTTTACTACAAGGAT------GGA 633

Qy       162 SerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArg 181
                  |||                        :::  :::   ||||||:::
Db       634 AAACAGCTTCCTAAT--------------------AGTTATAATTTAGAGAAGATCACA 672

Qy       182 ValAsp------AsnArgAspTyrLysLysTyr-------------------------- 190
             |||:::      :::||||||      ||||||
Db       673 GTGAATTCAGTCTCCAGGGATAATAGCAAATATCATTGTACTGCTTATAGGAAGTTTTAC 732

Qy       191 --------------------------------ThrValGluCysGlnGluGlySerAla 199
                                             ::::::   ||||||
Db       733 ATACTTGACATTGAAGTAACTTCAAAACCCCTAAATATCCAAGTTCAAGAGCTGTTTCTA 792

Qy       200 CysProAla------AlaGluGluSerLeuProIleGluValValValAspAlaIleHis 217
               |||         |||      |||   |||||||||            :::
Db       793 CATCCTGTGCTGAGAGCCAGCTCTTCCACGCCCATAGAG---------GGGAGTCCCATG 843

Qy       218 LysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAsp 237
                |||      |||         |||
Db       844 ACCCTGACCTGTGAGACCCAGCTCTCT-----------------------CCACAGAGG 879

Qy       238 ProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrp 257
             |||         ||||||             ::::::|||:::   :::   :::   |||
Db       880 CCAGATGTCCAGCTGCAATTCTCCCTCTTCAGAGATAGCCAGACCCTCGGATTGGGCTGG 939

Qy       258 ------------------GluTyrProAspThrTrpSerThrProHis---SerTyrPhe 270
                           :::   |||      |||:::             ||||||:::
Db       940 AGCAGGTCCCCCAAACTCCAGATCCCTGCCATGTGGACTGAAGACTCAGGGTCTTACTGG 999

Qy       271 -----------SerLeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLys 286
                     ::::::|||      ::::::   :::         ::::::   :::
Db      1000 TGTGAGGTGGAGACAGTGACTCACAGCATCAAAAAAAGGAGCCTGAGATCTCAGATACGT 1059

Qy       287 LysAspArgLeuSerValAspLysThrSerAlaLysVal--------------------- 299
               |||:::   |||         :::   ::::::
Db      1060 GTACAGAGAGTCCCTGTGTCTAATGTGAATCTAGAGATCCGGCCCACCGGAGGGCAGCTG 1119

Qy       300 ------------------------ValCys------------------------------ 301
                                      :::|||
Db      1120 ATTGAAGGAGAAAATATGGTCCTTATTTGCTCAGTAGCCCAGGGTTCAGGGACTGTCACA 1179

Qy       302 ---------HisLysAspAlaLysIleArgValGlnAlaArg------------------ 312
                     ||||||:::   :::::|||         |||
Db      1180 TTCTCCTGGCACAAAGAAGGAAGAGTAAGAAGCCTGGGTAGAAAGACCCAGCGTTCCCTG 1239

Qy       313 ----------------------------------------AspArgTyrTyr------ 316
                                                    |||||||||
Db      1240 TTGGCAGAGCTGCATGTTCTCACCGTGAAGGAGAGTGATGCAGGGAGATACTACTGTGCA 1299

Qy       317 ---------------SerSerSerTrpSerAsnTrpAlaSerVal--------------- 326
                           |||     |||   |||     |||
Db      1300 GCTGATAACGTTCACAGCCCCATCCTCAGCACGTGGATTCGAGTCACCGTGAGAATTCCG 1359

Qy       326 ------------------------------------------------------------ 326

Db      1360 GTATCTCACCCTGTCCTCACCTTCAGGGCTCCCAGGGCCCACACTGTGGTGGGGGACCTG 1419

Qy       326 ------------------------------------------------------------ 326

Db      1420 CTGGAGCTTCACTGTGAGTCCCTGAGAGGCTCTCCCCCGATCCTGTACCGATTTTATCAT 1479

Qy       327 ---------------------SerCysSerGlyGlyGlyGlyGlySerArgAsnLeu 339
                                    |||   :::      |||||||||   |||   ||||||
Db      1480 GAGGATGTCACCCTGGGGAACAGCTCAGCCCCCTCTGGAGGAGGAGCCTCCTTCAACCTC 1539

Qy       340 ProThrProThrProSerProGlyMetPheGlnCys---------------------Leu 352
                                       |||   :::   |||
Db      1540 TCTCTGACTGCAGAACATTCTGGAAACTACTCCTGTGATGCAGACAATGGCCTGGGGGCC 1599

Qy       353 AsnHisSerGlnThrLeu------------------------------------------ 358
                ||||||      :::
Db      1600 CAGCACAGTCATGGAGTGAGTCTCAGGGTCACAGTTCCGGTGTCTCGCCCCGTCCTCACC 1659

Qy       359 LeuArgAla-----------------IleSerAsnThrLeuGlnLysAlaArgGlnThr 372
             |||||||||                  :::   :::   |||:::         ::::::
Db      1660 CTCAGGGCTCCCGGGGCCCAGGCTGTGGTGGGGGACCTGCTGGAGCTTCACTGTGAGTCC 1719

Qy       373 LeuGlu------------------------PheTyrSerCysThrSerGluGluIleAsp 384
             |||                          ||||||
Db      1720 CTGAGAGGCTCCTTCCCGATCCTGTACTGGTTTTAT----------------------- 1755

Qy       385 HisGluAspIleThrLysAspLysThrSer--------------------ThrValGlu 397
             |||||||||   |||                |||                 :::
Db      1756 CACGAGGATGACACCTTGGGGAACATCTCGGCCCACTCTGGAGGAGGGGCATCCTTCAAC 1815

Qy       398 AlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAla--------------- 412
                |||      |||   :::   |||   ||||||   |||
Db      1816 CTCTCTCTGACTACAGAACATTCTGGAAACTACTCATGTGAGGCTGACAATGGCCTGGGG 1875

Qy       413 ---------SerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLys 429
                      |||:::   ::::::|||         |||:::         ||||||
Db      1876 GCCCAGCACAGTAAAGTGGTGACACTCAATGTTACAGGAACT---------TCCAGGAAC 1926

Qy       430 ThrSerPheMetThrThrLeuCysLeuSerSerIle 441
                ::   :::|||         ::::::   :::
Db      1927 AGAACAGGCCTTACCGCTGCGGGAATCACGGGGCTG 1962
```

RESULT 6
US-10-511-937-349
; Sequence 349, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 349
; LENGTH: 2341
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-511-937-349

Alignment Scores:

Pred. No.:	0.111	Length:	2341
Score:	114.00	Matches:	77
Percent Similarity:	32.2%	Conservative:	39
Best Local Similarity:	21.4%	Mismatches:	101
Query Match:	4.1%	Indels:	144
DB:	6	Gaps:	15

US-10-821-670A-39 (1-533) x US-10-511-937-349 (1-2341)

```
Qy          3 ProGlnGlnLeuValIleAlaTrp--------------LeuSerLeuValLeuLeuAla 17
              |||   |||      |||   |||                  :::|||:::||||||
Db        275 CCTCTCCAGTGTGGCATCATGTGGCAGCTGCTCCTCCCAACTGCTCTGCTACTTCTAGTT 334

Qy         18 ProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrp 37
                  |||       :::|||   |||   |||       :::|||      |||
Db        335 TCAGCTGGCATGCGGACTGAAGATCTCCCAAAGGCTGTGGTGTTCCTGGAGCCTCAATGG 394

Qy         38 HisProAspAlaProGlyGluMetValValLeuThrCysAsn---------ThrProGlu 54
              :::                 :::   |||   |||   |||            :::||||||
Db        395 TACAGGGTGCTCGAGAAGGACAGTGTGACTCTGAAGTGCCAGGGAGCCTACTCCCCTGAG 454

Qy         55 GluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGlyLysThr 74
              ::::::         |||      ::::::|||      :::               :::
Db        455 GACAATTCCACACAGTGGTTTCACAATGAGAGCCTC---ATCTCAAGCCAGGCCTCGAGC 511

Qy         75 LeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGly 94
                 |||                 |||:::|||:::|||   |||
Db        512 TACTTCATTGACGCTGCCACAGTCGACGACAGTGGAGAGTACAGGTGCCAGACAAACCTC 571

Qy         95 GluValLeuSerHisSerPheLeuLeu-------------------------------- 103
                 ||||||          |||
Db        572 TCCACCCTCAGTGACCCGGTGCAGCTAGAAGTCCATATCGGCTGGCTGTTGCTCCAGGCC 631

Qy        104 ---------IleHisLysLysGluAspGlyIle-----------------TrpSerThr 114
                    :::   |||:::||||||   |||                  |||
Db        632 CCTCGGTGGGTGTTCAAGGAGGAAGACCCTATTCACCTGAGGTGTCACAGCTGGAAGAAC 691

Qy        115 AspIleLeu-------------------------------------------------- 117
                 |||
Db        692 ACTGCTCTGCATAAGGTCACATATTTACAGAATGGCAAAGGCAGGAAGTATTTTCATCAT 751

Qy        118 ---------------------------------------------------------Arg 118
                                                                       |||
Db        752 AATTCTGACTTCTACATTCCAAAAGCCACACTCAAAGACAGCGGCTCCTACTTCTGCAGG 811

Qy        119 GluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGly 138
                  |||||||||   :::|||      ||||||      :::::::|||
Db        812 GGGCTTGTTGGGAGTAAAAATGT-GTCTTCAGAGACTGTGAACATCACCATCACTCA--- 867

Qy        139 ArgPhe--------------------------ThrCysTrp-Trp-------------- 144
              ||||||                          :::   ||| :::
Db        868 AGGTTTGGCAGTGTCAACCATCTCATCATTCTTTCCACCTGGGTACCAAGTCTCTTTCTG 927

Qy        145 ---------------LeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSe 159
                          |||   |||:::   |||   |||   |||:::||||||:::::
Db        928 CTTGGTGATGGTACTCCTTTTTGCAGTGGACACAGGACTATATTTCTCTGTGAAGACAAA 987

Qy        159 rArgGlySerSer-------------------------------------AspProGl 166
              :      ||||||                                    ||||||||
Db        988 CATTCGAAGCTCAACAAGAGACTGGAAGGACCATAAATTTAAATGGAGAAAGGACCCTCA 1047

Qy        166 n-----------------------------------------------------GluVa 168
              |                                                     |||
Db       1048 AGACAAATGACCCCCATCCCATGGGGGTAATAAGAGCAGTAGCAGCAGCATCTCTGAACA 1107

Qy        168 lThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLy 188
                 |||   ||||||||||||:::      :::        :::|||   :::::
Db       1108 TTTCTCTGGATTTGCAACCCTATCATCCTCAGGCCTCTCTACAAGCAGCAGGAAACATAG 1167

Qy        188 sLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeu-- 207
```

```
              :                  |||                 |||      :::   ||||||
Db       1168 A---------------ACTCAGAGCCAGATCCCTTATCCAACTCTCGACTTTTCCTTGGT 1212

Qy        208 ----------------------------------------ProIleGluValValVa 213
                                                     |||   |||
Db       1213 CTCCAGTGGAAGGGAAAAGCCCATGATCTTCAAGCAGGGAAGCCCCAGTGAG-------- 1264

Qy        213 lAspAlaIleHis------LysLeuLysTyrGluAsnTyrThrSerSerPhePheIle 230
                  :::|||     |||||||||:::::::|||||:::::|||   :::
Db       1265 ----TAGCTGCATTCCTAGAAATTGAAGTTTCAGAGCTACACAAACACTTTTTCTGTC 1318

RESULT 7
US-11-217-529-76356
; Sequence 76356, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76356
;   LENGTH: 3123
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-76356
```

Alignment Scores:

Pred. No.:	0.239	Length:	3123
Score:	112.50	Matches:	110
Percent Similarity:	31.6%	Conservative:	63
Best Local Similarity:	20.1%	Mismatches:	168
Query Match:	4.0%	Indels:	206
DB:	7	Gaps:	24

US-10-821-670A-39 (1-533) x US-11-217-529-76356 (1-3123)

```
Qy         85 AlaGlyGlnTyrThrCysHisLys---GlyGlyGluValLeuSerHisSerPheLeuLeu 103
                 |||   ::::::      ||||||      |||:::::::|||              |||
Db        853 GCCTCTAGATTCCAGAAGCACAAAATATCGGGTAAAATTTTGTTA---GAGTTAGAGCTT 909

Qy        104 IleHisLysLysGluAspGlyIleTrpSer------------ThrAspIleLeuArgGlu 119
                 :::|||   ||||||   ||||||   |||          :::|||   :::|||
Db        910 GTTCATTTAAAAGAGTTGGGCATAAATTCTTTTGGGACAAGATTTGAGATTTTCAAAGAA 969

Qy        120 GlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsn------------ 135
                    ::::::   |||      |||                 :::   |||
Db        970 ATAGAAAAAATCAAAGAGGCTATTAGAACTAATGGCCGCTCCCTGAATAGAGCTAGTAAG 1029

Qy        135 ---------------------------------------------------------- 135

Db       1030 ACCAATAACTCTAACATTTATAACCAATTGATGCCTCCCGCAAACGTTGACCAGAGAGCT 1089

Qy        136 ---TyrSerGly------ArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeu 152
                   |||   |||      |||   |||                |||      :::   :::
Db       1090 TCCTACAGAGGCCATGTTAGAAAGACTTCACAGTCGTTAGAGGACCTTCCGTCACAACAG 1149

Qy        153 LysPhe------ThrValLysSerSerArgGlySerSerAspProGlnGluValThrCys 170
                 |||      |||   ::::::::|||   |||
Db       1150 AATTTTATCCCCACTCCCAGAAATACTAGGAACTCC------------------------ 1185

Qy        171 GlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyr 190
                        ||||||   |||   |||                       |||
Db       1186 ---------------TCAGCTTCCAAGCACCGGCCT---------------AAATCTTTA 1215
```

```
Qy        191 ThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGlu 210
Db       1216 GTTTTTGATTCACAAGAGGCTAATGCTAATATAGCTCCAGATGTTCAAATTCCT---CAG 1272

Qy        211 ValValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIle 230
Db       1273 GTGGTAGAGGAAATGGCAGGT--------------------AATGAAAATTTGTTTGTT 1311

Qy        231 ------ArgAspIleIleLysPro--------------------AspProProLysAsn 241
Db       1312 TCTCCGAGGAGAGCCCCCAAACCCCCATCTTACCCTAGTCCAGCACAACCTCCAAAATCG 1371

Qy        242 LeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAsp 261
Db       1372 ------------CCCCTATTGAATAACACAAGGACGTCACCTTCTCCTACTCAACTTTAT 1419

Qy        262 ThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLys 281
Db       1420 TCATGGCAATCACCTACTTTATCTTTCTCA----------------------GGGCCT 1455

Qy        282 AsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCys 301
Db       1456 AAAAGGACTTCTTATATCGATCAA---------------------------------- 1479

Qy        302 HisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSer 321
Db       1480 ----------------------------------------TATTCTTCATCAGATTCT 1497

Qy        322 AsnTrpAlaSerValSerCys------------SerGlyGlyGlyGlyGlyGlySerArg 337
Db       1498 AATTTCAATTCCCGTTCCGCACTCCCAAAGAACAACCAAGGCGGTGGGAAGGCGTTGTCA 1557

Qy        338 AsnLeuProThrProThr---------------------------------------- 343
Db       1558 CCTATTCCATCCCCCACCCGTAATTCTGTTAGAAATGAAGATAGTGAAGGCAAGCTAACA 1617

Qy        344 ------------------------------------------------ProSerPro 346
Db       1618 TCGTCCTCGAAGAGGAATTCTGTCCCTTATTATGGATACGCTCCTGAATCTTCTTCGGAT 1677

Qy        347 GlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeu 366
Db       1678 AGAAAATCCTCTTGTTCCAGCCATGAGGAAGAGCAGTTTCAAGAAACAATGAACACATTC 1737

Qy        367 GlnLysAlaArgGlnThrLeuGluPheTyr--------------------SerCysThr 379
Db       1738 GAA------AGACCCACGTCCAGTATATACGCTGATGGATCTACCATTGCATCCATAAGT 1791

Qy        380 SerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCys 399
Db       1792 AATGACAGATTGGCACATGAGAAGGAGGGGAAGAAAAAACCA------------------ 1833

Qy        400 LeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIle 419
Db       1834 ---------------ACGAGACACTCGTCTTCATTATCTTCTAAATCAAAAAGCGATTCC 1878

Qy        420 ThrAsnGlySerCysLeu---------------AlaSerArgLysThrSerPheMetThr 434
Db       1879 AGGAGGAACTCGTCTTTAAAGAGAAGCAGCAGTGCATCGCGAACTAGTTCATTC------ 1932

Qy        435 ThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAla 454
Db       1932 ---------------------------------------------------------- 1932

Qy        455 MetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAsp------------ 470
Db       1933 AAAAAAAGTTCCTTCATGCTAAGTCCCTTTAGGCAACAATTTACTGATAATGCTGCTCGC 1992

Qy        471 ---------------GlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsn 485
Db       1993 TCTTCAAGTCCTGAAGAGAATCCCATAACCTCAATGCCGTCAGAAAAAAACAGCTCACCG 2052

Qy        486 ValAsnSer-ValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysTh 505
Db       2053 ATAGTTGATAAAAAGTCTTCCAAAAAGAGTAGATCTAAAAGAAGATCAGTTAGCGCAAAG 2112

Qy        505 rLysIleLysLeu------------------CysIleLeuLeuHisAlaPheArgIleAr 519
Db       2113 GAAGCTGAAATTTTTACCGAAACTGTGAAAGATGATAAAAATAAGAGGTCTGCGAGTGAG 2172

Qy        519 gAlaValThrIleAsnArg 525
Db       2173 GCTATTAAAGGTGAAACGC 2191
```

RESULT 8
US-10-511-937-358
; Sequence 358, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 358
; LENGTH: 3646
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-358

Alignment Scores:

Pred. No.:	0.927	Length:	3646
Score:	107.50	Matches:	115
Percent Similarity:	35.6%	Conservative:	83
Best Local Similarity:	20.7%	Mismatches:	211
Query Match:	3.8%	Indels:	149
DB:	6	Gaps:	26

US-10-821-670A-39 (1-533) x US-10-511-937-358 (1-3646)

```
Qy         39 ProAspAlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIle 58
Db        611 CCACAGAAACCTGCTGCCCTGCTCTGCAGAGGCCTCACTCAGCCT-----------CTG 658

Qy         59 ThrTrpThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGln 78
Db        659 CTCTGGACCAGTCTCCATGTGCTCAGCCCACAATGCCCTGGCAAGATGGA-CCAAAGCAG 717

Qy         79 ValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSer 98
Db        718 ACCTCCCCAAGTAGAGAAGCTTCAGCTCTGACAGCAGAGGGTGGAAGCTGCCTCATCTCA 777

Qy         99 -----------------HisSerPheLeuLeuIleHisLysLysGluAspGlyIle--- 111
Db        778 GGACTCCAGCCTGGCAACTCCTACTGGCTGCAGCTGCGCAGCGAACCTGATGGGATCTCC 837

Qy        112 --------------------TrpSerThrAspIleLeuArgGluGlnLysGluSerLys 124
Db        838 CTCGGTGGCTCCTGGGGATCCTGGTCCCTCCCTGTGACTGTGGACCTGCCTGGAGATGCA 897
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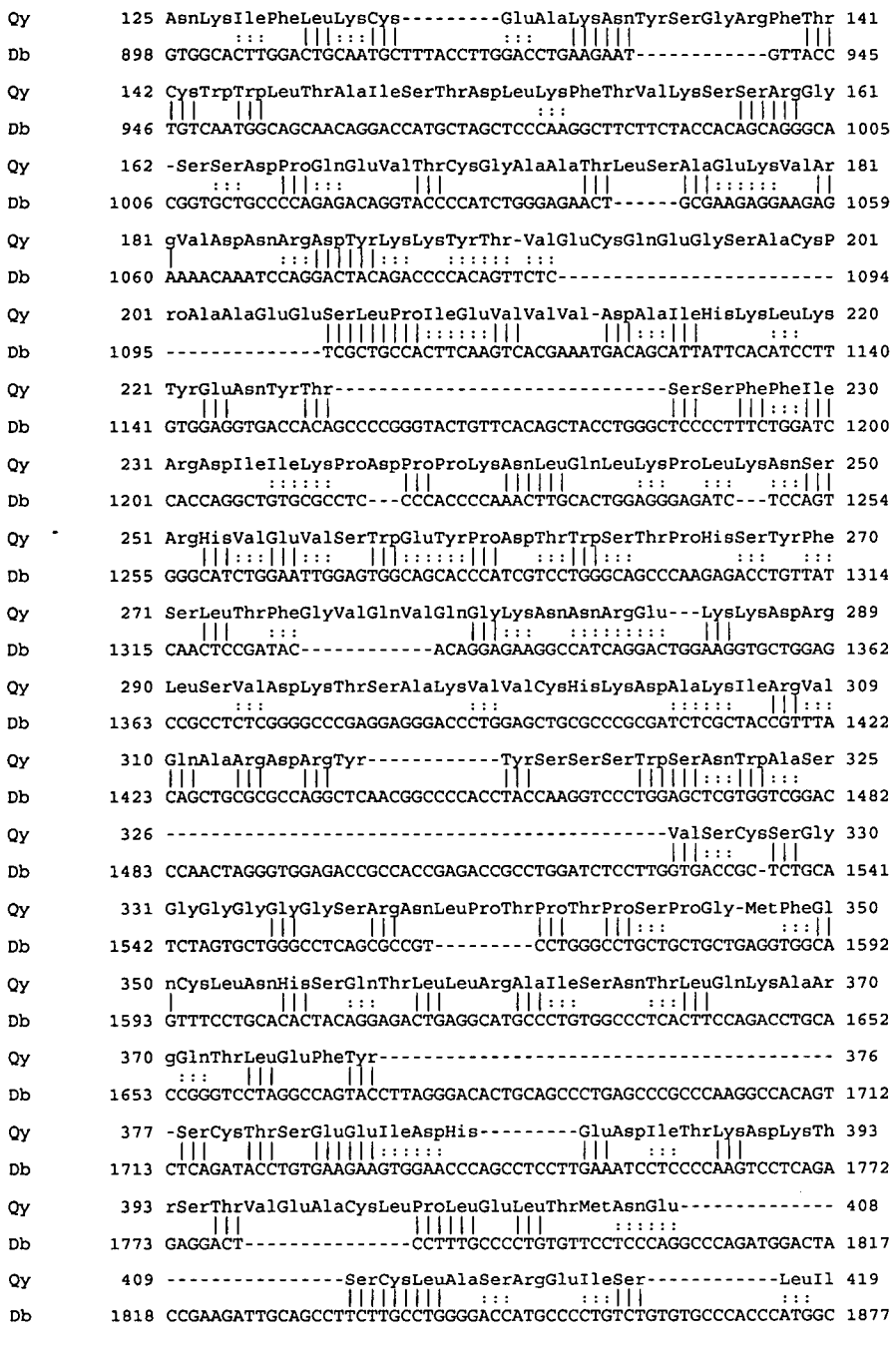

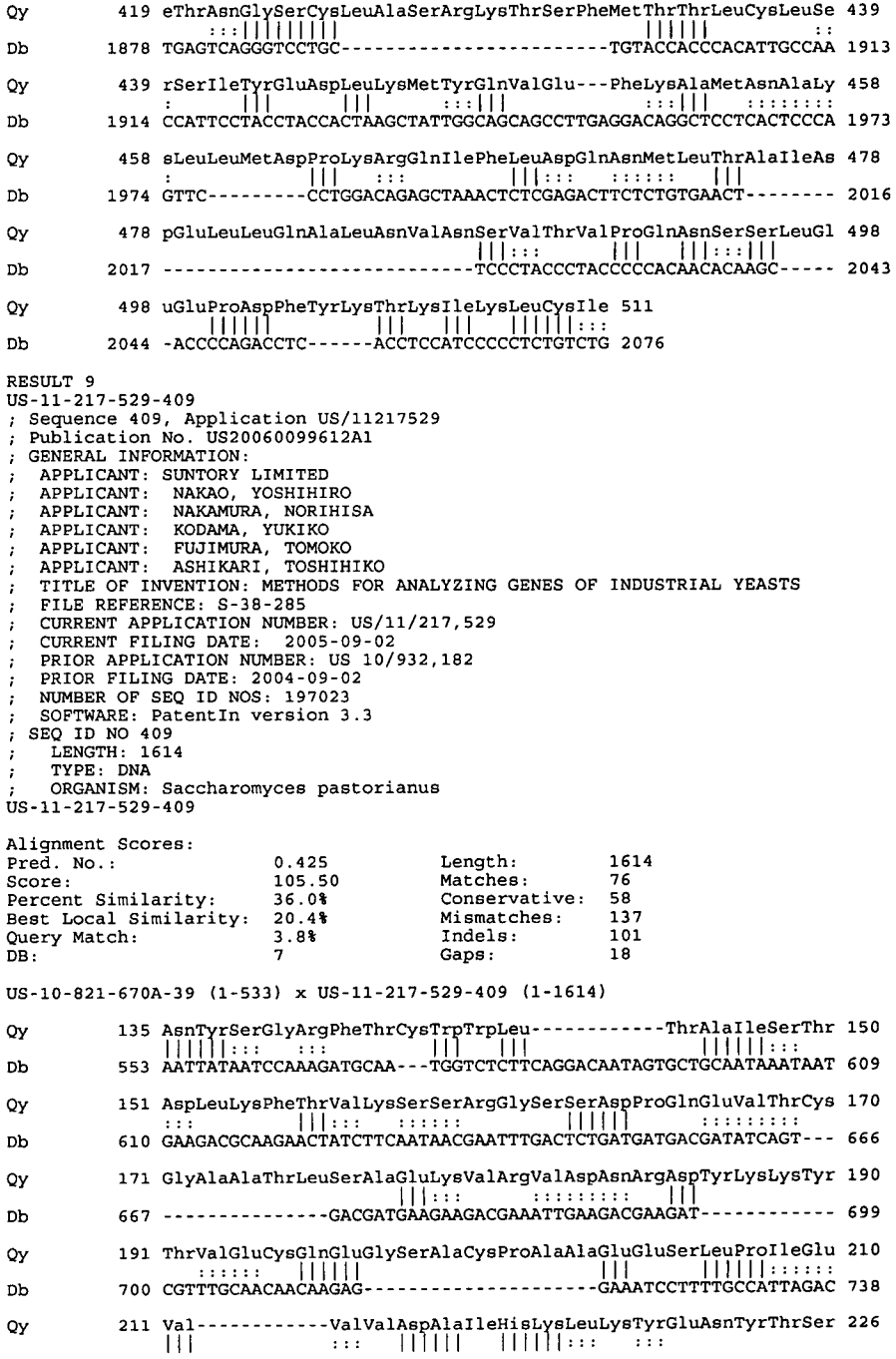

RESULT 9
US-11-217-529-409
; Sequence 409, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 409
; LENGTH: 1614
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-409

Alignment Scores:

Pred. No.:	0.425	Length:	1614
Score:	105.50	Matches:	76
Percent Similarity:	36.0%	Conservative:	58
Best Local Similarity:	20.4%	Mismatches:	137
Query Match:	3.8%	Indels:	101
DB:	7	Gaps:	18

US-10-821-670A-39 (1-533) x US-11-217-529-409 (1-1614)

```
Db        739 GTCACCTCAGTATCGATATTTGATGCCGATCATAAAATAAATCAT---------- 783

Qy        227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGlnLeuLysPro 246

Db        783 ---------------------------------------------------------- 783

Qy        247 LeuLysAsnSerArgHisValGluValSerTrpGluTyrProAsp---------- 261

Db        784 TTAAAGAGTGCTGGTCATGTATTTAATGAATACAGTTACGTTGATTCTAATACAGACGAC 843

Qy        262 ---ThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280

Db        844 ACAACCAACATCACACCCAAAAATACGTTAGAAGAACAGGAAAATGCAAACGCTGAGGAA 903

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAsp---------- 293

Db        904 GGGGGTGAGGAGGAAGATAACGATCTTCTCGACGAAGATGATTTATATGATATTTCTCTT 963

Qy        294 ---------LysThrSerAlaLysValValCysHisLysAsp---------- 304

Db        964 TTGAAGAACAAAAGGAAGCAAAGTTTTGTACTCAATAAGAATACCGTTGGTTTTGAAAGA 1023

Qy        305 --------------AlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSer 319

Db       1024 CTATCGTCTCCATCAACTCCGGTAAAGGTACCGTCTAACACTACTACTACTACTACTAAA 1083

Qy        320 TrpSerAsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeu 339

Db       1084 AGGAAATCTACAAAGTCGTTCAATAATAGTGGTGGCACTAACAGTAATAACGAAAACACC 1143

Qy        340 Pro---------------ThrProThrProSerProGlyMetPheGlnCysLeuAsnHis 354

Db       1144 CCGATGGAAAGAATAAAGAAACCGACTTCGTCC-----------------GTGTCAAAT 1185

Qy        355 SerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLys------AlaArgGlnThr 372

Db       1186 TCTAATAGTAGTAGGCGGAAACTAATTAACTATACCAAAAAACATCTATCATCACATCCT 1245

Qy        373 LeuGluPheTyrSer------------CysThrSerGluGluIleAspHisGluAspIle 388

Db       1246 ACACCATTCAGTTCGAGCCCAAGTCCTACAACCACATCATCTTCGGCACACGCGTCG--- 1302

Qy        389 ThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGlu 408

Db       1303 TCTTCGGACGGTAGCAACGAAATATTTGCGTGCCAAATCATGAATCTTACTAGTAATGAA 1362

Qy        409 SerCysLeuAla------SerArgGluIleSerLeuIleThrAsnGlySerCysLeu--- 425

Db       1363 CCATGTGGTGCACAATTTTCAAGATCATACGACTTGACAAGGCACCAAAATACCATACAT 1422

Qy        426 AlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeu 445

Db       1423 GCCAAGAGAAAGATTGTATTCCGTTGCTCTGAATGTATAAAAATTCTGGGATCAGAA--- 1479

Qy        446 LysMetTyrGlnValGluPheLysAlaMetAsnAla 457

Db       1480 ---GGTTATCAGAAGACATTTTCGAGATTAGACGCT 1512

RESULT 10
US-11-293-697-1946
; Sequence 1946, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1946
;   LENGTH: 2534
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1946

Alignment Scores:
Pred. No.:                0.839          Length:          2534
Score:                    105.50         Matches:         62
Percent Similarity:       35.6%          Conservative:    33
Best Local Similarity:    23.2%          Mismatches:      107
Query Match:              3.8%           Indels:          65
DB:                       7              Gaps:            13

US-10-821-670A-39 (1-533) x US-11-293-697-1946 (1-2534)

Qy         46 ValValLeuThrCysAsnThrProGlu---GluAspAspIleThrTrpThrSerAsp--- 63

Db        298 CTGGCCCTGCAGTGTGAAGTCTCTGACCCCGAGGCCCATGTGGTGTGGCGCAAAGATGGC 357

Qy         64 -----------------GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIle 77

Db        358 GTGCAGCTGGGCCCCAGTGACAAGTATGACTTCCTGCACACGGCGGGCACGCGGGGGCTC 417

Qy         78 GlnValLysGluPheAla------AspAlaGlyGlnTyrThrCysHisLysGlyGlyGlu 95

Db        418 GTGGTGCATGACGTGAGCCCTGAAGACGCCGGCCTGTACACCTGCCACGTGGGCTCCGAG 477

Qy         96 ValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAsp 115

Db        478 GAG---ACCCGGGCCCGGGTCCGCGTGCACGATCTGCACGTGGGCATC---------- 522

Qy        116 IleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsn 135

Db        523 ------------ACCAAGAGGCTGAAGACAATGGAGGTGCTGGAAGGGGAA--------- 561

Qy        136 TyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThr 155

Db        562 ---AGCTGCAGCTTTGAGTGC------------------------------------- 579

Qy        156 ValLysSerSerArgGlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeu 175

Db        580 GTCCTGTCCCACGAGAGTGCCAGCGACCCGGCCATGTGGACAGTCGGTGGGAAGACAGTG 639

Qy        176 SerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGln 195

Db        640 GGCAGCTCCAGCCGCTTCCAGGCCACACGTCAGGGCCGAAAATACATCCTGGTGGTCCGG 699

Qy        196 GluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValValValAspAla 215

Db        700 GAGGCTGCACCAAGTGATGCCGGGGAG--------------------GTGGTCTTCTCT 738

Qy        216 IleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLys 235

Db        739 GTGCGGGGCCTCACCTCCAAG---------GCCTCACTCATTGTCAGA------------ 777

Qy        236 ProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluVal 255

Db        778 ---GAGAGGCCGGCCACCATC---ATCAAGCCCCTGGAA--------------------- 810

Qy        256 SerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGly 275

Db        811 --------------GACCAGTGGGTGGCGCCAGGGGAGGACGTGGAGCTGCGCTGTGAG 855

Qy        276 ValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThr 295

Db        856 CTGTCACGGGCGGGAACGCCCGTGCACTGGCTGAAGGACAGGAAGGCCATCCGCAAGAGC 915

Qy        296 SerAla---LysValValCys 301

Db        916 CAGAAGTATGATGTGGTCTGC 936

RESULT 11
US-11-274-375-5
```

```
; Sequence 5, Application US/11274375
; Publication No. US20060106201A1
; GENERAL INFORMATION:
;  APPLICANT: Maeda, Masatsugu
;  APPLICANT:  Yaguchi, Noriko
;  TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
;  FILE REFERENCE: 06501-105US1
;  CURRENT APPLICATION NUMBER: US/11/274,375
;  CURRENT FILING DATE:  2005-11-14
;  PRIOR APPLICATION NUMBER: US/10/105,930
;  PRIOR FILING DATE: 2002-03-25
;  PRIOR APPLICATION NUMBER: PCT/JP00/06654
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: JP 2000-240397
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: JP 11-273358
;  PRIOR FILING DATE: 1999-09-27
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 2123
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (98)...(1984)
US-11-274-375-5

Alignment Scores:
Pred. No.:              0.804          Length:         2123
Score:                  104.50         Matches:        94
Percent Similarity:     33.1%          Conservative:   47
Best Local Similarity:  22.1%          Mismatches:     181
Query Match:            3.7%           Indels:         104
DB:                     7              Gaps:           18

US-10-821-670A-39 (1-533) x US-11-274-375-5 (1-2123)

Qy        131 CysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrp----------LeuThr 146
              |||             |||||||||     ||||||  |||           ||||||
Db        494 TGTGTCATTTATGAATATTCAGGCAACATGACTTGCACCTGGAATGCTGGGAGGCTCACC 553

Qy        147 AlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSerAspProGln 166
                  |||   |||                 |||||||||               :::   |||
Db        554 TACATAGACACAAAATACGTGGTACATGTGAAGAGTTTAGAGACAGAAGAAGAGCAACAG 613

Qy        167 GluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAsp 186
              :::|||                 :::|||   :::  :::             :::
Db        614 TATCTCACCTCAAGCTATATTAACATCTCCACTGATTCATTA-----------CAAGGT 661

Qy        187 TyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSer 206
                |||||||||   |||      |||      :::|||           |||||||||
Db        662 GGCAAGAAGTACTTGGTTTGGGTCCAAGCAGCAAACGCACTA---GGCATGGAAGAGTCA 718

Qy        207 LeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSer 226
                  :::::::::   :::|||   |||      |||               :::
Db        719 AAACAACTGCAAATTCACCTGGATGATATAGTGATACTTTCTGCAGCCGTCATTTCCAGG 778

Qy        227 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu---------- 242
              :::         :::   |||          ||||||   :::
Db        779 GCT-----------GAGACTATAAATGCTACAGTGCCCAAGACCATAATTTATTGGGAT 826

Qy        243 ---GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAsp 261
                  |||          |||   |||      :::
Db        827 AGTCAAACAACAATTGAAAAGGTTTCCTGTGAAATGAGATACAAGGCTACAACAAACCAA 886

Qy        262 ThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLys 281
              ||||||:::                |||          |||           |||   :::
Db        887 ACTTGGAATGTTAAAGAA------TTTGACACCAATTTTACATATGTGCAACAGTCAGAA 940

Qy        282 AsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCys 301
                        |||                                 |||         :::|||   |||
Db        941 TTCTACTTGGAGCCAAAC--------------ATTAAGTACGTATTTCAAGTGAGATGT 985

Qy        302 HisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSer 321
                  :::       |||                     ||||||            |||
Db        986 CAAGAAACAGGCAAA--------------------AGGTAC-----------TGGCAG 1012

Qy        322 AsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThr 341
                  |||:::|||:::                                          |||
Db       1013 CCTTGGAGTTCACTGTTTTTTCAT-----------------------------AAAACA 1042

Qy        342 ProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAla 361
              |||          |||                          |||         :::|||
Db       1043 CCTGAAACAGTTCCC-------------------------CAGGTCACATCAAAAGCA 1075

Qy        362 IleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGlu 381
                    :::             :::     |||:::         |||
Db       1076 TTCCAACATGACACATGGAATTCTGGGCTAACAGTTGCTTCCATCTCT----------- 1123

Qy        382 GluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuPro 401
                                  |||         ||||||              :::
Db       1124 --------------------ACAGGGCACCTTACTTCTGACAACAGAGGAGACATTGGA 1162

Qy        402 LeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsn 421
              |||   |||  |||           :::           :::|||||||||
Db       1163 CTTTTATTGGGAATGATCGTCTTTGCTGTTATGTTGTCAATTCTTTCTTTGATT------ 1216

Qy        422 GlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeu--------- 438
              |||:::       |||  :::|||          :::    |||
Db       1217 GGGACATTTAACAGATCATTCCGAACTGGGATTAAAAGAAGGATCTTATTGTTAATACCA 1276

Qy        439 SerSerIleTyrGluAspLeu--------------------------LysMetTyrGln 449
                  :::|||||||||:::                           ||||||   |||
Db       1277 AAGTGGCTTTATGAAGATATTCCTAATATGAAAAACAGCAATGTTGTGAAAATGCTACAG 1336

Qy        450 ValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeu 469
                        :::   ||||||          :::         |||:::
Db       1337 GAAAATAGTGAACTTATGAAT-----------AATAATTCCAGTGAGCAGGTCCTATAT 1384

Qy        470 AspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerVal 489
                    |||:::|||   |||   |||:::
Db       1385 GTTGATCCCATGATTACAGAGATAAAAGAAATCTTC---------------------- 1420

Qy        490 ThrValProGlnAsn----------------------------SerSerLeuGluGlu 499
                  :::|||::::::                                  ||||||
Db       1421 ---ATCCCAGAACACAAGCCTACAGACTACAAGAAGGAGAATACAGGACCCCTGGAGACA 1477

Qy        500 ProAspPhe-TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleAr 519
              |||:::    |||||:::          :::   |||:::   |||   |||
Db       1478 AGAGACTACCCGCAAAACTCGCTATTCGACAATACTACAGTTGTATATATTCCTGATCTC 1537

Qy        519 gAlaValThrIleAsn 524
                :::   ||||||
Db       1538 AACACTGGATATAAAC 1553

RESULT 12
US-11-217-529-774
; Sequence 774, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 774
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;   LENGTH: 3117
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-774

Alignment Scores:
Pred. No.:                1.61          Length:          3117
Score:                    104.00        Matches:         110
Percent Similarity:       33.1%         Conservative:    68
Best Local Similarity:    20.4%         Mismatches:      167
Query Match:              3.7%          Indels:          193
DB:                       7             Gaps:            25

US-10-821-670A-39 (1-533) x US-11-217-529-774 (1-3117)

Qy         53 ProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGly 72
Db        778 CCTGTTGAAGCGGAAATG---TGGACACCTGAAGAAATAACAGCATAT------------ 822

Qy         73 LysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLys 92
Db        823 ------TTTATCATGGAAGGATATGATGTCCAATCCGCCTCTAGGTTTCAAAAACATAAG 876

Qy         93 ---GlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIle 111
Db        877 ATATCAGGTAGAATTTTATTA---GAACTAGAACTAGTCCATTTAAAAGAGCTAGATATA 933

Qy        112 TrpSer------------ThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIle 127
Db        934 AATTCCTTTGGTACAAGATTTGAGATTTTCAAAGAAATTGAAAAAATCAAAGAGGCAATT 993

Qy        128 ------------------PheLeuLysCysGluAlaLysAsn------------------ 135
Db        994 AGGACAAATGGTCACTCATTTAACAGAGTTAGCAAGGCTAATAATAACACTAACAGTTAC 1053

Qy        136 ----------------------------------------TyrSerGly------Arg 139
Db       1054 AACCAATTGATGCCTCCTGCGAACGTCGACCAGAGGGTATCCTACAGGGGCCATGTCAGA 1113

Qy        140 PheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrVal--------- 156
Db       1114 AAAACTTCACAGTCGTTAGATGACCTTCCATCACAACAGAATTTTACTGCTACCCCTCAA 1173

Qy        157 ---------LysSerSerArgGlySerSerAspProGlnGluValThrCysGlyAlaAla 173
Db       1174 GGTAACAGAAATTCTTCAACAGGTAAACATAGACCG---------------------- 1209

Qy        174 ThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrValGlu 193
Db       1210 ----------------------------------------AAATCTTTAACTCTTGAT 1227

Qy        194 CysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValValVal 213
Db       1228 ACTCAAGAAGGCGATTCC------AGTGCTACTCCAAAAATTCAGATTCCTCAAGTTGTA 1281

Qy        214 AspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIle------Arg 231
Db       1282 GAAGAAATTGCTAGTAATGAATAT-----------------TTGTTTGTTTCCCCAAGA 1323

Qy        232 AspIleIleLysPro--------------------AspProProLysAsnLeuGlnLeu 244
Db       1324 AGGGCACCCAAACCTCCATCTTATCCAAGCCCTGCACAACCTCCCAAGTCA--------- 1374

Qy        245 LysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThrTrpSer 264
Db       1375 ---CCCCTCCTAAGTAATAGAAAGGCCTCACCGTCTCCCACCCAATTACATTCATGGCAA 1431

Qy        265 ThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsnAsnArg 284
Db       1432 TCACCAAGTTCATCTTACTCG---------------------------------------- 1452

Qy        285 GluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHisLysAsp 304
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Db       1453 GACTCAAAAAAAAATTTGTATACCGACCAATCTTCATCGAAT----------------- 1494

Qy        305 AlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAla 324
Db       1495 ----------------------------------TCTAATTCAAATTCCCGTTTTGCA 1518

Qy        325 SerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrProThrPro 344
Db       1519 CTTTCAAAAAACAACCAAGGGAACGGGAGGCCATTGTCTCCTATTCCTCCCCCCACT--- 1575

Qy        345 SerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsn 364
Db       1576 ----------------------------------------CTTAAAGCAATTTCAAAT 1593

Qy        365 ThrLeuGlnLysAlaArgGlnThr---------------------------------- 372
Db       1594 TCTGCAGACAAAACGAAAGACACAAATACAGTATCTGCAAATAGAAATTCCGTTCTTTAT 1653

Qy        373 ----------------------------LeuGluPheTyrSerCysThrSerGluGlu 382
Db       1654 TCAGGATATGCTGTTGACTCTTTCAACAGAAAATCTTCTTATTCCAGTGGTGAGGAAGAG 1713

Qy        383 IleAspHisGlu------AspIleThrLysAspLysThrSerThrValGluAla------ 398
Db       1714 CACTTCCAAGAAACGTTGGATACACTCGAAAGACCCACATCCAGCATATACGCCGATGGG 1773

Qy        399 ------------------------CysLeuProLeuGlu---------------------- 403
Db       1774 TCTACAATCGCATCAATGAGTAATGCTAGGCCAATACAAGACAATGAAAAGAAGAAAAAA 1833

Qy        404 LeuThrMetAsnGluSerCysLeuAlaSer----------------------ArgGluIle 416
Db       1834 CCGACGAGACATTCTTCCTTGTTATCTTCAAAATCCAAAGGTGATCCCAAAAGGAACTCT 1893

Qy        417 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 436
Db       1894 TCTTTAAAGAGAAGCAGTAGC------GCATCAAGAACCAGTTCATTCAGAAAAAGCACT 1947

Qy        437 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 456
Db       1948 TTTATG-----------------CTAAGTCCCTTTAGACAACAGTTCACTGAAAATGCG 1989

Qy        457 AlaLysLeuLeuMetAspPro-LysArgGlnIlePheLeuAspGlnAsnMetLeuThrAl 476
Db       1990 GCTCGTTCTTCACCAAGTCCTGAAAAAAATTCTATGGCTTCAACGCCACTATCCCCAACC 2049

Qy        476 aIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGln 493
Db       2050 GATAACAAATCTTCCAAGGACAAATCAAAAGCAAGATCTGTCAGCGCCAAAG 2101

RESULT 13
US-10-511-937-448
; Sequence 448, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
;  APPLICANT: EXPRESSION DIAGNOSTICS, INC.
;  APPLICANT:  Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  APPLICANT:  Prentice, James
;  APPLICANT:  Morris, MacDonald
;  APPLICANT:  Rosenberg, Steven
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
;  TITLE OF INVENTION:  AND MONITORING TRANSPLANT REJECTION
;  FILE REFERENCE: 506612000104
;  CURRENT APPLICATION NUMBER: US/10/511,937
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: PCT/US2003/012946
;  PRIOR FILING DATE: 2003-04-24
;  PRIOR APPLICATION NUMBER: US 10/131,831
;  PRIOR FILING DATE: 2002-04-24
;  PRIOR APPLICATION NUMBER: US 10/325,899
```

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;  PRIOR FILING DATE: 2002-12-20
;  NUMBER OF SEQ ID NOS: 3117
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 448
;   LENGTH: 3084
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-511-937-448

Alignment Scores:
Pred. No.:              1.77          Length:          3084
Score:                  103.50        Matches:         94
Percent Similarity:     31.2%         Conservative:    47
Best Local Similarity:  20.8%         Mismatches:      137
Query Match:            3.7%          Indels:          174
DB:                     6             Gaps:            24

US-10-821-670A-39 (1-533) x US-10-511-937-448 (1-3084)

Qy         38 HisProAspAla-ProGlyGluMetValValLeuThrCysAsnThrPro------GluGl 55
Db        542 CACCCACCTGCTTCAGGGGCAGAGCCTGACCCTGACCTTGGAGAGCCCCCCTGGTAGTAG 601

Qy         55 uAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLe 75
Db        602 CCCCTCAGTGCAATGTAGGAGTCCAAGGGGTAAAAACATACAGGGG---GGGAAGACCCT 658

Qy         75 uThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCys-------------- 90
Db        659 CTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGCACCTGGACATGCACTGTCTTGCAGAA 718

Qy         91 -HisLysGlyGlyGlu------------------------ValLeuSerHisSerPheLe 102
Db        719 CCAGAAGAAGGTGGAGTTCAAAATAGACATCGTGGTGCTAGCTTTCCAGAAGGCCTCCAG 778

Qy        102 uLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGl 122
Db        779 CATAGTCTATAAGAAAGAGGGG--------------------------GAACAGGTGGA 811

Qy        122 uSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCy 142
Db        812 GTTCTCCTTCCCACTCGCCTTTACAGTTGAAAAGCTGACGGGCAGTGGCGAGCTG----- 866

Qy        142 sTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySe 162
Db        867 -TGGTGG---------------------------------CAGGCGGAGAGGGCTTC 889

Qy        162 rSerAspProGlnGluValThrCysGlyAlaAlaThr------LeuSerAlaGluLysVa 180
Db        890 CTCCTCCAAGTCTTGGATCACCTTTGACCTGAAGAACAAGGAAGTGTCTGTAAAACGGGT 949

Qy        180 lArgValAspAsnArgAspTyr------LysLysTyrThrValGluCysGlnGluGlySe 198
Db        950 TACCCAGGACCCTAAGCTCCAGATGGGCAAGAAGCTCCCGCTCCACCTCACCCTGCCCCA 1009

Qy        198 rAlaCysPro------------AlaAlaGluGluSerLeuProIleGluValValValAs 214
Db       1010 GGCCTTGCCTCAGTATGCTGGCTCTGGAAACCTCACCCTGGCCCTTGAAGCGAAAACAGG 1069

Qy        214 pAlaIleHisLys----------------------------LeuLysTyrGluAsnTy 224
Db       1070 AAAGTTGCATCAGGAAGTGAACCTGGTGGTGATGAGAGCCACTCAGCTCCAGAAAAATTT 1129

Qy        224 rThrSerSerPhePheIleArgAspIleIleLysProAspProProLys---------- 240
Db       1130 GACCTGT--------------GAGGTGTGGGGACCCACCTCCCCTAAGCTGATGCTGAG 1174

Qy        241 ----AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrp----- 257
Db       1175 CTTGAAACTGGAGAACAAGGAGGCAAAGGTCTCGAAGCGGGAGAAGGCGGTGTGGGTGCT 1234

Qy        257 ------------------------------------------------------------ 257

Db       1235 GAACCCTGAGGCGGGGATGTGGCAGTGTCTGCTGAGTGACTCGGGACAGGTCCTGCTGGA 1294

Qy        258 ----------GluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeuThrPh 274
Db       1295 ATCCAACATCAAGGTTCTGCCCACATGGTCCACCCCGGTGCAGCCAATGGCCCTGATTGT 1354

Qy        274 e------GlyValGln-------------------------------------ValGl 279
Db       1355 GCTGGGGGGCGTCGCCGGCCTCCTGCTTTTCATTGGGCTAGGCATCTTCTTCTGTGTCAG 1414

Qy        279 nGlyLysAsnAsnArgGluLysLysAspArgLeuSerValAspLys------ThrSerAl 297
Db       1415 GTGCCGGCACCGAAGGCGCCAAGCAGAGCGGATGTCTCAGATCAAGAGACTCCTCAGTGA 1474

Qy        297 aLysValValCysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSe 317
Db       1475 GAAGAAGACCTGC----------------------CAGTGCCCTCACCGGTTTCAGAA 1510

Qy        317 rSerSerTrpSerAsnTrpAlaSerValSerCysSer---------GlyGlyGlyGlyGl 334
Db       1511 G--------------------------ACATGTAGCCCCATTTGAGGCACGAGGCCAGG 1543

Qy        334 yGlySerArg------------------------------------------------- 337
Db       1544 CAGATCCCACTTGCAGCCTCCCCAGGTGTCTGCCCCGCGTTTCCTGCCTGCGGACCAGAT 1603

Qy        338 -AsnLeuProThrProThrPro------------------------------------- 344
Db       1604 GAATGTAGCAGATCCCAGGCCTCTGGCCTCCTGTTCGCCTCCTCTACAATTTGCCATTGT 1663

Qy        345 -SerProGlyMet-----------------------------------PheGlnCysLe 352
Db       1664 TTCTCCTGGGTTAGGCCCCGGCTTCACTGGTTGAGTGTTGCTCTCTAGTTTCCAGAGGCT 1723

Qy        352 uAsnHisSerGlnThrLeuLeuArgAlaIleSer 363
Db       1724 TAATCAC------ACCGTCCTCCACGCCATTTCC 1751

RESULT 14
US-11-217-529-191047
; Sequence 191047, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 191047
;   LENGTH: 3510
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-191047

Alignment Scores:
Pred. No.:              2.4           Length:          3510
Score:                  103.00        Matches:         105
Percent Similarity:     32.7%         Conservative:    69
Best Local Similarity:  19.7%         Mismatches:      214
Query Match:            3.7%          Indels:          144
DB:                     7             Gaps:            20

US-10-821-670A-39 (1-533) x US-11-217-529-191047 (1-3510)
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Qy        31 TyrValValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCys 50
Db       976 TATGTCACTAGCTCTTCCTGG-----------TCGTCCAGTGAAGTCTGTACAGAGTGC 1023

Qy        51 AsnThrProGluGluAspAsp--------------IleThrTrpThrSerAspGlnSer 65
Db      1024 ACCGAGACCGAGTCTACTAGCACCTCTACTCCATATGTCACCAGCTCTTCCTCGTCGTCC 1083

Qy        66 SerGluVal-----------------LeuGlySerGlyLysThrLeuThrIleGlnVal 79
Db      1084 AGTGAAGTCTGTACGGAGTGCACCGAAACTGAGTCTACCAGTTATGTGACACCATATGTC 1143

Qy        80 LysGluPheAlaAspAlaGlyGlnTyrThr-------------------------Cys 90
Db      1144 AGCTCGTCTACTGCTGCCGCAAACTACACTAGCTCATTCTCATCGTCCAGTGAAGTCTGT 1203

Qy        91 HisLysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGly 110
Db      1204 ACAGAGTGCACCGAAACTGAGTCTACTAGCACCTCTACTCCATATGTCACTAGCTCTTCC 1263

Qy       111 IleTrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeu--- 129
Db      1264 TGGTCGTCCAGTGAAGTCTGTACAGAGTGCACCGAGACCGAGTCTACCAGTTATGTGACA 1323

Qy       130 --------------LysCysGluAlaLysAsnTyrSerGlyArgPheThr--------- 141
Db      1324 CCATATGTCAGCTCGTCTACTGCTGCCGCAAACTACACTAGCTCATTCTCATCGTCCAGT 1383

Qy       142 --------------CysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrVal 156
Db      1384 GAAGTCTGTACAGAGTGCACCGAAACTGAGTCTACTAGCACCTCTACTCCATATGTCACT 1443

Qy       157 LysSerSerArgGlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSer 176
Db      1444 AGCTCTTCCTCGTCGTCCAGTGAA----------------------------GTCTGT 1473

Qy       177 AlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGlu 196
Db      1474 ACAGAGTGCACCGAGACCGAGTCTACCAGTTATGTGACACCATATGTCAGCTCGTCTACT 1533

Qy       197 GlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIle 216
Db      1534 GCTGCCGCA---------------------------------------------------- 1542

Qy       217 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 236
Db      1543 ------------------AACTACACTAGCTCTTTC----------------------- 1560

Qy       237 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSer 256
Db      1561 ------------------------------------TCATCGTCCAGTGAAGTCTGT 1581

Qy       257 TrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyVal 276
Db      1582 ACAGAGTGCACCGAAACCGAGTCTACTAGCACCTCTACTCCATATGTCACC--------- 1632

Qy       277 GlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSer 296
Db      1633 ---------------AGCTCTTCCTGGTCGTCCAGTGAAGTCTGTACAGAGTGCACCGAG 1677

Qy       297 AlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyr 316
Db      1678 ACCGAGTCTACCAGTTATGTGACACCATATGTCAGCTCGTCTACTGCTGCCGCAAACTAC 1737

Qy       317 SerSerSerTrpSerAsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlySer 336
Db      1738 ACTAGCTCATTCTCATCGTCCAGTGAAGTC---TGTACAGAGTGCACCGAAACCGAGTCT 1794

Qy       337 ArgAsnLeuProThrPro------ThrProSerProGlyMetPheGlnCysLeuAsnHis 354
Db      1795 ACAAGCACATCCACTCCATATGCAACCTCATCTACTGGCACA----------------- 1836

Qy       355 SerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln------Thr 372

Db      1837 GCTACTTCATTTACCGCTTCAACTTCCAATACCATGACGTCTTTGGTCCAAACAGACACA 1896

Qy       373 LeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLys 392
Db      1897 ACCGTTTCTTTCAGCCTATCTTCAACTGTAAGCGAGCAT---------ACCAACGCTCCA 1947

Qy       393 ThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAla 412
Db      1948 ACTTCATCTGTAGAGTCAAATGCTAGTACTTTCATATCGTCAAATAAAGGCAGCGTTAAA 2007

Qy       413 SerArgGluIleSer-------------------------------------LeuIle 419
Db      2008 AGTTATGTTACGTCATCCATACATAGCATTACGCCCATGTATCCTAGTAACCAAACCGTA 2067

Qy       420 ThrAsnGlySerCysLeuAla-----------------SerArgLysThrSerPheMet 433
Db      2068 ACATCTAGCTCTGTTGTCTCCACACCAATTACTTCCGAATCTTCTGAATCCTCGGCCTCA 2127

Qy       434 ThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLys 453
Db      2128 GTTACCATTCTACCCTCAACTATCACTTCTGAATTCAAACCATCTACAATGAAAACGAAG 2187

Qy       454 AlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMet 473
Db      2188 GTCGTTAGT------ATCTCCTCATCACCA--------------------ACTAATTTG 2220

Qy       474 LeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThr------Val 491
Db      2221 ATTACCAGCTATGACACTACATCTAAGGATTCAACTGTTGGTTCATCCACATCGTCTGTA 2280

Qy       492 ProGlnAsnSerSerLeuGluGluProAspPheTyr 503
Db      2281 AGCCTGATCTCTAGTATTTCTCTACCAAGTAGTTAT 2316
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RESULT 15
US-11-145-307A-22
; Sequence 22, Application US/11145307A
; Publication No. US20060094035A1
; GENERAL INFORMATION:
; APPLICANT: Arcturus Bioscience, Inc.
; APPLICANT: Erlander, Mark G.
; APPLICANT: Ma, Xiao-Jun
; TITLE OF INVENTION: Identification of Tumors
; FILE REFERENCE: 022041-002020US
; CURRENT APPLICATION NUMBER: US/11/145,307A
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 60/577,084
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 2832
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-145-307A-22

Alignment Scores:

Pred. No.:	1.95	Length:	2832
Score:	102.50	Matches:	91
Percent Similarity:	36.3%	Conservative:	87
Best Local Similarity:	18.5%	Mismatches:	151
Query Match:	3.7%	Indels:	164
DB:	7	Gaps:	22

US-10-821-670A-39 (1-533) x US-11-145-307A-22 (1-2832)

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Qy        82 PheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeu------------ 97
Db       186 TTCAGTGGAATGGGCAGAAGGAGGTGCCACAAAGGGCA-AAGAGATTGATTTTGATGATG 244

Qy        98 --------------------SerHisSerPheLeuLeuIleHisLysLysGluAspGly 110
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Db        245 TGGCTGCAATAAACCCAGAACTCTTACAGCTTCTTCCC-TTACATCCGAAG---GACAAT 300

Qy        111 IleTrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLys 130

Db        301 CTGCCCTTGCAGGAAAATGTAACAATCCAGAAACAAAAACGGAGATCCGTCAACTCCAAA 360

Qy        131 CysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThr 150

Db        361 ATTCCTGCTCCAAAAGAAAGTCTTCGAAGCCGCTCCACTCGCATGTCCACTGTCTCA--- 417

Qy        151 AspLeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGluValThrCys 170

Db        418 GAGCTTCGCATCACGGCTCAG--------------GAGAATGACATGGAGGTGGAGCTG 462

Qy        171 GlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyr 190

Db        463 CCTGCAGCTGCAAACTCCCGCAAGCAGTTTTCAGTTCCTCCTGCCCCCACTAGG------ 516

Qy        191 ThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGlu 210

Db        517 --------------------CCTTCCTGCCCTGCAGTGGCTGAA---ATACCATTGAGG 552

Qy        211 ValValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIle 230

Db        553 ATGGTCAGCGAGGAGATGGAAGAGCAAGTCCATTCC--------------------ATC 591

Qy        231 ArgAspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSer 250

Db        592 CGAGGCAGCTCTTCTGCAAACCCTGTGAACTCAGTTCGGAGGAAATCATGTCTT---GTG 648

Qy        251 ArgHisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPhe 270

Db        649 AAGGAAGTGGAA---------------------------------------------- 660

Qy        271 SerLeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeu 290

Db        661 ----------------------AAAATGAAGAACAAGCGAGAAGAGAAGAAGGCC--- 693

Qy        291 SerValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGln 310

Db        694 ----------------------------------CAGAACTCTGAAATGAGAATGAAG 717

Qy        311 AlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrp-------------------- 323

Db        718 ---AGAGCTCAGGAGTATGACAGTAGTTTTCCAAACTGGGAATTTGCCCGAATGATTAAA 774

Qy        324 ---------AlaSerValSerCysSerGlyGlyGlyGlyGlySerArgAsnLeuPro 340

Db        775 GAATTTCGGGCTACTTTGGAATGTCAT-----------------CCACTTACTATGACT 816

Qy        341 ThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArg 360

Db        817 GATCCTATCGAAGAGCACAGAATATGTGTCTGTGTTAGG-----------------AAA 858

Qy        361 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 380

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Qy        381 Glu------GluIleAspHisGlu--------------AspIleThrLys--------- 390

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Qy        391 ------------------------------AspLysThrSerThrValGlu--------- 397

Db        979 AACCAAGCATTCTGCTTTGACTTTGCATTTGATGAAACAGCTTCGAATGAAGTTGTCTAC 1038

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Qy        409 ------------------------------------------------------------ 409

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Qy        410 --------------------------CysLeuAlaSerArgGluIleSerLeuIleThr 420

Db       1159 GCCCAGAATGCATCCAAAGGGATCTATGCCATGGCCTCCCGGGACGTCTTCCTCCTGAAG 1218

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Db       1219 AATCAACCCTGCTAC------CGGAAGTTGGGCCTGGAAGTCTATGTGACATTCTTCGAG 1272

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Qy        461 MetAspProLysArgGln---------IlePheLeuAspGlnAsnMetLeuThrAlaIle 477

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Search completed: June 10, 2006, 01:22:03
Job time : 52.7307 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 10, 2006, 03:13:25 ; Search time 6314.34 Seconds
(without alignments)
15525.205 Million cell updates/sec

Title: US-10-821-670A-43
Perfect score: 1533
Sequence: 1 atatgggaactggagaaaaa.....tgagctatctgaatgcttcc 1533

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
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10: gb_vi:*
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12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1533	100.0	1599	2	AR595956	AR595956 Sequence
c 4	1533	100.0	1599	2	AR595957	AR595957 Sequence
5	1373	89.6	1533	2	AR595973	AR595973 Sequence
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13	921	60.1	921	2	AR595948	AR595948 Sequence
c 14	921	60.1	921	2	AR595949	AR595949 Sequence
15	921	60.1	1006	14	FCIL12P40	Y07762 Felis catus
16	919.4	60.0	921	2	AR242436	AR242436 Sequence
17	919.4	60.0	921	2	AR280204	AR280204 Sequence
18	919.4	60.0	921	2	AR322419	AR322419 Sequence
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ALIGNMENTS

RESULT 1
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DEFINITION Sequence 43 from patent US 6818444.
ACCESSION AR595959
VERSION AR595959.1 GI:56646940
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1533)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 43 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .1533
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 100.0%; Score 1533; DB 2; Length 1533;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Qy       241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Db       241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy       301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy       361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy       421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Db       421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy       481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Db       481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

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Db       541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy       601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Db       601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy       661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
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Qy       721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
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Db       721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy       781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy       841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy       901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy       961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020

Qy      1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080

Qy      1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy      1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200

Qy      1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260

Qy      1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320

Qy      1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380

Qy      1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
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Db      1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440

Qy      1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500

Qy      1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
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Db      1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
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RESULT 2
AR595960/c
LOCUS AR595960 1533 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 45 from patent US 6818444.
ACCESSION AR595960
VERSION AR595960.1 GI:56646941
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1533)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 45 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .1533
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 100.0%; Score 1533; DB 2; Length 1533;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy        61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy       121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy       181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Db      1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy       241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy       301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy       361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy       421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054
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Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
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Db        633 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        961 ACTCCATCCCCGGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 ACTCCATCCCCGGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
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Db        333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
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RESULT 3
AR595956
LOCUS       AR595956                1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 38 from patent US 6818444.
ACCESSION   AR595956
VERSION     AR595956.1  GI:56646937
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 38 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
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ORIGIN

  Query Match             100.0%;  Score 1533;  DB 2;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1533;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
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Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
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Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
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Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
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Db        967 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026

Qy        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
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Db       1027 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1086

Qy       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
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Db       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1146

Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
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Db       1147 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
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Db       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1266

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1267 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1326

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
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Db       1327 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1386

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
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Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
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Db       1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1506

Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1566

Qy       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
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RESULT 4
AR595957/c
LOCUS       AR595957               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 40 from patent US 6818444.
ACCESSION   AR595957
VERSION     AR595957.1  GI:56646938
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 40 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
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ORIGIN

  Query Match             100.0%;  Score 1533;  DB 2;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1533;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
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Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
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Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574
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Qy        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
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Db        573 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
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Db        333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
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Db        213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
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Db        153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
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Db         33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
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RESULT 5
AR595973
LOCUS AR595973 1533 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 66 from patent US 6818444.
ACCESSION AR595973
VERSION AR595973.1 GI:56646954
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1533)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 66 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .1533
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 89.6%; Score 1373; DB 2; Length 1533;
Best Local Similarity 93.5%; Pred. No. 0;
Matches 1433; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

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Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              |||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              | |||||||||||||||||||| |||||||||||| |||||||||||  ||  ||||
Db        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              |||| |||||||| ||||||||||||||||||||||||||||||||| ||||||||||||
Db        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||  |||
Db        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              |||||||||||||||||||| |||||||||||| ||||||||| |||||||||| |
Db        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| |||||| |||||||||| |||||| |||||||||| ||||||||||
Db        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              || |||||||||| |||||||||||||| ||||| || |||||||||||||| ||||||
Db        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              |||||||||||||||||||||||| | |||||| || |||||| ||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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Db        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
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Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
              |||||||| ||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
              |||||||||||||| |||||||| ||  | ||||||||||||||| || || ||||| ||
Db        961 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 1020

Qy       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
              |||||||||||||||||||||||||||||||||||| || ||||||||||||||||||||
Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 1080

Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db       1081 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1200
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Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
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Db       1201 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1260

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
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Db       1261 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1320

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
             || || ||||||||||||||||||||||||||||||||||||| ||||||||||||||||
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Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
             ||||||||| |||||||||||||||||||||||| |||||| | ||||| |||||||||
Db       1381 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1440

Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
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Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1500

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Db       1501 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1533


RESULT 6
AR595974/c
LOCUS       AR595974               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 68 from patent US 6818444.
ACCESSION   AR595974
VERSION     AR595974.1  GI:56646955
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 68 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             89.6%;  Score 1373;  DB 2;  Length 1533;
  Best Local Similarity   93.5%;  Pred. No. 0;
  Matches 1433;  Conservative    0;  Mismatches  100;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              |||||||||||||||| | ||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
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Db       1473 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              |  |||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1413 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Db       1353 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
               |||| |||||||| |||||||||||||||||||||||||||||| ||||||||||||
Db       1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
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Db       1233 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db       1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Db       1113 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              || |||||||||| |||||||||||||| ||||| || |||||||||||||| ||||||
Db        873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              |||||||||||||||||||||||||| | |||||| || |||||| ||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || |||||||||||||| ||||||| ||||||||||||||||||||||||||||||||
Db        753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

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Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 634

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Db        633 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
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Db        573 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 514

Qy       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 454

Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         453 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||| |||
Db         393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 334

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
              |||||||||||||||  ||||| ||||||||||||||  ||||||||||||||| ||||||
Db         333 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 274

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
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Db         273 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 214

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
              || || ||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db         213 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 154

Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
              ||||||||| |||||||||||||||||||||||| |||||| | ||||| |||||||||
Db         153 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 94
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Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
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Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 34

Qy       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
             |||||||||||||||  |||  ||||  |||||
Db         33 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1


RESULT 7
AR595971
LOCUS       AR595971                1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 61 from patent US 6818444.
ACCESSION   AR595971
VERSION     AR595971.1  GI:56646952
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 61 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
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ORIGIN

  Query Match             89.6%;  Score 1373;  DB 2;  Length 1599;
  Best Local Similarity   93.5%;  Pred. No. 0;
  Matches 1433;  Conservative    0;  Mismatches  100;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              |||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
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Db        127 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
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Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
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Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
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Db        787 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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Db        847 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
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Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
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Db        967 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026

Qy        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
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Qy       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
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Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
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Db       1147 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
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Db       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1266

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
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Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
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Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
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Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
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Db       1447 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1506

Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
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Db       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1566

Qy       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
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RESULT 8
AR595972/c
LOCUS       AR595972                1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 63 from patent US 6818444.
ACCESSION   AR595972
VERSION     AR595972.1  GI:56646953
KEYWORDS    .
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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 63 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
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ORIGIN

  Query Match             89.6%;  Score 1373;  DB 2;  Length 1599;
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Db       1533 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

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Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Db       1413 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Db       1353 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
               |||| |||||||| ||||||||||||||||||||||||||||||| ||||||||||||
Db       1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
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Db       1233 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
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Db       1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
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Db        873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
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Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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Qy       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
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Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 454

Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
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Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
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Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 334

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
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Db        333 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 274

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
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Db        273 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 214

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
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Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
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Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
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RESULT 9
AF401989
LOCUS       AF401989               1626 bp    mRNA    linear   SYN 14-FEB-2002
DEFINITION  Synthetic construct single chain interleukin-12 mRNA, complete cds.
ACCESSION   AF401989
VERSION     AF401989.1  GI:18656516
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 1626)
  AUTHORS   McMonagle,E.L.J., Taylor,S., van Zuilekom,H., Sanders,L.,
            Scholtes,N., Keanie,L.J., Hopkins,C.A., Logan,N.A., Bain,D.,
            Argyle,D.J., Onions,D.E., Schijns,V.E. and Nicolson,L.
  TITLE     Production of biologically active equine interleukin 12 through
            expression of p35, p40 and single chain IL-12 in mammalian and
            baculovirus expression systems
  JOURNAL   Equine Vet. J. 33 (7), 693-698 (2001)
   PUBMED   11770992
REFERENCE   2  (bases 1 to 1626)
  AUTHORS   McMonagle,L.J., Taylor,S., Keanie,L.J., Hopkins,C.A., Logan,N.A.,
            Argyle,D.J., Onions,D.E. and Nicolson,L.
  TITLE     Direct Submission
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  JOURNAL   Submitted (24-JUL-2001) Veterinary Pathology, Glasgow Veterinary
            School, Bearsden Rd, Glasgow G61 1QH, UK
FEATURES             Location/Qualifiers
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ORIGIN

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Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACCCCTGAAGAAGAAGGCATCACCTGGACCTCG 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Db        247 GGAGATGCTGGCTGGTACACCTGTCACAAAGGAGGCGAGGTTCTGAGCCATTCTCACCTG 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Qy        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
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Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Db        607 GCCGAGGAGAGCCTGCCCATTGAGATCGTGGTGGATGCTGTTCACAAGCTCAAGTATGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
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Db        907 AAGGATGGCCAGATCCGTGTCCAAGCCAGGGACCGCTACTACAGCTCATCCTGGAGCGAA 966

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGG----------------------CGGTGGCGGC 936
              |||||||||| |||||||||||||                      ||||||||||
Db        967 TGGGCATCCGTATCCTGCAGTGGTGGCGGTGGCTCGGGCGGTGGTGGATCCGGTGGCGGC 1026

Qy        937 GGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCAC 996
              |||||||| ||| | || ||  | || |||  ||| || ||||||||||||||||||||
Db       1027 GGATCTAGGAACCTCCCCACAGCCACACCAGGCCCAGGAATGTTCCAGTGCCTCAACCAC 1086

Qy        997 TCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAA 1056
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Db       1087 TCCCAAAACCTGCTGAGGACCGTCAGCAACACGCTTCAGAAGGCCAGGCAAACCCTAGAA 1146

Qy       1057 TTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGC 1116
              || |||||||||||||| |||||||| |||||||||||||||| || | ||||
Db       1147 TTCTACTCCTGCACTTCTGAAGAGATCGATCATGAGGATATCACAAAAGACAAGAGCAGC 1206

Qy       1117 ACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGA 1176
              || |||| ||||||| | || |||||| |  ||  ||| |||||||||||||||||||||
Db       1207 ACCGTGGCGGCCTGCCTCCCCCTGGAACTCGCCCCGAACGAGAGTTGCCTGGCTTCCAGA 1266

Qy       1177 GAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACG 1236
              ||||||||| | |||||||||||||||||||| || || ||||| |||||| ||||| |
Db       1267 GAGATCTCTTTCATAACTAATGGGAGTTGCCTGACCCCCGGAAAGGCCTCTTCTATGATG 1326

Qy       1237 ACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCC 1296
              || |||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db       1327 ACGCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCC 1386

Qy       1297 ATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 1356
              |||||||| |||||||| || |||||| | |||||||||||||||||| | |||||||||
Db       1387 ATGAATGCCAAGCTGTTGATAGATCCTCAGAGGCAGATCTTTCTGGATGAGAACATGCTG 1446

Qy       1357 ACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAAC 1416
              ||||| |||||  ||||| | |||||||||| |||||||| |||||||||||| ||
Db       1447 ACAGCCATTGACAAGCTGATGCAGGCCCTGAACTTCAACAGTGAGACTGTGCCACAAAAG 1506

Qy       1417 TCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1476
              ||||| | |||| || |||||||||||||||||| |||||||||||| |||||||||
Db       1507 CCCTCCCTTGAAGGACTGGATTTTTATAAAACTAAAGTCAAGCTCTGCATCCTTCTTCAT 1566

Qy       1477 GCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
              || |||||||| || |||||||||||||| || |||||| ||||||||||||||||
Db       1567 GCCTTCAGAATCCGCGCAGTGACCATCAACAGGATGATGGGCTATCTGAATGCTTCC 1623

RESULT 10
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AR091395
LOCUS       AR091395                1560 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 11 from patent US 5994104.
ACCESSION   AR091395
VERSION     AR091395.1  GI:10018150
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1560)
  AUTHORS   Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
  TITLE     Interleukin-12 fusion protein
  JOURNAL   Patent: US 5994104-A 11 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .1560
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                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           78.2%;  Score 1198.2;  DB 2;  Length 1560;
  Best Local Similarity   86.8%;  Pred. No. 0;
  Matches 1352;  Conservative    0;  Mismatches  178;  Indels   27;  Gaps    2;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              |||||||||||| ||||| | |||||||| ||||| ||||| ||| | || ||||||||
Db          4 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 63

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              |||||||||||||||||||||||  | || ||||||||||||  ||||||||||||
Db         64 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 123

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              |||||||||||||| ||| |||||||||| ||||| ||||||||||||||||||| |||
Db        124 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 183

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              | ||||||||||||||| |||||||| |||||||||||||||| ||||||||| ||||
Db        184 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 243

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Db        244 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 303

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              |||||||||||| |||||||| ||| ||||| ||||||||||||||||||||||||||||
Db        304 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 363

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              |||||||||||| |||||||||| ||||||| ||||| ||||||||||||||||||||
Db        364 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 423

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| |||||| || ||||| || |||||||| |||||||  ||||||| |
Db        424 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 483

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||| ||| |||    ||||| |||||||||| ||||||| |||||||||||| |||
Db        484 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              || |||||||| || |||||||| ||| ||||||| ||  ||||||||||||||| |||
Db        541 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||| ||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              || |||||||||||||| |||||||||| ||||| || |||||||| ||||||||||||
Db        661 CAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||| || |||||||||||||||||| | |||||  |||| ||||||||||||||||| |

Db        721 TGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || |||||||||||||| ||| ||| |  |||||||||||||||||| |||| | |||| |
Db        781 AAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||  ||||||  ||  ||||||  |||   |||||||||||||||||||| |||||| |
Db        841 AAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAA 900

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGT----------------------GGCGGC 936
              ||||||| ||| ||||||||||||||||                      || |||
Db        901 TGGGCATCTGTGCCCTGCAGTGGTGGCGGTGGAAGCGGCGGTGGCGGAAGCGGCGGTGGC 960

Qy        937 GGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCAC 996
              ||    |||||| | ||     | ||||||  ||| || |||||||  |||||  |||||
Db        961 GGCAGCAGAAACCTCCCCCTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCAC 1020

Qy        997 TCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAA 1056
              ||||||| ||||||| | ||| ||||||||| ||| ||||||||||||||||||||||||
Db       1021 TCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAA 1080

Qy       1057 TTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGC 1116
              |||||| | |||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1081 TTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGC 1140

Qy       1117 ACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGA 1176
              |||||||||||||| |||||| |||||||||||| ||||||||||||||   ||||||
Db       1141 ACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGA 1200

Qy       1177 GAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACG 1236
              |||| |||| | |||||||||||||||||||||||||||||||||||||||||||| |
Db       1201 GAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATG 1260

Qy       1237 ACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCC 1296
              |||||||||||| ||||| ||||| |||||||||||||||||||||||||||||||| ||
Db       1261 GCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACC 1320

Qy       1297 ATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 1356
              |||||||||||||  | |||||||||| |||||||||||| ||||||||||||||||
Db       1321 ATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTG 1380

Qy       1357 ACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAAC 1416
              ||| |||||||||||| | |||||||||| ||||||||| |||||||||||| ||
Db       1381 GCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAA 1440

Qy       1417 TCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1476
              |||||| | |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1500

Qy       1477 GCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
              |||||||||||||| |||||||| ||  | ||| ||| ||||||||||||||||||
Db       1501 GCTTTCAGAATTCGGGCAGTGACTATTGACAGAGTGACGAGCTATCTGAATGCTTCC 1557


RESULT 11
AR091394
LOCUS       AR091394                1623 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 9 from patent US 5994104.
ACCESSION   AR091394
VERSION     AR091394.1  GI:10018149
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1623)
  AUTHORS   Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
  TITLE     Interleukin-12 fusion protein
  JOURNAL   Patent: US 5994104-A 9 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .1623
                     /organism="unknown"
                     /mol_type="unassigned DNA"
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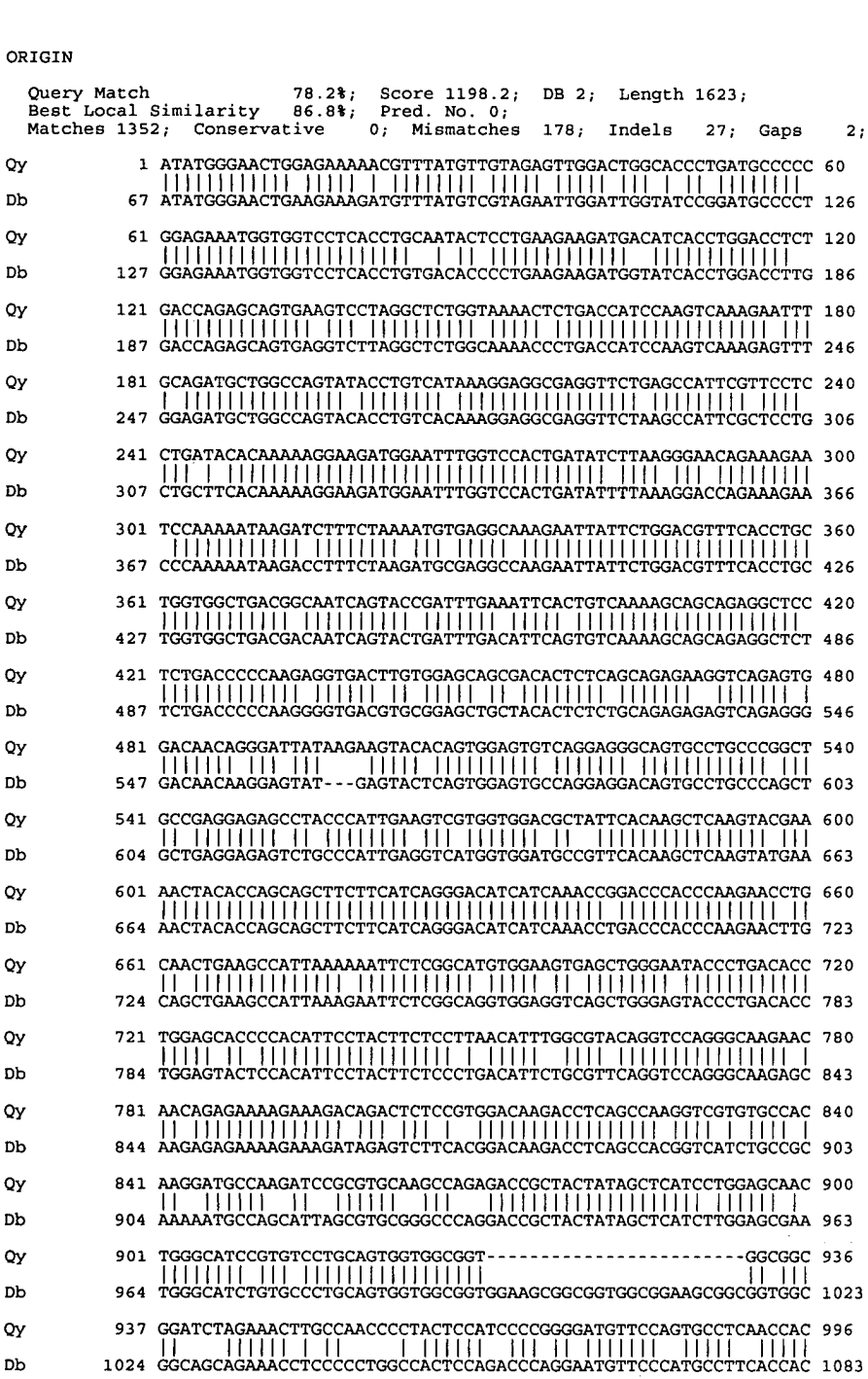
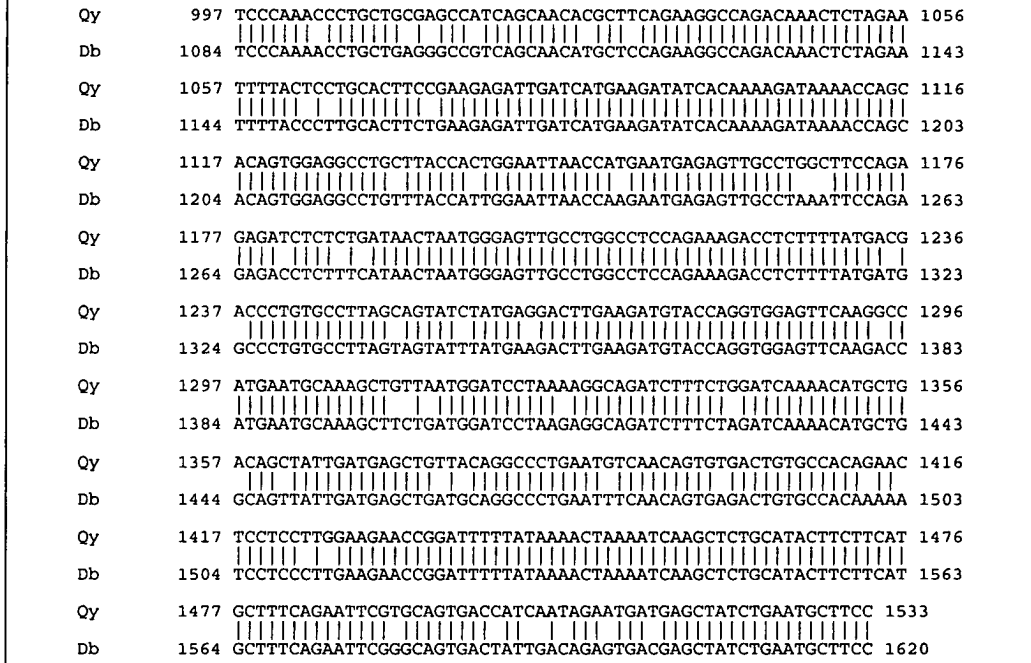
ORIGIN

Query Match 78.2%; Score 1198.2; DB 2; Length 1623;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 1352; Conservative 0; Mismatches 178; Indels 27; Gaps 2;





RESULT 12
AR091393
LOCUS AR091393 6139 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 7 from patent US 5994104.
ACCESSION AR091393
VERSION AR091393.1 GI:10018148
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 6139)
AUTHORS Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
TITLE Interleukin-12 fusion protein
JOURNAL Patent: US 5994104-A 7 30-NOV-1999;
FEATURES Location/Qualifiers
source 1. .6139
/organism="unknown"
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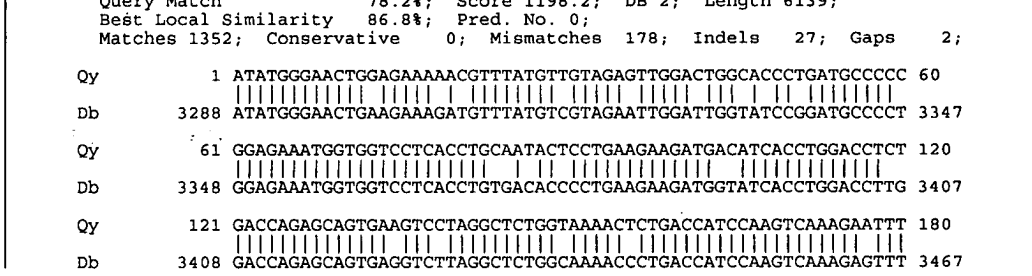
ORIGIN

Query Match 78.2%; Score 1198.2; DB 2; Length 6139;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 1352; Conservative 0; Mismatches 178; Indels 27; Gaps 2;



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Qy       181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
Db      3468 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 3527

Qy       241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
Db      3528 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 3587

Qy       301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
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Qy       361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
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Qy       421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
Db      3708 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 3767

Qy       481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
Db      3768 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 3824

Qy       541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
Db      3825 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAA 3884

Qy       601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
Db      3885 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTG 3944

Qy       661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
Db      3945 CAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACC 4004

Qy       721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
Db      4005 TGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGC 4064

Qy       781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
Db      4065 AAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGC 4124

Qy       841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
Db      4125 AAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAA 4184

Qy       901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGT----------------------GGCGGC 936
Db      4185 TGGGCATCTGTGCCCTGCAGTGGTGGCGGTGGAAGCGGCGGTGGCGGAAGCGGCGGTGGC 4244

Qy       937 GGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCAC 996
Db      4245 GGCAGCAGAAACCTCCCCCTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCAC 4304

Qy       997 TCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAA 1056
Db      4305 TCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAA 4364

Qy      1057 TTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGC 1116
Db      4365 TTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGC 4424

Qy      1117 ACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGA 1176
Db      4425 ACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGA 4484

Qy      1177 GAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACG 1236
Db      4485 GAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATG 4544

Qy      1237 ACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCC 1296
Db      4545 GCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACC 4604

Qy      1297 ATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 1356
Db      4605 ATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTG 4664

Qy      1357 ACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAAC 1416
Db      4665 GCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAA 4724

Qy      1417 TCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1476
Db      4725 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 4784

Qy      1477 GCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
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RESULT 13
AR595948
LOCUS AR595948 921 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 26 from patent US 6818444.
ACCESSION AR595948
VERSION AR595948.1 GI:56646929
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 921)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 26 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .921
/organism="unknown"
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ORIGIN

Query Match 60.1%; Score 921; DB 2; Length 921;
Best Local Similarity 100.0%; Pred. No. 7.9e-262;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
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Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
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Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
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Qy        901 TGGGCATCCGTGTCCTGCAGT 921
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Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 14
AR595949/c
LOCUS       AR595949                921 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 28 from patent US 6818444.
ACCESSION   AR595949
VERSION     AR595949.1  GI:56646930
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 28 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             60.1%;  Score 921;  DB 2;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-262;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

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Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

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Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

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Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

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Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
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Qy        901 TGGGCATCCGTGTCCTGCAGT 921
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Db         21 TGGGCATCCGTGTCCTGCAGT 1


RESULT 15
FCIL12P40
LOCUS       FCIL12P40               1006 bp    mRNA    linear   MAM 18-APR-2005
DEFINITION  Felis catus mRNA for interleukin-12 p40 chain.
ACCESSION   Y07762
VERSION     Y07762.1  GI:2102664
KEYWORDS    interleukin-12 p40.
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1
  AUTHORS   Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
  TITLE     Molecular cloning of cat interleukin-12
  JOURNAL   Immunogenetics 45 (6), 462-463 (1997)
   PUBMED   9089110
REFERENCE   2  (bases 1 to 1006)
```

```
  AUTHORS   Schijns,V.E.C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
            Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
            Utrecht, NETHERLANDS
FEATURES             Location/Qualifiers
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                     /tissue_type="peripheral blood"
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     CDS             1. .990
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                     /note="heterodimer with IL-12 p35 chain"
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ORIGIN

  Query Match           60.1%;  Score 921;  DB 14;  Length 1006;
  Best Local Similarity  100.0%;  Pred. No. 8e-262;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

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Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
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Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

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Searched: 5244920 seqs, 3486124231 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	3	1533	100.0	1533	14	ADV34697	Adv34697 Feline si
	4	1533	100.0	1533	14	ADV34695	Adv34695 Feline si
	5	1533	100.0	1599	6	ABK98950	Abk98950 Feline in
c	6	1533	100.0	1599	6	ABK98951	Abk98951 Feline in
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c	8	1533	100.0	1599	14	ADV34693	Adv34693 Feline si
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c	11	1373	89.6	1533	14	ADV34718	Adv34718 Canine si
	12	1373	89.6	1533	14	ADV34716	Adv34716 Canine si
	13	1373	89.6	1599	6	ABK98965	Abk98965 Canine in
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	16	1373	89.6	1599	14	ADV34713	Adv34713 Canine si
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	21	1198.2	78.2	6139	3	AAZ40023	Aaz40023 Interleuk
	22	1193.8	77.9	8578	6	AAD31546	Aad31546 pIRES-hB7
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	24	1193.8	77.9	8623	6	AAD31547	Aad31547 pIRES-hB7
	25	1193.8	77.9	8644	6	AAD31551	Aad31551 pIRES-IL1
	26	1178.8	76.9	8638	6	AAD31549	Aad31549 pIRES-hB7
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	37	919.4	60.0	2193	2	AAV56625	Aav56625 Feline FL
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c	39	917.4	59.8	985	6	ABK98962	Abk98962 Feline in
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	41	917.4	59.8	985	14	ADV34707	Adv34707 Feline N-
c	42	917.4	59.8	985	14	ADV34709	Adv34709 Feline N-
	43	916.2	59.8	990	4	AAF26082	Aaf26082 Feline IL
	44	916.2	59.8	990	4	AAF26085	Aaf26085 Feline IL
	45	916.2	59.8	4522	4	AAF26076	Aaf26076 Feline IL

ALIGNMENTS

RESULT 1
ABK98954/c
ID ABK98954 standard; cDNA; 1533 BP.
XX
AC ABK98954;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12-1533 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 66-67; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,

```
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 1533;  DB 6;  Length 1533;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1533;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
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Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
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Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
              |||||||||||||||||||||||||||||||||
Db         33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 2
ABK98953
ID   ABK98953 standard; cDNA; 1533 BP.
XX
AC   ABK98953;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1533 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
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PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69307.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 63-64; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

Query Match 100.0%; Score 1533; DB 6; Length 1533;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020

Qy       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080

Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380

Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440

Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500

Qy       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
              |||||||||||||||||||||||||||||||||
Db       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
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RESULT 3
ADV34697/c
ID ADV34697 standard; DNA; 1533 BP.
XX
AC ADV34697;
XX
DT 24-FEB-2005 (first entry)
XX

DE Feline single chain IL-12 complementary DNA, nFeIL-12 1533.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Felis catus.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 3; SEQ ID NO 45; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain IL-12 complementary DNA.
XX
SQ Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

Query Match 100.0%; Score 1533; DB 14; Length 1533;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
              ||||||||||||||||||||||||||||||||
Db         33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
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RESULT 4
ADV34695
ID   ADV34695 standard; cDNA; 1533 BP.
XX
AC   ADV34695;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1533
FT                   /*tag=  a
FT                   /product= "PFeIL-12 511 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34696.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 43; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 1533;  DB 14;  Length 1533;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1533;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020

Qy       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080

Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380

Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440

Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500

Qy       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
                ||||||||||||||||||||||||||||||||
Db       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533


RESULT 5
ABK98950
ID   ABK98950 standard; cDNA; 1599 BP.
XX
AC   ABK98950;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1599 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69306.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 58-60; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 1533;  DB 6;  Length 1599;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1533;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGAACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026

Qy        961 ACTCCATCCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1086
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Qy       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1146

Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1147 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1266

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1267 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1326

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1327 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1386

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1387 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1446

Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1506

Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1566

Qy       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
             |||||||||||||||||||||||||||||||||
Db       1567 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
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RESULT 6
ABK98951/c
ID ABK98951 standard; cDNA; 1599 BP.
XX
AC ABK98951;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12-1599 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 61-62; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

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  Query Match             100.0%;  Score 1533;  DB 6;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1533;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754
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Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
              |||||||||||||||||||||||||||||||||
Db          33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1


RESULT 7
ADV34691
ID   ADV34691 standard; cDNA; 1599 BP.
XX
AC   ADV34691;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1599
FT                   /*tag=  a
FT                   /product= "PFeIL-12p533 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34692.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 38; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1533;  DB 14;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1533;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026

Qy        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1086

Qy       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1146

Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1147 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1266

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1267 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1326

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1327 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1386

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1387 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1446

Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1506

Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1566

Qy       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
              |||||||||||||||||||||||||||||||||
Db       1567 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
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RESULT 8
ADV34693/c

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ID   ADV34693 standard; DNA; 1599 BP.
XX
AC   ADV34693;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 complementary DNA, nFeIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 40; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 complementary DNA.
XX
SQ   Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 1533;  DB 14;  Length 1599;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1533;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174
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Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
              |||||||||||||||||||||||||||||||||
Db         33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
```

RESULT 9
ABK98967
ID ABK98967 standard; cDNA; 1533 BP.
XX
AC ABK98967;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12-1533 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69314.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 83-85; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1533 BP; 446 A; 368 C; 369 G; 350 T; 0 U; 0 Other;

```
  Query Match             89.6%;  Score 1373;  DB 6;  Length 1533;
  Best Local Similarity   93.5%;  Pred. No. 0;
  Matches 1433;  Conservative    0;  Mismatches  100;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              |||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              |||||||||||||||||||||| |||| |||||||||||||||||||| ||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120
```

```
Qy       121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
Db       121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy       181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
Db       181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240

Qy       241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
Db       241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300

Qy       301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
Db       301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360

Qy       361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
Db       361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420

Qy       421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
Db       421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480

Qy       481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
Db       481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540

Qy       541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
Db       541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy       601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
Db       601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660

Qy       661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
Db       661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720

Qy       721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
Db       721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780

Qy       781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
Db       781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy       841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
Db       841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900

Qy       901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
Db       901 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy       961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
Db       961 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 1020

Qy      1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
Db      1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 1080

Qy      1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
Db      1081 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy      1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
Db      1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1200

Qy      1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
Db      1201 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1260

Qy      1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
Db      1261 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1320

Qy      1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
Db      1321 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 1380

Qy      1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
Db      1381 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1440

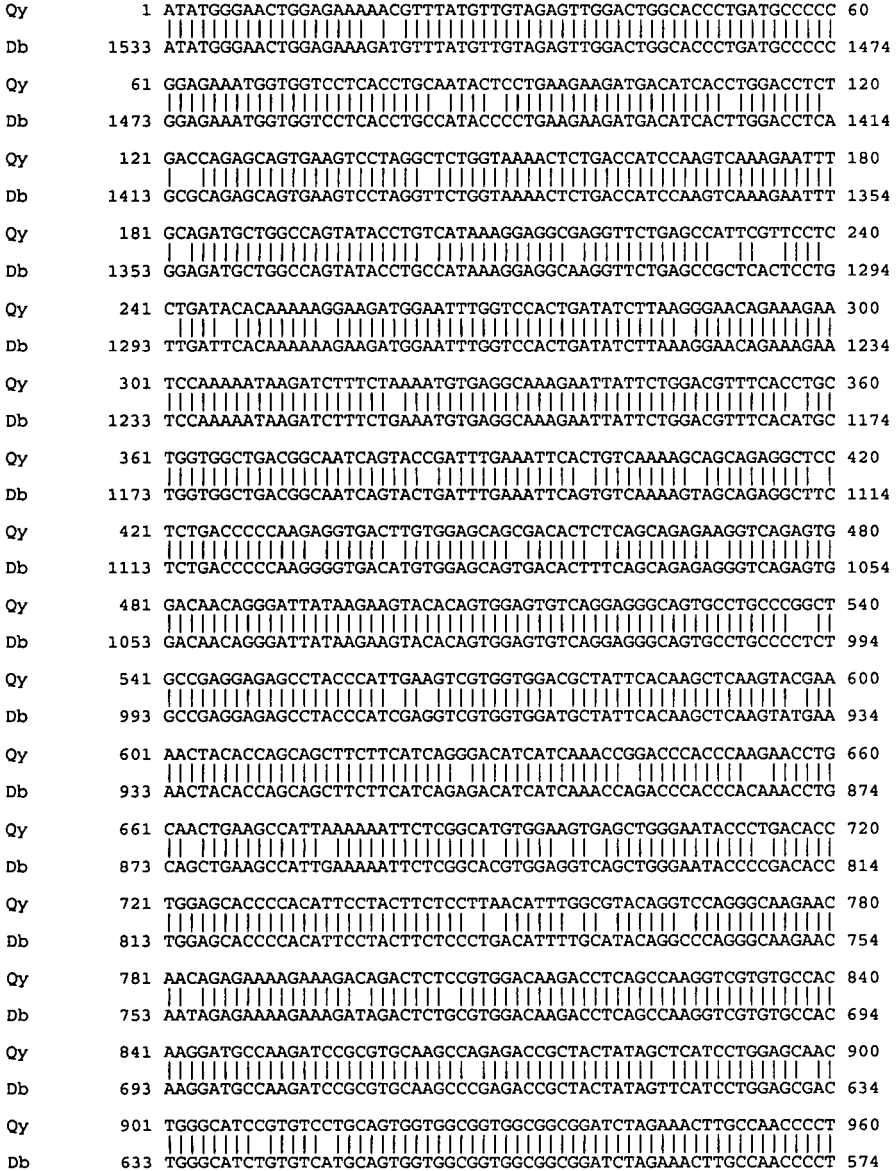
Qy      1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
Db      1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1500

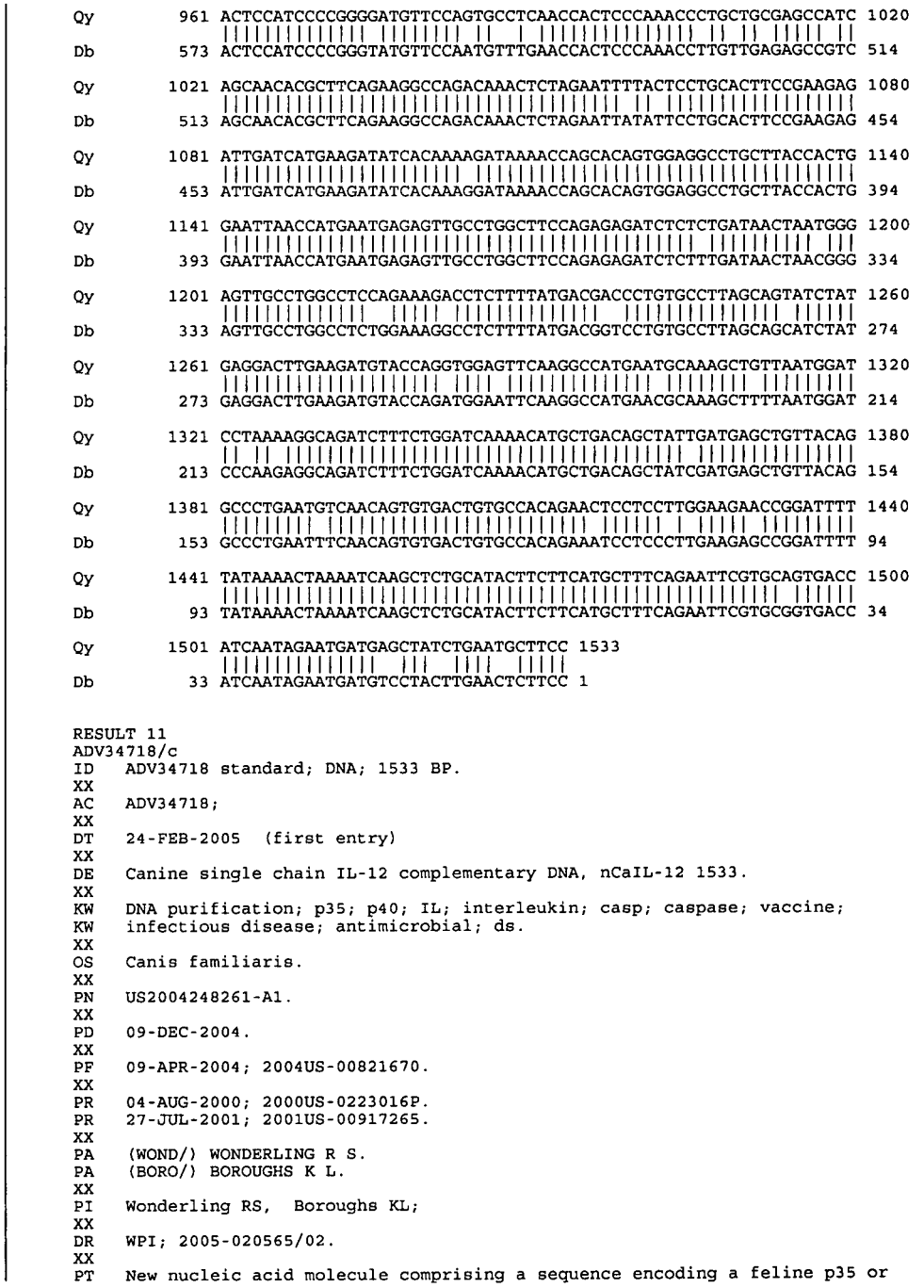
Qy      1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
Db      1501 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1533
```

RESULT 10
ABK98968/c
ID ABK98968 standard; cDNA; 1533 BP.
XX
AC ABK98968;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12-1533 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 86-87; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid

CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

Query Match 89.6%; Score 1373; DB 6; Length 1533;
Best Local Similarity 93.5%; Pred. No. 0;
Matches 1433; Conservative 0; Mismatches 100; Indels 0; Gaps 0;





RESULT 11
ADV34718/c
ID ADV34718 standard; DNA; 1533 BP.
XX
AC ADV34718;
XX
DT 24-FEB-2005 (first entry)
XX
DE Canine single chain IL-12 complementary DNA, nCaIL-12 1533.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Canis familiaris.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or

```
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 68; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 complementary DNA.
XX
SQ   Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

  Query Match            89.6%;  Score 1373;  DB 14;  Length 1533;
  Best Local Similarity  93.5%;  Pred. No. 0;
  Matches 1433;  Conservative    0;  Mismatches  100;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              |||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              | |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       1413 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              | |||||||||||||||||||| |||||||||||| |||||||||||||   ||  ||||
Db       1353 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              |||| |||||||| |||||||||||||||||||||||||||||||| ||||||||||||
Db       1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||| |||
Db       1233 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              |||||||||||||||||||||| |||||||||||| |||||||| |||||||||| |
Db       1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||||| |||||| |||||||||| |||||| |||||||||| ||||||||||
Db       1113 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              |||||||||||||||||| || |||||||||| |||||||||||||||||||| |||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              |||||||||||||||||||||||| |||||||||||| |||||||||  ||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              || |||||||||| |||||||||||||| ||||| || |||||||||||||| ||||||
Db        873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              |||||||||||||||||||||||||| | |||||| || |||||| ||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || |||||||||||||| ||||||| ||||||||||||||||||||||||||||||||||

Db        753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              |||||||||||||||||||||||||||| |||||||||||||||| |||||||||||| ||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
              |||||||| ||||| |||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
              ||||||||||||| |||||||| ||  | |||||||||||||| || || ||||| ||
Db        573 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 514

Qy       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
              |||||||||||||||||||||||||||||||||||| || ||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 454

Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 334

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
              |||||||||||||  ||||| ||||||||||||  |||||||||||||| ||||||
Db        333 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 274

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
              |||||||||||||||||||||| |||| |||||||||||||| |||||||| |||||||||
Db        273 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 214

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
              || || ||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        213 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 154

Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
              ||||||||| |||||||||||||||||||||| |||||| | ||||| |||||||||
Db        153 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 94

Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 34

Qy       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
              ||||||||||||||  |||  ||||  |||||
Db         33 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1

RESULT 12
ADV34716
ID   ADV34716 standard; cDNA; 1533 BP.
XX
AC   ADV34716;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12 protein cDNA, nCaIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1533
FT                   /*tag=  a
FT                   /product= "PCaIL-12 511 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
```

```
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34717.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 66; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1533 BP; 446 A; 368 C; 369 G; 350 T; 0 U; 0 Other;

  Query Match           89.6%;  Score 1373;  DB 14;  Length 1533;
  Best Local Similarity   93.5%;  Pred. No. 0;
  Matches 1433;  Conservative    0;  Mismatches  100;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              |||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              |||||||||||||||||||||||| |||| |||||||||||||||||||| ||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              | |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              | |||||||||||||||||||| |||||||||||| |||||||||||   ||  ||||
Db        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
               |||| |||||||| |||||||||||||||||||||||||||||||| ||||||||||||
Db        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300

Qy        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||| |||
Db        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              |||||||||||||||||||| |||||||||||| |||||||| |||||||||| |
Db        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||||| |||||| |||||||||| |||||| |||||||||| ||||||||||
Db        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              |||||||||||||||||||| || |||||||||| |||||||||||||||||||| |||
Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              |||||||||||||||||||||||||| |||||||||||| |||||||||| ||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              || |||||||||| |||||||||||||| ||||| || |||||||||||||| ||||||
Db        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              |||||||||||||||||||||||||| | |||||| || |||||| ||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || |||||||||||||| ||||||| ||||||||||||||||||||||||||||||||||
Db        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              |||||||||||||||||||||||||| |||||||||||||||| |||||||||||| ||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
              |||||||| ||||| |||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
              |||||||||||||| |||||||| ||  | |||||||||||||| || || ||||| ||
Db        961 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 1020

Qy       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
              |||||||||||||||||||||||||||||||||||||||||| || ||||||||||||||||
Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 1080

Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db       1081 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||
Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1200

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
              |||||||||||||| ||||| |||||||||||||| |||||||||||||| ||||||
Db       1201 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1260

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
              |||||||||||||||||||| |||| |||||||||||||| |||||||| ||||||||||
Db       1261 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1320

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
              || || |||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       1321 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 1380

Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
              ||||||||| |||||||||||||||||||||||| |||||| | ||||| |||||||||
Db       1381 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1440

Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1500

Qy       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
              ||||||||||||||   |||  ||||  |||||
Db       1501 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1533


RESULT 13
ABK98965
ID   ABK98965 standard; cDNA; 1599 BP.
XX
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AC ABK98965;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12-1599 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69313.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 79-80; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1599 BP; 452 A; 392 C; 383 G; 372 T; 0 U; 0 Other;

Query Match 89.6%; Score 1373; DB 6; Length 1599;
Best Local Similarity 93.5%; Pred. No. 0;
Matches 1433; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

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Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              |||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              |||||||||||||||||||||||| |||| |||||||||||||||||||| ||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              | ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db        187 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              | |||||||||||||||||| |||||||||||| |||||||||||  ||  ||||
Db        247 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              |||| |||||||| ||||||||||||||||||||||||||||||| ||||||||||||||
Db        307 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||| |||
Db        367 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              |||||||||||||||||||||||| |||||||||||| ||||||||| |||||||||| |
Db        427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| |||||| |||||||||| |||||| |||||||||| ||||||||||
Db        487 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              |||||||||||||||||| || |||||||||| |||||||||||||||||||| |||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              |||||||||||||||||||||||||||||||| |||||||||||||| ||||||||||  ||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              || |||||||||| |||||||||||||| ||||| || |||||||||||||| ||||||
Db        727 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              |||||||||||||||||||||||||| | |||||| || |||||| ||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || |||||||||||||| ||||||| ||||||||||||||||||||||||||||||||||
Db        847 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              |||||||||||||||||||||||||| |||||||||||||| |||||||||||| ||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
              |||||||| ||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        967 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026

Qy        961 ACTCCATCCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
              |||||||||||||| |||||||| ||  | |||||||||||||| || || |||| ||
Db       1027 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 1086

Qy       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
              |||||||||||||||||||||||||||||||||||||||| || ||||||||||||||||||
Db       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 1146

Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       1147 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1266

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
              |||||||||||||| ||||| |||||||||||||| |||||||||||||| ||||||
Db       1267 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1326

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
              |||||||||||||||||||| |||| |||||||||||||| |||||||| |||||||||
Db       1327 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1386

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
              || || |||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db       1387 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 1446
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Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
             ||||||||| |||||||||||||||||||||||| |||||| | ||||| |||||||||
Db       1447 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1506

Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1566

Qy       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
              ||||||||||||||  |||  ||||  |||||
Db       1567 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1599


RESULT 14
ABK98966/c
ID   ABK98966 standard; cDNA; 1599 BP.
XX
AC   ABK98966;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1599 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 82-83; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 372 A; 383 C; 392 G; 452 T; 0 U; 0 Other;

  Query Match           89.6%;  Score 1373;  DB 6;  Length 1599;
  Best Local Similarity   93.5%;  Pred. No. 0;
  Matches 1433;  Conservative    0;  Mismatches  100;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              |||||||||||||||| | ||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              |||||||||||||||||||||||| |||| |||||||||||||||||||| ||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              | |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db       1413 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              | |||||||||||||||||||| |||||||||||| |||||||||||  ||  ||||
Db       1353 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              |||| |||||||| ||||||||||||||||||||||||||||||| ||||||||||||
Db       1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||| |||
Db       1233 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              |||||||||||||||||||| |||||||||||| |||||||| |||||||||| |
Db       1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| |||||| ||||||||| |||||| |||||||||| ||||||||||
Db       1113 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              |||||||||||||||||||| || |||||||||| |||||||||||||||||||| |||
Db       993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              |||||||||||||||||||||||| |||||||||||||| |||||||||| ||||||
Db       933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              || |||||||||| |||||||||||||| ||||| || |||||||||||||| ||||||
Db       873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              |||||||||||||||||||||||||||| | |||||| || |||||| |||||||||||||
Db       813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || |||||||||||||| ||||||| ||||||||||||||||||||||||||||||||||
Db       753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              |||||||||||||||||||||||| |||||||||||||| |||||||||||| ||
Db       693 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
              |||||||| |||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       633 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
              |||||||||||||| |||||||| ||  | |||||||||||||| || || ||||| ||
Db       573 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 514

Qy       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
              |||||||||||||||||||||||||||||||||||||||||| || ||||||||||||||
Db       513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 454

Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db       453 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394
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Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||| |||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 334

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
             |||||||||||||||  ||||| |||||||||||||||  |||||||||||||||| ||||||
Db        333 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 274

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
             |||||||||||||||||||| |||| |||||||||||||| |||||||| |||||||||
Db        273 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 214

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
             || || ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        213 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 154

Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
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Db        153 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 94

Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db          93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 34

Qy       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
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Db          33 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1
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RESULT 15
ADV34715/c
ID ADV34715 standard; DNA; 1599 BP.
XX
AC ADV34715;
XX
DT 24-FEB-2005 (first entry)
XX
DE Canine single chain IL-12 complementary DNA, nCaIL-12 1599.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Canis familiaris.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 4; SEQ ID NO 63; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the canine single chain IL-12 complementary DNA.

XX
SQ Sequence 1599 BP; 372 A; 383 C; 392 G; 452 T; 0 U; 0 Other;

Query Match 89.6%; Score 1373; DB 14; Length 1599;
Best Local Similarity 93.5%; Pred. No. 0;
Matches 1433; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

```
Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              |||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              |||||||||||||||||||||||| |||| |||||||||||||||||| ||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              | |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1413 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              | |||||||||||||||||||| |||||||||||| |||||||||||  ||  ||||
Db       1353 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              |||| |||||||| ||||||||||||||||||||||||||||| ||||||||||||
Db       1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||| |||
Db       1233 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              |||||||||||||||||||| |||||||||||| ||||||||| |||||||||| |
Db       1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| |||||| |||||||||| |||||| |||||||||| ||||||||||
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Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              || |||||||||| |||||||||||||| ||||| || |||||||||||||| ||||||
Db        873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              |||||||||||||||||||||||||| | |||||| || |||||| ||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || |||||||||||||| ||||||| ||||||||||||||||||||||||||||||||||
Db        753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
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Db        633 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
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```

```
Db        573 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 514

Qy       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
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Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 454

Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
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Db        453 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
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Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 334

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
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Db        333 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 274

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
              |||||||||||||||||||| |||| |||||||||||||| |||||||| |||||||||
Db        273 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 214

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
              || || ||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        213 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 154

Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
              ||||||||| |||||||||||||||||||||||| |||||| | ||||| |||||||||
Db        153 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 94

Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 34

Qy       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
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Db         33 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1
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Search completed: June 10, 2006, 04:50:55
Job time : 1134.44 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 10, 2006, 03:16:38 ; Search time 8952.62 Seconds
(without alignments)
9575.336 Million cell updates/sec

Title: US-10-821-670A-43
Perfect score: 1533
Sequence: 1 atatgggaactggagaaaaa.....tgagctatctgaatgcttcc 1533

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	528.4	34.5	756	5	CK130264	CK130264 AGENCOURT
	2	526.4	34.3	735	5	CD559605	CD559605 AGENCOURT
	3	519	33.9	747	5	CD559607	CD559607 AGENCOURT
	4	515.4	33.6	772	5	CD559604	CD559604 AGENCOURT
c	5	507.6	33.1	785	5	CD559448	CD559448 AGENCOURT
c	6	506.4	33.0	772	5	CD559450	CD559450 AGENCOURT
c	7	501.4	32.7	736	5	CD559453	CD559453 AGENCOURT
c	8	499.8	32.6	762	5	CD559451	CD559451 AGENCOURT
	9	495.4	32.3	762	14	DQ033872	DQ033872 Homo sapi
	10	490.6	32.0	762	14	DQ033873	DQ033873 Pan trogl
c	11	477.4	31.1	754	5	CD559452	CD559452 AGENCOURT
c	12	471.8	30.8	766	5	CD559449	CD559449 AGENCOURT
	13	468	30.5	1839	6	AK162981	AK162981 Mus muscu
	14	461.8	30.1	745	5	CD559602	CD559602 AGENCOURT
	15	457	29.8	2908	6	AK155593	AK155593 Mus muscu
c	16	436	28.4	725	5	CD559454	CD559454 AGENCOURT
	17	409.4	26.7	935	4	CD013914	CD013914 90138124
	18	408.8	26.7	1136	4	CD013915	CD013915 90138132
	19	365.6	23.8	724	5	CD559603	CD559603 AGENCOURT
	20	350	22.8	1042	5	CD559606	CD559606 AGENCOURT
	21	331.2	21.6	863	4	CD013916	CD013916 90138296
	22	313.4	20.4	649	5	CJ134671	CJ134671 CJ134671
	23	258	16.8	1938	6	BC035571	BC035571 Homo sapi
	24	230.6	15.0	475	7	BF704417	BF704417 MI-P-E6-a
	25	227.4	14.8	812	2	BG702253	BG702253 602683459
	26	218	14.2	589	1	AI050362	AI050362 ub30a07.r
	27	215.8	14.1	563	3	BU698113	BU698113 LL2in1206
c	28	215	14.0	1099	2	BI523344	BI523344 603175938
	29	207.8	13.6	417	8	CO949904	CO949904 UMC-pd12c
c	30	207.6	13.5	778	1	AJ820622	AJ820622 AJ820622
	31	200	13.0	373	7	BF552757	BF552757 UI-R-C0-i
	32	198.2	12.9	700	12	CE093997	CE093997 tigr-gss-
	33	190	12.4	561	3	BU699383	BU699383 LL2in1157
	34	185.6	12.1	387	4	BY167742	BY167742 BY167742
	35	180.4	11.8	535	11	AZ441303	AZ441303 1M0232M24
	36	180.2	11.8	252	10	DV799576	DV799576 est_t_tru
	37	178.4	11.6	423	4	BY218447	BY218447 BY218447
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c	40	173.8	11.3	777	4	CB168830	CB168830 CWI602769
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	43	168	11.0	375	4	BY222535	BY222535 BY222535
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ALIGNMENTS

RESULT 1
CK130264
LOCUS CK130264 756 bp mRNA linear EST 02-DEC-2003
DEFINITION AGENCOURT_14496566 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971871 5', mRNA sequence.
ACCESSION CK130264
VERSION CK130264.1 GI:38622200
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 756)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: h column: 02
High quality sequence start: 5
High quality sequence stop: 731.
FEATURES Location/Qualifiers
source 1. .756
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971871"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:

loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 34.5%; Score 528.4; DB 5; Length 756;
Best Local Similarity 88.6%; Pred. No. 7.7e-143;
Matches 584; Conservative 0; Mismatches 72; Indels 3; Gaps 1;

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Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db        100 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 159

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              ||||||||||||||||||||||  | || ||||||||||||  ||||||||||||
Db        160 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 219

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Db        220 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 279

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              | |||||||||||||| |||||||| |||||||||||||||| ||||||||| ||||
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Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||| | |||||||||||||||||||||||||||||||||| |||| ||| |||||||||
Db        340 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 399

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Db        400 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 459

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
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Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Db        580 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 636

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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              |||||||||||||||||||||||||||||||||| |||| ||||||||||||||| |
Db        697 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCNAACCTGACCCACCCAAGAACTT 755
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RESULT 2
CD559605
LOCUS CD559605 735 bp mRNA linear EST 26-NOV-2003
DEFINITION AGENCOURT_14496534 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971870 5', mRNA sequence.
ACCESSION CD559605
VERSION CD559605.2 GI:38558937
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 735)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585673.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: IRBK2 row: h column: 01
High quality sequence stop: 709.
FEATURES Location/Qualifiers
source 1. .735
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/mol_type="mRNA"
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/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 34.3%; Score 526.4; DB 5; Length 735;
Best Local Similarity 88.7%; Pred. No. 2.9e-142;
Matches 582; Conservative 0; Mismatches 71; Indels 3; Gaps 1;

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Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db         83 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 142

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||  | || ||||||||||||  ||||||||||||
Db        143 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 202

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Db        203 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 262

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Db        263 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 322
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Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Db        323 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 382

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
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Db        383 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 442

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
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Db        443 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAGAGCAGCAGAGGCTCT 502

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Db        503 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 562

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Db        620 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAA 679

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAA 656
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Db        680 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAA 735
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RESULT 3
CD559607
LOCUS CD559607 747 bp mRNA linear EST 26-NOV-2003
DEFINITION AGENCOURT_14497061 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971868 5', mRNA sequence.
ACCESSION CD559607
VERSION CD559607.2 GI:38558941
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 747)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585675.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: g column: 11
High quality sequence start: 14
High quality sequence stop: 671.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971868"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.data Note: this is a NIH_MGC Library."
ORIGIN

Query Match 33.9%; Score 519; DB 5; Length 747;
Best Local Similarity 88.1%; Pred. No. 4.4e-140;
Matches 577; Conservative 0; Mismatches 75; Indels 3; Gaps 1;

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Db         95 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 154

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
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Db        155 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 214

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Db        215 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 274

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Db        275 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 334

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Db        335 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 394

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
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Db        395 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 454

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              |||||||||||| |||||||||| ||||||| ||||| ||||||||||||||||||||
Db        455 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 514

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||||| |||||| || ||||| || |||||||| |||||||  ||||||| |
Db        515 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 574

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Db        632 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATTGCGTTCACAAGCTCCAGTATGAA 691

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGA 655
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Db        692 AACTACACCCGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAAA 746
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RESULT 4
CD559604
LOCUS CD559604 772 bp mRNA linear EST 26-NOV-2003
DEFINITION AGENCOURT_14496598 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971872 5', mRNA sequence.
ACCESSION CD559604

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VERSION     CD559604.2  GI:38558934
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 772)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585672.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 03
            High quality sequence start: 13
            High quality sequence stop: 750.
FEATURES             Location/Qualifiers
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                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN
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  Query Match             33.6%;  Score 515.4;  DB 5;  Length 772;
  Best Local Similarity   87.9%;  Pred. No. 5.1e-139;
  Matches  574;  Conservative    0;  Mismatches   76;  Indels    3;  Gaps    1;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db        104 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 163

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||  | || ||||||||||||  ||||||||||||
Db        164 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 223

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||| ||||||||||||| ||||| ||||||||||||||||||| |||
Db        224 GACCAGAGCAGTGAGGTCCTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 283

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Db        284 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 343

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Db        344 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 403

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
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Db        404 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 463

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              |||||||||||| |||||||||| ||||||| ||||| ||||||||||||||||||||||
Db        464 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 523

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Db        524 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 583

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Db        584 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 640

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAA 653
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Db        701 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAACCTGACCAACCCAAA 753
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RESULT 5
CD559448/c
LOCUS       CD559448                785 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496712 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971874 5', mRNA sequence.
ACCESSION   CD559448
VERSION     CD559448.2  GI:38453466
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 785)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585516.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 05
            High quality sequence stop: 696.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971874"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
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loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 33.1%; Score 507.6; DB 5; Length 785;
Best Local Similarity 85.7%; Pred. No. 9.9e-137;
Matches 588; Conservative 0; Mismatches 94; Indels 4; Gaps 2;

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Qy      296 AAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCA 355
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Db      715 AAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCA 656

Qy      356 CCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAG 415
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Db      655 CCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAG 596

Qy      416 GCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCA 475
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Db      595 GCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCA 536

Qy      476 GAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCC 535
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Db      535 GAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCC 479

Qy      536 CGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGT 595
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Db      478 CAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGT 419

Qy      596 ACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGA 655
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Qy      656 ACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTG 715
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Db      358 ACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTG 299

Qy      716 ACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCA 775
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Db      298 ACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCA 239

Qy      776 AGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGT 835
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Qy      896 GCAACTGGGCATCCGTGTCCTGCAGT 921
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Db      118 GCGAATGGGCATCTGTGCCCTGCAGT 93
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RESULT 6
CD559450/c

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LOCUS       CD559450                772 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496612 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971872 5', mRNA sequence.
ACCESSION   CD559450
VERSION     CD559450.2  GI:38453469
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 772)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585518.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 03
            High quality sequence start: 2
            High quality sequence stop: 753.
FEATURES              Location/Qualifiers
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                      /lab_host="DH5A (T1 phage-resistant)"
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                      /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                      loxP-HindIII; Clones from this library have been
                      PCR-amplified using gene-specific primers to contain the
                      complete open reading frame (based on known gene sequences
                      available from NCBI's RefSeq). Template for PCR is cDNA
                      derived from either pooled cytoplasmic polyA RNA from 30
                      cells lines or pooled total RNA from 10 different tissues
                      (from BD Biosciences/Clontech and Washington University).
                      PCR products are directionally cloned into the loxP sites
                      of the pDNR-Dual vector. Library constructed by Dr.
                      Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                      Expression Laboratory, Research Technology Program, SAIC
                      Frederick, NCI-Frederick, Frederick, MD 21702). For
                      information on which gene each clone represents, please
                      visit our anonymous ftp site at
                      ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                      a Note: this is a NIH_MGC Library."
ORIGIN
```

Query Match 33.0%; Score 506.4; DB 5; Length 772;
Best Local Similarity 86.5%; Pred. No. 2.2e-136;
Matches 582; Conservative 0; Mismatches 87; Indels 4; Gaps 2;

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Qy      249 CAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAA 308
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Db      770 CACAAAAGGAAGATGAATTNGGTCCACTGATAT-TTAAAGGACCAGAAAGAACCCAAAAA 712

Qy      309 TAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCT 368
            ||||| |||||||| ||| ||||| ||||||||||||||||||||||||||||||||||||
Db      711 TAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCT 652

Qy      369 GACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCC 428
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Db        651 GACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCTGACCC 592

Qy        429 CCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAG 488

Db        591 CCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAACAA 532

Qy        489 GGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGA 548

Db        531 GGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCTGAGGA 475

Qy        549 GAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACAC 608

Db        474 GAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACAC 415

Qy        609 CAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAA 668

Db        414 CAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAA 355

Qy        669 GCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCAC 728

Db        354 GCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTAC 295

Qy        729 CCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGA 788

Db        294 TCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGCAAGAGAGA 235

Qy        789 AAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGC 848

Db        234 AAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGCAAAAATGC 175

Qy        849 CAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATC 908

Db        174 CAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAATGGGCATC 115

Qy        909 CGTGTCCTGCAGT 921

Db        114 TGTGCCCTGCAGT 102


RESULT 7
CD559453/c
LOCUS       CD559453                736 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14497154 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971869 5', mRNA sequence.
ACCESSION   CD559453
VERSION     CD559453.2  GI:38453475
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 736)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585521.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: g  column: 12
            High quality sequence stop: 683.
FEATURES             Location/Qualifiers
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                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
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                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             32.7%;  Score 501.4;  DB 5;  Length 736;
  Best Local Similarity   87.1%;  Pred. No. 6.3e-135;
  Matches  574;  Conservative    0;  Mismatches   81;  Indels    4;  Gaps    2;

Qy        263 GAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAA 322

Db        732 GGAATTGGTCCACTGATAT-TTAAAGGACCAGAAAGAACCCAAAAATAAGACCTTTCTAA 674

Qy        323 AATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTA 382

Db        673 GATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGACAATCAGTA 614

Qy        383 CCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTT 442

Db        613 CTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGT 554

Qy        443 GTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGT 502

Db        553 GCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAACAAGGAGTAT---GAGT 497

Qy        503 ACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTG 562

Db        496 ACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCTGAGGAGAGTCTGCCCATTG 437

Qy        563 AAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCA 622

Db        436 AGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCA 377

Qy        623 TCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATT 682

Db        376 TCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATT 317

Qy        683 CTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACT 742

Db        316 CTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACATTCCTACT 257

Qy        743 TCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGAC 802

Db        256 TCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGCAAGAGAGAAAAGAAAGATAGAG 197

Qy        803 TCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGC 862

Db        196 TCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGCAAAAATGCCAGCATTAGCGTGC 137

Qy        863 AAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 921

Db        136 GGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAATGGGCATCTGTGCCCTGCAGT 78
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RESULT 8
CD559451/c
LOCUS       CD559451                762 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496580 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971871 5', mRNA sequence.
ACCESSION   CD559451
VERSION     CD559451.2  GI:38453471
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585519.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 02
            High quality sequence start: 38
            High quality sequence stop: 761.
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                     /clone="IMAGE:6971871"
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                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match            32.6%;  Score 499.8;  DB 5;  Length 762;
  Best Local Similarity  86.9%;  Pred. No. 1.9e-134;
  Matches  573;  Conservative    0;  Mismatches   82;  Indels    4;  Gaps    2;

Qy        263 GAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAA 322
              | | ||||||||||||||| |||| ||| ||||||||| |||||||||||| || |||||
Db        753 GGAATTGGTCCACTGATAT-TTAAAGGACCAGAAAGAACCCAAAAATAAGACCTCTCTAA 695

Qy        323 AATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTA 382
              ||| ||||| ||||||||||||||||||||||||||||||||||||||||| |||||||||

Db        694 GATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGACAATCAGTA 635

Qy        383 CCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTT 442
              | ||||||| ||||| |||||||||||||||||||||| |||||||||||| |||||| |
Db        634 CTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGT 575

Qy        443 GTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGT 502
              | ||||| || |||||||| |||||||  |||||||| ||||||| ||| |||    |||
Db        574 GCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAACAAGGAGTAT---GAGT 518

Qy        503 ACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTG 562
              || |||||||||| ||||||| |||||||||||| ||||| |||||||| || |||||||
Db        517 ACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCTGAGGAGAGTCTGCCCATTG 458

Qy        563 AAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCA 622
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Db        457 AGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCA 398

Qy        623 TCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATT 682
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Db        397 TCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATT 338

Qy        683 CTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACT 742
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Db        337 CTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACATTCCTACT 278

Qy        743 TCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGAC 802
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Db        277 TCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGCAAGAGAGAAAAGAAAGATAGAG 218

Qy        803 TCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGC 862
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Qy        863 AAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 921
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RESULT 9
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LOCUS       DQ033872                762 bp    DNA     linear   GSS 02-JUN-2005
DEFINITION  Homo sapiens IL12A gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   DQ033872
VERSION     DQ033872.1  GI:66885081
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     A Scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
  JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
   PUBMED   15869325
REFERENCE   2  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.  Translation starts at the beginning of
            alignment.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
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  Best Local Similarity   89.7%;  Pred. No. 3.7e-133;
  Matches  532;  Conservative    0;  Mismatches   61;  Indels    0;  Gaps    0;

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Qy       1001 AAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTT 1060
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Db        227 AAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTTT 286

Qy       1061 ACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAG 1120
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Db        287 ACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAG 346

Qy       1121 TGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGA 1180
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Db        347 TGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGAGAGA 406

Qy       1181 TCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCC 1240
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Db        407 CCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATGGCCC 466

Qy       1241 TGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGA 1300
              |||||||||| ||||| ||||| ||||||||||||||||||||||||||||| ||||||
Db        467 TGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGA 526

Qy       1301 ATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAG 1360
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Db        527 ATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCAG 586

Qy       1361 CTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCT 1420
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Qy       1481 TCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
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RESULT 10
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LOCUS       DQ033873                762 bp    DNA     linear   GSS 02-JUN-2005
DEFINITION  Pan troglodytes IL12A gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   DQ033873
VERSION     DQ033873.1  GI:66885082
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     A Scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
  JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
   PUBMED   15869325
REFERENCE   2  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.  Translation starts at the beginning of
            alignment.
FEATURES             Location/Qualifiers
     source          1. .762
                     /organism="Pan troglodytes"
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                     /db_xref="taxon:9598"
     gene            <1. .>762
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                     /locus_tag="HC3464"
ORIGIN

  Query Match             32.0%;  Score 490.6;  DB 14;  Length 762;
  Best Local Similarity   89.2%;  Pred. No. 9.5e-132;
  Matches  529;  Conservative    0;  Mismatches   64;  Indels    0;  Gaps    0;

Qy        941 CTAGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCC 1000
              | |||||| | ||      | || |||  ||| || |||||||  |||||  |||||||||
Db        167 CCAGAAACCTCCCCGTGGCCACCCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCC 226

Qy       1001 AAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTT 1060
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Db        227 AAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTTT 286

Qy       1061 ACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAG 1120
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Db        287 ACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAG 346

Qy       1121 TGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGA 1180
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Db        347 TGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGAGAGA 406

Qy       1181 TCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCC 1240
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Qy       1241 TGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGA 1300
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Qy       1301 ATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAG 1360
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Db        527 ATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCAG 586

Qy       1361 CTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCT 1420
              ||||||||||||| | |||||||||||| ||||||||| |||||||||||| || ||||
Db        587 TTATTGACGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCT 646

Qy       1421 CCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTT 1480
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Db        647 CCCTTGAAGAACTGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTT 706

Qy       1481 TCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
              |||||||||| ||||||||  ||||| ||||||||||||||||||||||||
Db        707 TCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTCC 759


RESULT 11
CD559452/c
LOCUS       CD559452                754 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496548 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971870 5', mRNA sequence.
ACCESSION   CD559452
VERSION     CD559452.2  GI:38453473
```

```
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 754)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585520.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 01
            High quality sequence start: 130
            High quality sequence stop: 572.
FEATURES             Location/Qualifiers
     source          1. .754
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971870"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match           31.1%;  Score 477.4;  DB 5;  Length 754;
  Best Local Similarity   84.8%;  Pred. No. 7e-128;
  Matches  559;  Conservative    0;  Mismatches   96;  Indels    4;  Gaps    2;

Qy        263 GAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAA 322
              ||||||||||||  ||||||  ||||  |||  |||||||||  ||||||||||||  ||||||||
Db        752 GAATTTGGTCCAATGATAT-TTAAAGGACCAGAAAGAACCCAAAAATAAGACCTTTCTAA 694

Qy        323 AATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTA 382
               |||  |||||  ||||||||||||||||||||||||||||||||||||||||  |||||||||
Db        693 GATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGACAATCAGTA 634

Qy        383 CCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTT 442
              | |||||||  |||||  ||||||  ||||||||||||   | ||||||||||| ||||||  |
Db        633 CTGATTTGACATTCAGTGTCAAGAGCAGCAGAGGCTTTTTTGACCCCCAAGGGGTGACGT 574

Qy        443 GTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGT 502
              | |||||  ||  |||||||  |||||||  |||||||  ||||||||  |||  |||     |||
Db        573 GCGGAGCTGCTACACTCTTTGCAGAGAGAGTCAGAGGGGACAACAAGGAGTAT---GAGT 517

Qy        503 ACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTG 562
              ||  |||||||||  |||||||  ||||||||||||  ||||   ||||||||   | |||||||
Db        516 ACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGGTGAGGAGAGTTTGCCCATTG 457

Qy        563 AAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCA 622
              | |||  |||||||  ||   ||||||||||||||||  ||||||||||||||||||  ||  ||||
Db        456 AGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACCAGCAGGTTTTTCA 397

Qy        623 TCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATT 682
              ||||||||||||||||||  ||||||||||||||  ||||  ||||||||||||||  ||||
Db        396 TCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATT 337

Qy        683 CTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACT 742
              ||  ||||  |||||  ||  ||||||||  ||||||||||||||||||  ||  ||||||||||| |
Db        336 CTTGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACATTCCTAAT 277

Qy        743 TCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGAC 802
              | |||  | ||||||  ||||  |||||  ||||||||||  |||  ||||||||||||||  |||
Db        276 TTTCCCTGACATTTTGCGTTCAGGTTCAGGGCAAGAGCAAGAGAGAAAAGAAAGATAGAG 217

Qy        803 TCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGC 862
              | | |  ||||||||||||  |||||  ||||  |  ||||  |||  ||||||  ||  ||||||
Db        216 TTTTCACGGACAAGACCTTAGCCACGGTCATTTGCCGCAAAAATGCCAGCATTAGCGTGC 157

Qy        863 AAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 921
                |||   |||||  ||||||||||||||  ||||||  |  |||||||  |||  ||||||||
Db        156 GGGCCCAGGACCGGTACTATAGCTCATTTTGGAGCGAATGGGCATTTGTGCCCTGCAGT 98


RESULT 12
CD559449/c
LOCUS       CD559449                766 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496649 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971873 5', mRNA sequence.
ACCESSION   CD559449
VERSION     CD559449.2  GI:38453467
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 766)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585517.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 04
            High quality sequence stop: 641.
FEATURES             Location/Qualifiers
     source          1. .766
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971873"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
```

PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 30.8%; Score 471.8; DB 5; Length 766;
Best Local Similarity 85.6%; Pred. No. 3.1e-126;
Matches 537; Conservative 0; Mismatches 87; Indels 3; Gaps 1;

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Qy        295 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 354
              |  | || | ||  ||  |||||||| ||| ||||| ||||| ||||||||||||||||
Db        714 AGAAGAACCCAGAAATAGTACTTTCTAAGATGCGAGGCCAAGAAGTATTCTGGACGTTTC 655

Qy        355 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 414
              ||||| |||||||||||| |||||||||| ||||||| ||||| ||||||||||||||||
Db        654 ACCTGGTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 595

Qy        415 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 474
              ||||| |||||||||||||| |||||| || ||||| || |||||||| |||||||  |||
Db        594 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 535

Qy        475 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 534
              |||| |||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||
Db        534 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 478

Qy        535 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 594
              || ||||| |||||||| || |||||||| ||| ||||||| ||  ||||||||||||||
Db        477 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 418

Qy        595 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 654
              || ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        417 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 358

Qy        655 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 714
              ||| |||| |||||||||||||| |||||||||| ||||| || |||||||| ||||||
Db        357 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 298

Qy        715 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 774
              |||||||||| || |||||||||||||||||| | |||||  |||| ||||||||||||
Db        297 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 238

Qy        775 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 834
              |||| ||| |||||||||||||| ||| ||| |  |||||||||||||||| |||| |
Db        237 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 178

Qy        835 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 894
              |||| ||| |||||| || |||||| ||| |||||||||||||||||||| |||
Db        177 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 118

Qy        895 AGCAACTGGGCATCCGTGTCCTGCAGT 921
              ||| | |||||||| ||| ||||||||
Db        117 AGCGAATGGGCATCTGTGCCCTGCAGT 91
```

RESULT 13
AK162981
LOCUS AK162981 1839 bp mRNA linear HTC 21-SEP-2005
DEFINITION Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430014H12 product:interleukin 12b, full insert sequence.
ACCESSION AK162981
VERSION AK162981.1 GI:74188061
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
CONSRTM RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
PUBMED 11217851
REFERENCE 5
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,

Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420 (6915), 563-573 (2002)

PUBMED 12466851

REFERENCE 6

AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE The transcriptional landscape of the mammalian genome

JOURNAL Science 309 (5740), 1559-1563 (2005)

PUBMED 16141072

REFERENCE 7

AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.

CONSRTM RIKEN Genome Exploration Research Group

TITLE Antisense transcription in the mammalian transcriptome

JOURNAL Science 309 (5740), 1564-1566 (2005)

PUBMED 16141073

REFERENCE 8 (bases 1 to 1839)

AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

source 1. .1839
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/mol_type="mRNA"
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/dev_stage="0 day neonate"

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S"

ORIGIN

Query Match 30.5%; Score 468; DB 6; Length 1839;
Best Local Similarity 72.1%; Pred. No. 5.8e-125;
Matches 682; Conservative 0; Mismatches 225; Indels 39; Gaps 4;

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Db        124 ATGTGGGAGCTGGAGAAAGACGTTTATGTTGTAGAGGTGGACTGGACTCCCGATGCCCCT 183

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              |||||||  |||  |||||||||  | || ||||||||||||||||||||||||||||||
Db        184 GGAGAAACAGTGAACCTCACCTGTGACACGCCTGAAGAAGATGACATCACCTGGACCTCA 243

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Db        415 TTCAAAAACAAGACTTTCCTGAAGTGTGAAGCACCAAATTACTCCGGACGGTTCACGTGC 474

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

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Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

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Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Db        595 GACCAAAGGGACTATGAGAAGTATTCAGTGTCCTGCCAGGAGGATGTCACCTGCCCAACT 654

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Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Db        715 AACTACAGCACCAGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTG 774

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Db        775 CAGATGAAGCCTTTGAAGAACTC---ACAGGTGGAGGTCAGCTGGGAGTACCCTGACTCC 831

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Db        832 TGGAGCACTCCCCATTCCTACTTCTCCCTCAAGTTCTTTGTTCGAATCCAGCGCAAGAAA 891

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Db        952 ACATCTACCGAAGTCCAATG---CAAAGGCGGGAATGTCTGCGTGCAAGCTCAGGATCGC 1008

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Db       1009 TATTACAATTCCTCATGCAGCAAGTGGGCATGTGTTCCCTGCAGGG 1054


RESULT 14
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DEFINITION  AGENCOURT_14496684 NIH_MGC_195 Homo sapiens cDNA clone
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ACCESSION   CD559602
VERSION     CD559602.2  GI:38558930
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 745)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585670.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 05
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                     /lab_host="DH5A (T1 phage-resistant)"
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                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
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                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match           30.1%;  Score 461.8;  DB 5;  Length 745;
  Best Local Similarity   86.2%;  Pred. No. 2.6e-123;
  Matches  535;  Conservative    0;  Mismatches   82;  Indels    4;  Gaps    2;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

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Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Db        132 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 191

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

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Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

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Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Db        432 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 491

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Db        492 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 551

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Db        552 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 608

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RESULT 15
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LOCUS AK155593 2908 bp mRNA linear HTC 21-SEP-2005
DEFINITION Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F730005O03 product:interleukin 12b, full insert sequence.
ACCESSION AK155593
VERSION AK155593.1 GI:74212721
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
CONSRTM RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
PUBMED 11217851
REFERENCE 5
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
CONSRTM FANTOM Consortium
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420 (6915), 563-573 (2002)
PUBMED 12466851
REFERENCE 6
AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.
CONSRTM FANTOM Consortium
TITLE The transcriptional landscape of the mammalian genome
JOURNAL Science 309 (5740), 1559-1563 (2005)
PUBMED 16141072

```
REFERENCE   7
  AUTHORS   Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M.,
            Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H.,
            Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T.,
            Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L.,
            Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A.,
            Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and
            Wahlestedt,C.
  CONSRTM   RIKEN Genome Exploration Research Group
  TITLE     Antisense transcription in the mammalian transcriptome
  JOURNAL   Science 309 (5740), 1564-1566 (2005)
   PUBMED   16141073
REFERENCE   8  (bases 1 to 2908)
  AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K.,
            Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S.,
            Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N.,
            Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D.,
            Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
            Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
            Trust/MRC building Addenbrookes Hospital Cambridge) whose
            assistance we gratefully acknowledge.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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; Sequence 43, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)
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; Sequence 45, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
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US-09-917-265A-45

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Db        453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
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Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
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Db        333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
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Db        273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
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Db        213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

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Db        153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
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Db         33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
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RESULT 3
US-09-917-265A-38
; Sequence 38, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-09-917-265A-38

  Query Match            100.0%;  Score 1533;  DB 3;  Length 1599;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1533;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
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Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
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Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026

Qy        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
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Db       1027 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1086

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Db       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1146

Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
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Db       1147 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1266

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
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Db       1267 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1326

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
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Db       1327 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1386

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
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Db       1387 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1446

Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
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Db       1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1506

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Db       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1566

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Db       1567 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599


RESULT 4
US-09-917-265A-40/c
; Sequence 40, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-40

  Query Match            100.0%;  Score 1533;  DB 3;  Length 1599;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1533;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

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Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

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Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
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Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

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Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
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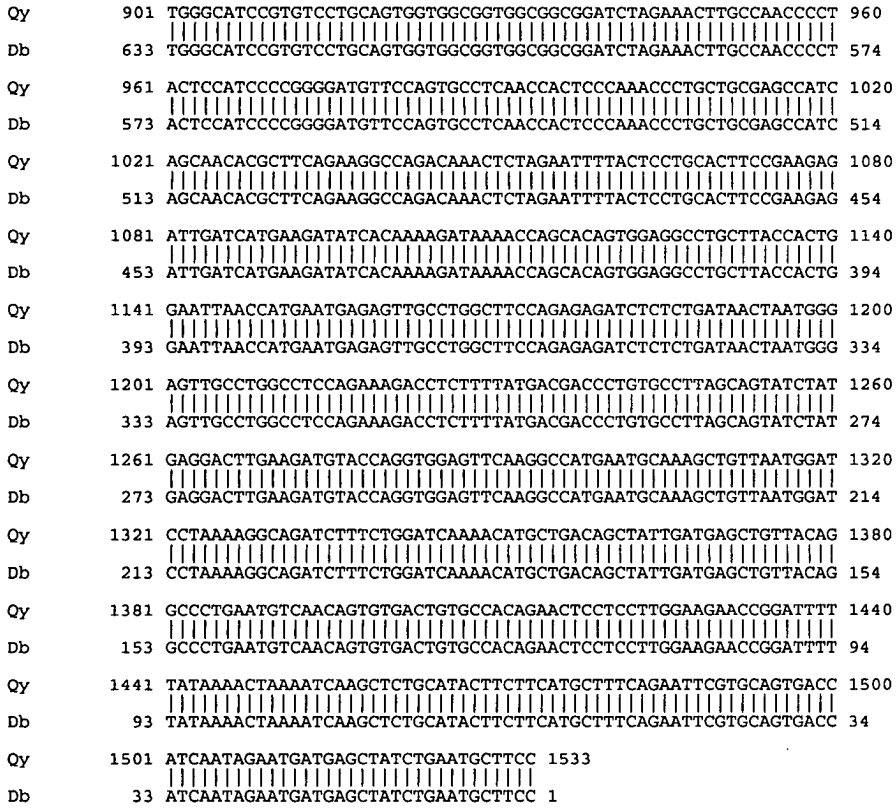
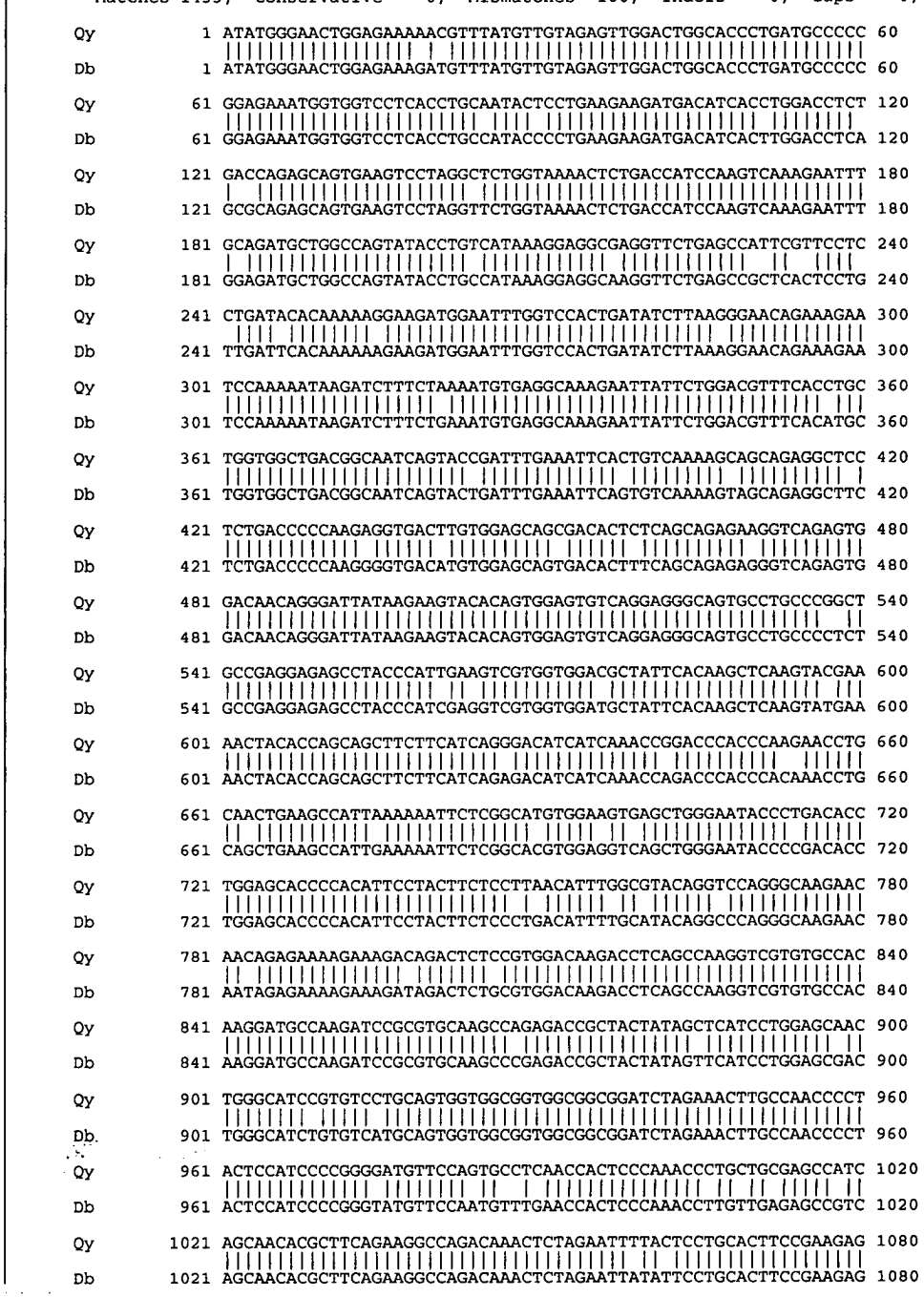


RESULT 5
US-09-917-265A-66
; Sequence 66, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)
US-09-917-265A-66

Query Match 89.6%; Score 1373; DB 3; Length 1533;
Best Local Similarity 93.5%; Pred. No. 0;



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Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
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Db       1081 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
             ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||
Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1200

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
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Db       1201 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1260

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
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Db       1261 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1320

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
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Db       1321 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 1380

Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
             ||||||||| |||||||||||||||||||||||||| |||||| | ||||| |||||||||
Db       1381 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1440

Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
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Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1500

Qy       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
             ||||||||||||||| ||| |||| |||||
Db       1501 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1533


RESULT 6
US-09-917-265A-68/c
; Sequence 68, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-68

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  Best Local Similarity   93.5%;  Pred. No. 0;
  Matches 1433;  Conservative    0;  Mismatches  100;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              |||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
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Db       1233 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              |||||||||||||||||||||||| |||||||||||| ||||||||| |||||||||| |
Db       1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| |||||| |||||| ||||||||| ||||||||| ||||||||||
Db       1113 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              |||||||||||||||||||| || |||||||||| |||||||||||||||||||| |||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              |||||||||||||||||||||||||||||||| |||||||||||| |||||||||| ||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              || |||||||||| |||||||||||||| ||||| || |||||||||||||| ||||||
Db        873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              |||||||||||||||||||||||||||| | |||||| || |||||| ||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || |||||||||||||| ||||||| |||||||||||||||||||||||||||||||||
Db        753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              |||||||||||||||||||||||||||| |||||||||||||||| |||||||||||| ||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
              |||||||| ||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
              |||||||||||||| |||||||| ||  | |||||||||||||||| || || ||||| ||
Db        573 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 514

Qy       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
              |||||||||||||||||||||||||||||||||||||||| || ||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 454

Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 334

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
              |||||||||||||  ||||| |||||||||||||  ||||||||||||||| ||||||
Db        333 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 274

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
              |||||||||||||||||||| |||| |||||||||||||| |||||||| |||||||||
```

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Db        273 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 214

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
              || || |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        213 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 154

Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
              ||||||||| |||||||||||||||||||||||||||| |||||| | ||||| |||||||||
Db        153 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 94

Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db          93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 34

Qy       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
              ||||||||||||||||  |||  ||||  |||||
Db          33 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1


RESULT 7
US-09-917-265A-61
; Sequence 61, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-09-917-265A-61

  Query Match             89.6%;  Score 1373;  DB 3;  Length 1599;
  Best Local Similarity   93.5%;  Pred. No. 0;
  Matches 1433;  Conservative    0;  Mismatches  100;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              |||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              |||||||||||||||||||||||| |||| |||||||||||||||||||| ||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              |  |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db        187 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              | |||||||||||||||||||| |||||||||||| ||||||||||   ||  ||||
Db        247 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              |||| |||||||| |||||||||||||||||||||||||||||||| ||||||||||||||
Db        307 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||| |||
Db        367 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              |||||||||||||||||||||||| |||||||||||| ||||||||| |||||||||| |
Db        427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| |||||| |||||||||| |||||| |||||||||| ||||||||||
Db        487 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              |||||||||||||||||| || |||||||||| |||||||||||||||||||| |||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              |||||||||||||||||||||||||||||||| |||||||||||||| ||||||||| ||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              || |||||||||| |||||||||||||| ||||| || |||||||||||||| ||||||
Db        727 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              |||||||||||||||||||||||||| | |||||| || |||||| ||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || |||||||||||||||| ||||||| |||||||||||||||||||||||||||||||
Db        847 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              |||||||||||||||||||||||||||| |||||||||||||||| |||||||||||| ||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
              |||||||| |||| |||||||||||||||||||||||||||||||||||||||||||||||
Db        967 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026

Qy        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
              |||||||||||||| |||||||| ||  | |||||||||||||||| || || |||| ||
Db       1027 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 1086

Qy       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
              |||||||||||||||||||||||||||||||||||||||| || ||||||||||||||||
Db       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 1146

Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1147 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||| |||
Db       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1266

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
              |||||||||||||  ||||| ||||||||||||||  |||||||||||||||| ||||||
Db       1267 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1326

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
              |||||||||||||||||||| |||| |||||||||||||| |||||||| |||||||||
Db       1327 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1386

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
              || || |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       1387 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 1446

Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
              ||||||||| |||||||||||||||||||||||||||| |||||| | ||||| |||||||||
Db       1447 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1506

Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
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Db       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1566

Qy       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
                ||||||||||||||||  |||  ||||  |||||
Db       1567 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1599


RESULT 8
US-09-917-265A-63/c
; Sequence 63, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-63

  Query Match             89.6%;  Score 1373;  DB 3;  Length 1599;
  Best Local Similarity   93.5%;  Pred. No. 0;
  Matches 1433;  Conservative    0;  Mismatches  100;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              |||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              |||||||||||||||||||||||| |||| |||||||||||||||||||| ||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              | |||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db       1413 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              | |||||||||||||||||||| |||||||||||  ||   ||||
Db       1353 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
               |||| |||||||| |||||||||||||||||||||||||||||||| ||||||||||||
Db       1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||| |||
Db       1233 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              |||||||||||||||||||| |||||||||||| |||||||||| |||||||||| | |
Db       1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||||| |||||| |||||||||| |||||| |||||||||| ||||||||||
Db       1113 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              |||||||||||||||||||| || |||||||||| |||||||||||||||||||| |||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              |||||||||||||||||||||||||| |||||||||||||| ||||||||||  ||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              || |||||||||| |||||||||||||| ||||| || ||||||||||||||| ||||||
Db        873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              |||||||||||||||||||||||||| | |||||| || |||||| ||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || |||||||||||||| ||||||| ||||||||||||||||||||||||||||||||||
Db        753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              |||||||||||||||||||||||||| |||||||||||||| |||||||||||| ||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
              |||||||| ||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
              |||||||||||||| |||||||| ||  | |||||||||||||| || || ||||| ||
Db        573 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 514

Qy       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
              |||||||||||||||||||||||||||||||||||||| || ||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 454

Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 334

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
              |||||||||||||  ||||| ||||||||||||||  ||||||||||||||| ||||||
Db        333 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 274

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
              |||||||||||||||||||| |||| |||||||||||||| |||||||| |||||||||
Db        273 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 214

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
              || || |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 154

Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
              ||||||||| |||||||||||||||||||||||| |||||| | ||||| |||||||||
Db        153 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 94

Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 34

Qy       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
              ||||||||||||||||  |||  ||||  |||||
Db         33 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1


RESULT 9
US-08-751-767A-11
; Sequence 11, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
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;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1560 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1557
US-08-751-767A-11

  Query Match             78.2%;  Score 1198.2;  DB 2;  Length 1560;
  Best Local Similarity   86.8%;  Pred. No. 0;
  Matches 1352;  Conservative    0;  Mismatches  178;  Indels   27;  Gaps    2;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||| ||||| | |||||||| ||||| ||||| ||| | || ||||||||
Db          4 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 63

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              |||||||||||||||||||||  | || ||||||||||||  ||||||||||||
Db         64 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 123

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              |||||||||||||| ||| |||||||||| ||||| ||||||||||||||||||||| |||
Db        124 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 183

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              | ||||||||||||||| |||||||| |||||||||||||||| ||||||||| ||||
Db        184 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 243

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||| | ||||||||||||||||||||||||||||||||||| |||| ||| |||||||||
Db        244 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 303

Qy        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              |||||||||||| |||||||| ||| ||||| ||||||||||||||||||||||||||||
Db        304 CCCAAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 363

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              |||||||||||| |||||||| ||||||| ||||| ||||||||||||||||||||||
Db        364 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 423

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| |||||| || ||||| || |||||||| ||||||| |||||||| |
Db        424 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 483

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||| ||| |||    ||||| |||||||||| ||||||| |||||||||||| |||
Db        484 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              || |||||||| || |||||||| ||| ||||||| ||  ||||||||||||||| |||
Db        541 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||| ||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              || |||||||||||||| |||||||||| ||||| || |||||||| ||||||||||
Db        661 CAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||| || |||||||||||||||||| | |||||  |||| ||||||||||||||||| |
Db        721 TGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || |||||||||||||| ||| ||| |  |||||||||||||||||| |||| | |||| |
Db        781 AAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||  ||||||  ||  ||||||  |||  ||||||||||||||||||||||  |||||| |
Db        841 AAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAA 900

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGT----------------------GGCGGC 936
              |||||||| ||| ||||||||||||||||                      || |||
Db        901 TGGGCATCTGTGCCCTGCAGTGGTGGCGGTGGAAGCGGCGGTGGCGGAAGCGGCGGTGGC 960

Qy        937 GGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCAC 996
              ||    |||||| | ||    | ||||||  ||| || |||||||  |||||  |||||
Db        961 GGCAGCAGAAACCTCCCCCTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCAC 1020

Qy        997 TCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAA 1056
              ||||||| ||||||| | ||| |||||||| ||| ||||||||||||||||||||||||
Db       1021 TCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAA 1080

Qy       1057 TTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGC 1116
              |||||| | |||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1081 TTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGC 1140

Qy       1117 ACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGA 1176
              |||||||||||||  |||||| |||||||||||||||  |||||||
Db       1141 ACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGA 1200

Qy       1177 GAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACG 1236
              |||| |||| | ||||||||||||||||||||||||||||||||||||||||||||| |
Db       1201 GAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATG 1260

Qy       1237 ACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCC 1296
              |||||||||||||  |||||  ||||| ||||||||||||||||||||||||||||| ||
Db       1261 GCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACC 1320

Qy       1297 ATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 1356
              |||||||||||||  | ||||||||||  |||||||||||||  ||||||||||||||
Db       1321 ATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTG 1380

Qy       1357 ACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAAC 1416
              ||| |||||||||||| | |||||||||| ||||||||| |||||||||||||||| ||
Db       1381 GCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAA 1440

Qy       1417 TCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1476
              |||||| | |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1500

Qy       1477 GCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
              |||||||||||||| |||||||| ||  | ||| ||| ||||||||||||||||||
Db       1501 GCTTTCAGAATTCGGGCAGTGACTATTGACAGAGTGACGAGCTATCTGAATGCTTCC 1557
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RESULT 10
US-08-751-767A-9
; Sequence 9, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;     APPLICANT:  ANDERSON, ROBERT J.
;     APPLICANT:  GRANT, HUGH
;     APPLICANT:  MACDONALD, IAN D.
;     TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;     NUMBER OF SEQUENCES:  80
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  NIXON & VANDERHYE P.C.
;       STREET:  1100 NORTH GLEBE ROAD
;       CITY:  ARLINGTON
;       STATE:  VA
;       COUNTRY:  USA
;       ZIP:  22201
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/751,767A
;       FILING DATE:  08-NOV-1996
;       CLASSIFICATION:  536
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  SADOFF, B.J.
;       REGISTRATION NUMBER:  36,663
;       REFERENCE/DOCKET NUMBER:  117-221
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  7038164091
;       TELEFAX:  7038164100
;   INFORMATION FOR SEQ ID NO:  9:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1623 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..1620
US-08-751-767A-9

  Query Match             78.2%;  Score 1198.2;  DB 2;  Length 1623;
  Best Local Similarity   86.8%;  Pred. No. 0;
  Matches 1352;  Conservative    0;  Mismatches  178;  Indels   27;  Gaps    2;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||  |||||  |  ||||||||  |||||  |||||  |||  |  ||  ||||||||
Db         67 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||  | ||  ||||||||||||||  ||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              |||||||||||||| |||  ||||||||||  |||||  ||||||||||||||||||| |||
Db        187 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              | ||||||||||||||| ||||||| ||||||||||||||||| |||||||| ||||
Db        247 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||| | |||||||||||||||||||||||||||||||||| |||| ||| |||||||||
Db        307 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 366

Qy        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||| |||||||| ||| ||||| ||||||||||||||||||||||||||||||
Db        367 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              |||||||||||| |||||||||| ||||||| ||||| |||||||||||||||||||||||
Db        427 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| |||||| || ||||| || |||||||| |||||||  |||||||  |
Db        487 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||| ||| |||    ||||| |||||||||| ||||||| |||||||||||| |||
Db        547 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 603

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              || |||||||| || |||||||| ||| ||||||| ||  |||||||||||||||| |||
Db        604 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAA 663

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Db        664 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTG 723

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              || |||||||||||||| |||||||||| |||||  || |||||||| ||||||||||||
Db        724 CAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACC 783

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              |||||  ||  |||||||||||||||||  |  |||||  ||||  |||||||||||||| |
Db        784 TGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGC 843

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || |||||||||||||| ||| ||| |  ||||||||||||||||| |||| | |||| |
Db        844 AAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGC 903

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||  ||||||  ||  ||||||  |||  |||||||||||||||||||| |||||| |
Db        904 AAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAA 963

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGT----------------------GGCGGC 936
              ||||||||  |||  |||||||||||||||||                    ||  |||
Db        964 TGGGCATCTGTGCCCTGCAGTGGTGGCGGTGGAAGCGGCGGTGGCGGAAGCGGCGGTGGC 1023

Qy        937 GGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCAC 996
              ||     ||||||  | ||      | ||||||  |||  || |||||||  |||||  |||||
Db       1024 GGCAGCAGAAACCTCCCCCTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCAC 1083

Qy        997 TCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAA 1056
              |||||||  |||||||  | |||  |||||||||  |||  |||||||||||||||||||||||
Db       1084 TCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAA 1143

Qy       1057 TTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGC 1116
              ||||||  |||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db       1144 TTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGC 1203

Qy       1117 ACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGA 1176
              |||||||||||||| ||||||  |||||||||||| ||||||||||||||    |||||||
Db       1204 ACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGA 1263

Qy       1177 GAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACG 1236
              |||| |||| | ||||||||||||||||||||||||||||||||||||||||||||| |
Db       1264 GAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATG 1323

Qy       1237 ACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCC 1296
              |||||||||||| |||||  ||||| |||||||||||||||||||||||||||||||| ||
Db       1324 GCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACC 1383

Qy       1297 ATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 1356
              |||||||||||||  | |||||||||| |||||||||||||| ||||||||||||||||
Db       1384 ATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTG 1443

Qy       1357 ACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAAC 1416
              |||  |||||||||||| | |||||||||||  |||||||||  |||||||||||| ||
Db       1444 GCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAA 1503

Qy       1417 TCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1476
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Db       1504 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1563

Qy       1477 GCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
              ||||||||||||||| |||||||| ||   | ||| ||| ||||||||||||||||||
Db       1564 GCTTTCAGAATTCGGGCAGTGACTATTGACAGAGTGACGAGCTATCTGAATGCTTCC 1620


RESULT 11
US-08-751-767A-7
; Sequence 7, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6139 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3222..4841
US-08-751-767A-7

  Query Match             78.2%;  Score 1198.2;  DB 2;  Length 6139;
  Best Local Similarity   86.8%;  Pred. No. 0;
  Matches 1352;  Conservative    0;  Mismatches  178;  Indels   27;  Gaps    2;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              |||||||||||| ||||| | |||||||| ||||| ||||| ||| | || ||||||||
Db       3288 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 3347

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              |||||||||||||||||||||||  | || ||||||||||||  ||||||||||||
Db       3348 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 3407

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              |||||||||||||| ||| |||||||||| ||||| |||||||||||||||||||| |||
Db       3408 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 3467

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              | |||||||||||||| |||||||| |||||||||||||||| ||||||||| ||||
Db       3468 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 3527

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||| | |||||||||||||||||||||||||||||||||||||||| |||| ||| |||||||||
Db       3528 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 3587

Qy        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              |||||||||||| |||||||| ||| ||||| |||||||||||||||||||||||||||||
Db       3588 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 3647

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              |||||||||||| |||||||||| ||||||| ||||| ||||||||||||||||||||||
Db       3648 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 3707

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| |||||| || ||||| || |||||||| |||||||  ||||||| |
Db       3708 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 3767

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||| ||| |||     ||||| |||||||||| ||||||| |||||||||||| |||
Db       3768 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 3824

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              || |||||||| || |||||||| ||| ||||||| ||  |||||||||||||||| |||
Db       3825 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAA 3884

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Db       3885 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTG 3944

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              || |||||||||||||| |||||||||| ||||| || |||||||| ||||||||||||
Db       3945 CAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACC 4004

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||| || |||||||||||||||||| | |||||  |||| ||||||||||||||| |
Db       4005 TGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGC 4064

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || |||||||||||||| ||| ||| |  |||||||||||||||| |||| | |||| |
Db       4065 AAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGC 4124

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||  ||||||  ||  ||||||  |||   |||||||||||||||||||| |||||| |
Db       4125 AAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAA 4184

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGT----------------------GGCGGC 936
              ||||||| ||| |||||||||||||||                      || |||
Db       4185 TGGGCATCTGTGCCCTGCAGTGGTGGCGGTGGAAGCGGCGGTGGCGGAAGCGGCGGTGGC 4244

Qy        937 GGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCAC 996
              ||    |||||| | ||     | ||||||  ||| || |||||||  |||||  |||||
Db       4245 GGCAGCAGAAACCTCCCCCTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCAC 4304

Qy        997 TCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAA 1056
              ||||||| ||||||| | ||| ||||||||| ||| ||||||||||||||||||||||||
Db       4305 TCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAA 4364

Qy       1057 TTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGC 1116
              |||||| | |||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       4365 TTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGC 4424

Qy       1117 ACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGA 1176
              |||||||||||||| |||||| |||||||||||| ||||||||||||   |||||||
Db       4425 ACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGA 4484

Qy       1177 GAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACG 1236
              |||| |||| | ||||||||||||||||||||||||||||||||||||||||||||| |
Db       4485 GAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATG 4544

Qy       1237 ACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCC 1296
              |||||||||||| ||||| ||||| |||||||||||||||||||||||||||||| ||
Db       4545 GCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACC 4604

Qy       1297 ATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 1356
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              |||||||||||||||  | ||||||||||| |||||||||||||| ||||||||||||||||
Db       4605 ATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTG 4664

Qy       1357 ACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAAC 1416
              ||| |||||||||||||| | |||||||||||| |||||||| |||||||||||| ||
Db       4665 GCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAA 4724

Qy       1417 TCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1476
              |||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4725 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 4784

Qy       1477 GCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
              |||||||||||||| |||||||| ||   | ||| ||| ||||||||||||||||||
Db       4785 GCTTTCAGAATTCGGGCAGTGACTATTGACAGAGTGACGAGCTATCTGAATGCTTCC 4841


RESULT 12
US-09-917-265A-26
; Sequence 26, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(921)
US-09-917-265A-26

  Query Match             60.1%;  Score 921;  DB 3;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-287;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 13
US-09-917-265A-28/c
; Sequence 28, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-28

  Query Match             60.1%;  Score 921;  DB 3;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-287;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCAGT 1


RESULT 14
US-09-011-143-6
; Sequence 6, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  921 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-6

  Query Match             60.0%;  Score 919.4;  DB 3;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 7e-287;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
                |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 15
US-09-302-495-6
; Sequence 6, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-302-495-6

  Query Match            60.0%;  Score 919.4;  DB 3;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 7e-287;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Job time : 331.925 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3		1533	100.0	1533	9	US-10-821-670-43	Sequence 43, Appl
c 4		1533	100.0	1533	9	US-10-821-670-45	Sequence 45, Appl
5		1533	100.0	1599	3	US-09-917-265-38	Sequence 38, Appl
c 6		1533	100.0	1599	3	US-09-917-265-40	Sequence 40, Appl
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c 10		1373	89.6	1533	3	US-09-917-265-68	Sequence 68, Appl
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c 12		1373	89.6	1533	9	US-10-821-670-68	Sequence 68, Appl
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24		1193.8	77.9	8644	3	US-09-828-825-13	Sequence 13, Appl
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39		917.4	59.8	985	3	US-09-917-265-55	Sequence 55, Appl
c 40		917.4	59.8	985	3	US-09-917-265-57	Sequence 57, Appl
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43		916.2	59.8	990	7	US-10-041-672C-1	Sequence 1, Appli
44		916.2	59.8	4522	7	US-10-041-672C-10	Sequence 10, Appl
45		825	53.8	921	3	US-09-917-265-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1
US-09-917-265-43
; Sequence 43, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)
; OTHER INFORMATION:
US-09-917-265-43

Query Match 100.0%; Score 1533; DB 3; Length 1533;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265-45

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy       901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       633 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy       961 ACTCCATCCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       573 ACTCCATCCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy      1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy      1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy      1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy      1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy      1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy      1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy      1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy      1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34
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Qy      1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
            |||||||||||||||||||||||||||||||||
Db        33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
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RESULT 3
US-10-821-670-43
; Sequence 43, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)
US-10-821-670-43

Query Match 100.0%; Score 1533; DB 9; Length 1533;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy        961 ACTCCATCCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020

Qy       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080

Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380

Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440

Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500

Qy       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
              |||||||||||||||||||||||||||||||||
Db       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
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RESULT 4
US-10-821-670-45/c
; Sequence 45, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
US-10-821-670-45

Query Match 100.0%; Score 1533; DB 9; Length 1533;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
              |||||||||||||||||||||||||||||||||
Db          33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
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RESULT 5
US-09-917-265-38
; Sequence 38, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
US-09-917-265-38

  Query Match           100.0%;  Score 1533;  DB 3;  Length 1599;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1533;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026

Qy        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1027 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1086

Qy       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1146

Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1147 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1266

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1267 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1326

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1327 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1386

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1387 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1446

Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1506

Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1566

Qy       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
             |||||||||||||||||||||||||||||||||
Db       1567 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599


RESULT 6
US-09-917-265-40/c
; Sequence 40, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-40

  Query Match            100.0%;  Score 1533;  DB 3;  Length 1599;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1533;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
             |||||||||||||||||||||||||||||||||
Db          33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
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RESULT 7
US-10-821-670-38
; Sequence 38, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1599)
US-10-821-670-38

Query Match 100.0%; Score 1533; DB 9; Length 1599;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026

Qy        961 ACTCCATCCCCGGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1086

Qy       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1146

Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1147 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1266

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1267 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1326

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1327 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1386

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
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Db       1387 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1446

Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
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Db       1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1506

Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1566

Qy       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
             |||||||||||||||||||||||||||||||||
Db       1567 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599


RESULT 8
US-10-821-670-40/c
; Sequence 40, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-40

  Query Match             100.0%;  Score 1533;  DB 9;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1533;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
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Db       1233 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
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Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
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Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
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Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
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Db        333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
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Db        213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
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Db        153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
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RESULT 9
US-09-917-265-66
; Sequence 66, Application US/09917265
; Patent No. US20020052030A1
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; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
;   OTHER INFORMATION:
US-09-917-265-66

  Query Match             89.6%;  Score 1373;  DB 3;  Length 1533;
  Best Local Similarity   93.5%;  Pred. No. 0;
  Matches 1433;  Conservative    0;  Mismatches  100;  Indels    0;  Gaps    0;

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Db          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
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Db         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Db        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Db        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Db        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
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Db        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
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Db        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Db        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540

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Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              || |||||||||| |||||||||||||| ||||| || |||||||||||||| ||||||
Db        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
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Db        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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Db        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
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Db        901 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
              |||||||||||||| |||||||| ||  | ||||||||||||||| || || ||||| ||
Db        961 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 1020

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              |||||||||||||||||||||||||||||||||||||||||||| || ||||||||||||
Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 1080

Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
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Db       1081 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
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Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1200

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
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Db       1201 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1260

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
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Db       1261 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1320

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Db       1381 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1440

Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
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Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1500

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Db       1501 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1533


RESULT 10
US-09-917-265-68/c
; Sequence 68, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
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;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-68

  Query Match             89.6%;  Score 1373;  DB 3;  Length 1533;
  Best Local Similarity   93.5%;  Pred. No. 0;
  Matches 1433;  Conservative    0;  Mismatches  100;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              |||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||
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Db       1473 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1414

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Db       1413 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Db       1353 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
               |||| |||||||| |||||||||||||||||||||||||||||| ||||||||||||
Db       1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||| |||
Db       1233 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              |||||||||||||||||| ||||||||||||| |||||||| |||||||||| |
Db       1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Db       1113 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Db       993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              |||||||||||||||||||||||| |||||||||||| |||||||||   ||||||
Db       933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              || |||||||||| |||||||||||||| ||||| || |||||||||||||| ||||||
Db       873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              |||||||||||||||||||||||||| | |||||| || |||||| ||||||||||||||
Db       813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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Db       753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
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Db       693 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
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Db       633 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
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Db       573 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 514

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Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 454

Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
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Db        453 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||| |||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 334

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
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Db        333 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 274

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
              |||||||||||||||||||| |||| |||||||||||||| |||||||| |||||||||
Db        273 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 214

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
              || || |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        213 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 154

Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
              ||||||||| |||||||||||||||||||||||| |||||| | ||||| |||||||||
Db        153 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 94

Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
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Db          93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 34

Qy       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
              |||||||||||||||  |||  ||||  |||||
Db          33 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1


RESULT 11
US-10-821-670-66
; Sequence 66, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-10-821-670-66

  Query Match             89.6%;  Score 1373;  DB 9;  Length 1533;
  Best Local Similarity   93.5%;  Pred. No. 0;
  Matches 1433;  Conservative    0;  Mismatches  100;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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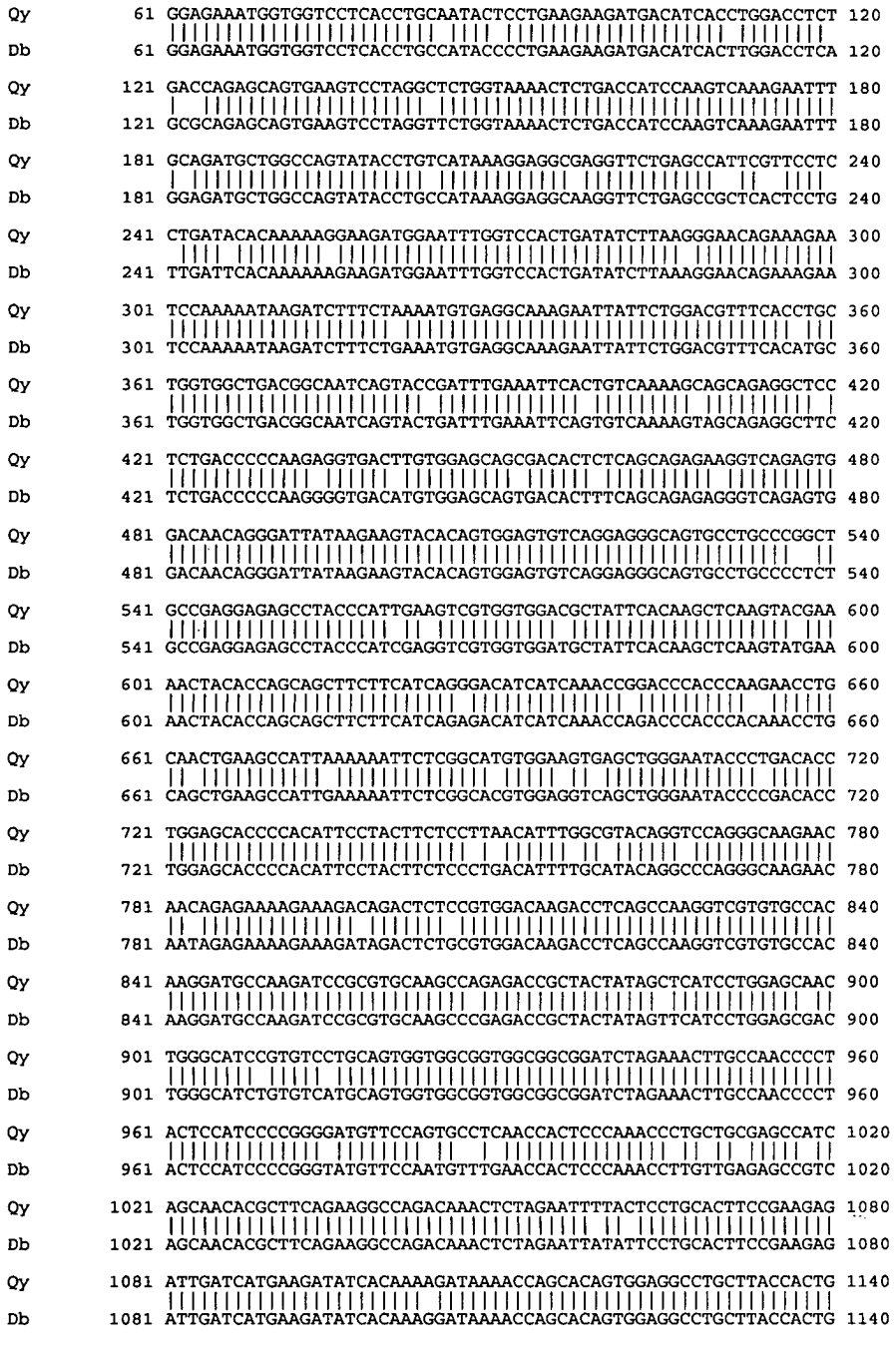

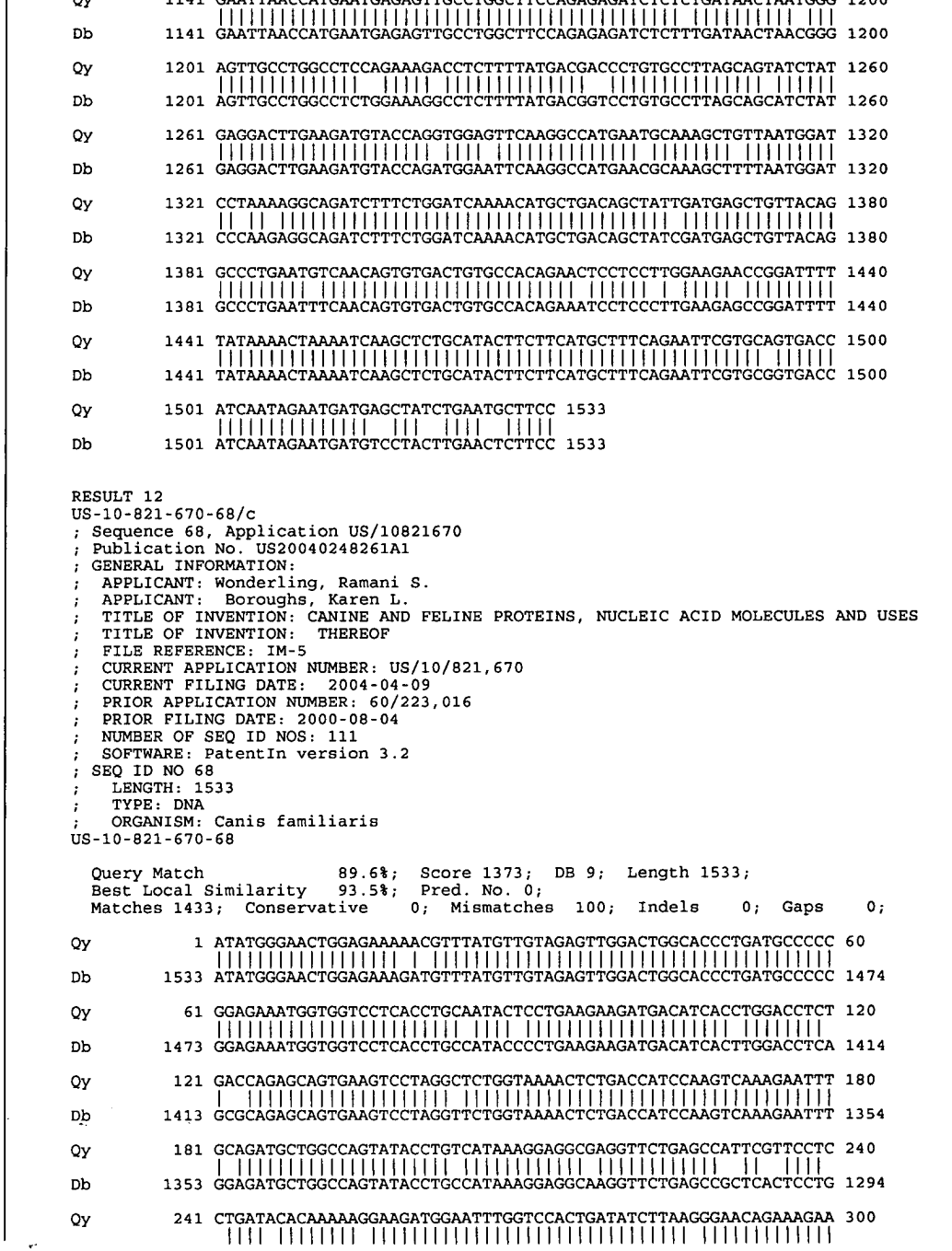

RESULT 12
US-10-821-670-68/c
; Sequence 68, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-821-670-68

Query Match 89.6%; Score 1373; DB 9; Length 1533;
Best Local Similarity 93.5%; Pred. No. 0;
Matches 1433; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

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Db       1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||| |||
Db       1233 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              |||||||||||||||||||| |||||||||||| ||||||||| |||||||||| |
Db       1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||| |||||| |||||||||| |||||| |||||||||| ||||||||||
Db       1113 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              |||||||||||||||||| || |||||||||| |||||||||||||||||||||| |||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              |||||||||||||||||||||||| |||||||||||||| ||||||||||   ||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              || |||||||||||| |||||||||||||| ||||| || |||||||||||||| ||||||
Db        873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              |||||||||||||||||||||||||| | |||||| || |||||| ||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              || |||||||||||||| ||||||| ||||||||||||||||||||||||||||||||||
Db        753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              |||||||||||||||||||||||||| |||||||||||||||| |||||||||||| ||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
              |||||||||||||| |||||||| ||  | ||||||||||||||| || || ||||| ||
Db        573 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 514

Qy       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
              |||||||||||||||||||||||||||||||||||| || ||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 454

Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 334

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260
              |||||||||||||| ||||| |||||||||||||| |||||||||||||| ||||||
Db        333 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 274

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
              |||||||||||||||||||| |||| |||||||||||||| |||||||| |||||||||
Db        273 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 214

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380
              || || |||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        213 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 154
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Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440
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Db        153 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 94

Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db          93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 34

Qy       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
              ||||||||||||||| ||| |||| |||||
Db          33 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1
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RESULT 13
US-09-917-265-61
; Sequence 61, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1599)
; OTHER INFORMATION:
US-09-917-265-61

Query Match 89.6%; Score 1373; DB 3; Length 1599;
Best Local Similarity 93.5%; Pred. No. 0;
Matches 1433; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

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Db         67 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
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Db        127 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Db        187 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              | |||||||||||||||||||| |||||||||||| |||||||||||| || ||||
Db        247 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Db        307 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||| |||
Db        367 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              |||||||||||||||||||| |||||||||||| ||||||||| |||||||||| |
Db        427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Db        487 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Db        727 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Db        787 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Db        847 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

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Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

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Qy        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020

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Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Db       1147 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200

Db       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1266

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260

Db       1267 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1326

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320

Db       1327 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1386

Qy       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380

Db       1387 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 1446

Qy       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440

Db       1447 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1506

Qy       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500

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Qy       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533

Db       1567 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1599
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RESULT 14
US-09-917-265-63/c
; Sequence 63, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-63

  Query Match            89.6%;  Score 1373;  DB 3;  Length 1599;
  Best Local Similarity  93.5%;  Pred. No. 0;
  Matches 1433;  Conservative    0;  Mismatches  100;  Indels    0;  Gaps    0;

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Db       1473 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Db       1413 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Db       1353 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Db       1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Db       1233 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Db       1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Db       1113 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

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Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
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Db        873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Db        813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Db        753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

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Qy        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

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Qy        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020

Db        573 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 514

Qy       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080

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Db        453 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200

Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 334

Qy       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260

Db        333 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 274

Qy       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320

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RESULT 15
US-10-821-670-61
; Sequence 61, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-10-821-670-61

  Query Match             89.6%;  Score 1373;  DB 9;  Length 1599;
  Best Local Similarity   93.5%;  Pred. No. 0;
  Matches 1433;  Conservative    0;  Mismatches  100;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

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Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

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Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

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Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Db        847 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

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Db        967 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026

Qy        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020
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Qy       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080
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Qy       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140
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Search completed: June 10, 2006, 18:16:37
Job time : 1750.73 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2006, 22:28:48 ; Search time 515.581 Seconds
(without alignments)
9006.379 Million cell updates/sec

Title: US-10-821-670A-32
Perfect score: 666
Sequence: 1 atgtgcccgccgcgtggcct.....tgagctatctgaatgcttcc 666

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 5244920 seqs, 3486124231 residues

Word size : 1

Total number of hits satisfying chosen parameters: 10489196

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 200 summaries

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1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
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7: geneseqn2002bs:*
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9: geneseqn2003bs:*
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11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	666	100.0	666	6	ABK98947	Abk98947 Feline in
	2	666	100.0	666	6	ABK98946	Abk98946 Feline in
	3	666	100.0	666	14	ADV34685	Adv34685 Feline si
c	4	666	100.0	666	14	ADV34687	Adv34687 Feline si
	5	602	90.4	1441	2	AAV56628	Aav56628 Feline FL
	6	558	83.8	561	6	ABK99001	Abk99001 Feline in
c	7	558	83.8	561	6	ABK99002	Abk99002 Feline in
	8	558	83.8	561	14	ADV34751	Adv34751 Feline N-
c	9	558	83.8	561	14	ADV34753	Adv34753 Feline N-
	10	540	81.1	591	6	ABK98948	Abk98948 Feline in
c	11	540	81.1	591	6	ABK98949	Abk98949 Feline in
	12	540	81.1	591	14	ADV34688	Adv34688 Feline si
c	13	540	81.1	591	14	ADV34690	Adv34690 Feline si
	14	527	79.1	591	2	AAV56629	Aav56629 Feline FL
c	15	507	76.1	1533	6	ABK98954	Abk98954 Feline in
	16	507	76.1	1533	6	ABK98953	Abk98953 Feline in
c	17	507	76.1	1533	14	ADV34697	Adv34697 Feline si
	18	507	76.1	1533	14	ADV34695	Adv34695 Feline si
	19	507	76.1	1599	6	ABK98950	Abk98950 Feline in
c	20	507	76.1	1599	6	ABK98951	Abk98951 Feline in
	21	507	76.1	1599	14	ADV34691	Adv34691 Feline si
c	22	507	76.1	1599	14	ADV34693	Adv34693 Feline si
	23	446	67.0	679	4	AAF26097	Aaf26097 Feline fi
	24	303	45.5	669	4	AAF26083	Aaf26083 Feline IL
	25	303	45.5	669	4	AAF26086	Aaf26086 Feline IL
	26	303	45.5	4201	4	AAF26077	Aaf26077 Feline IL
	27	248	37.2	689	2	AAV56641	Aav56641 Feline FL
	28	199	29.9	639	4	AAF26098	Aaf26098 Plasmid p
	29	178	26.7	660	5	AAD15214	Aad15214 Modified
	30	120	18.0	660	5	AAD15215	Aad15215 Modified
	31	115	17.3	660	5	AAD15213	Aad15213 Modified
	32	115	17.3	660	5	AAD15220	Aad15220 Modified
	33	102	15.3	660	5	AAD15218	Aad15218 Modified
	34	98	14.7	660	5	AAD15216	Aad15216 Modified
	35	84	12.6	660	5	AAD15219	Aad15219 Modified
	36	81	12.2	591	2	AAX18179	Aax18179 Canine ma
c	37	81	12.2	591	6	ABK98958	Abk98958 Canine in
	38	81	12.2	591	6	ABK98957	Abk98957 Canine in
	39	81	12.2	591	14	ADV34701	Adv34701 Canine si
c	40	81	12.2	591	14	ADV34703	Adv34703 Canine si
	41	81	12.2	666	6	ABK98955	Abk98955 Canine in
c	42	81	12.2	666	6	ABK98956	Abk98956 Canine in
c	43	81	12.2	666	14	ADV34700	Adv34700 Canine si
	44	81	12.2	666	14	ADV34698	Adv34698 Canine si
	45	81	12.2	669	2	AAV13818	Aav13818 Canine IL
	46	81	12.2	669	2	AAV13819	Aav13819 Canine IL
	47	81	12.2	669	2	AAX03163	Aax03163 Nucleic a
	48	81	12.2	669	2	AAX03153	Aax03153 Nucleic a
	49	81	12.2	669	2	AAX35616	Aax35616 Nucleic a
	50	81	12.2	669	2	AAX35626	Aax35626 Nucleic a
	51	81	12.2	669	4	AAI64389	Aai64389 Canine co
	52	81	12.2	669	4	AAI64379	Aai64379 Canine co
	53	81	12.2	669	11	ADZ25701	Adz25701 Canine in
	54	81	12.2	669	13	ADT04852	Adt04852 Canine in
	55	81	12.2	1282	2	AAX18178	Aax18178 Canine fu
	56	81	12.2	1455	6	ABK99003	Abk99003 Canine in
c	57	81	12.2	1455	6	ABK99004	Abk99004 Canine in
c	58	81	12.2	1455	14	ADV34756	Adv34756 Canine si
	59	81	12.2	1455	14	ADV34754	Adv34754 Canine si
	60	81	12.2	1533	6	ABK98967	Abk98967 Canine in
c	61	81	12.2	1533	6	ABK98968	Abk98968 Canine in
c	62	81	12.2	1533	14	ADV34718	Adv34718 Canine si
	63	81	12.2	1533	14	ADV34716	Adv34716 Canine si
	64	81	12.2	1599	6	ABK98965	Abk98965 Canine in
c	65	81	12.2	1599	6	ABK98966	Abk98966 Canine in
c	66	81	12.2	1599	14	ADV34715	Adv34715 Canine si
	67	81	12.2	1599	14	ADV34713	Adv34713 Canine si
	68	71	10.7	71	4	AAF26092	Aaf26092 Feline IL
	69	71	10.7	71	4	AAF26099	Aaf26099 Feline Il
	70	65	9.8	201	13	ADQ41825	Adq41825 Myocardia
	71	65	9.8	201	13	ADQ41824	Adq41824 Myocardia
	72	65	9.8	201	13	ADQ41835	Adq41835 Myocardia
	73	65	9.8	201	13	ADQ41829	Adq41829 Myocardia
	74	65	9.8	201	13	ADQ41838	Adq41838 Myocardia
	75	65	9.8	201	13	ADQ41833	Adq41833 Myocardia
	76	65	9.8	657	12	ADG39431	Adg39431 Human CLM
	77	65	9.8	660	2	AAQ97485	Aaq97485 Human int
	78	65	9.8	660	2	AAV07274	Aav07274 Human Int
	79	65	9.8	660	2	AAV07218	Aav07218 DNA encod
	80	65	9.8	660	2	AAZ40407	Aaz40407 Human int
	81	65	9.8	660	5	AAD15217	Aad15217 Modified
	82	65	9.8	660	5	AAD15221	Aad15221 Human cyt
	83	65	9.8	660	6	AAL44226	Aal44226 Human int
	84	65	9.8	660	6	ACC47589	Acc47589 Human int
	85	65	9.8	660	12	ADF77244	Adf77244 Human IL-
	86	65	9.8	702	12	ADP88401	Adp88401 Human int
	87	65	9.8	721	2	AAQ67880	Aaq67880 EPV 42 kD
	88	65	9.8	721	2	AAZ08515	Aaz08515 Vaccinia
	89	65	9.8	721	13	ADR21891	Adr21891 Vaccinia
	90	65	9.8	761	10	ADK98708	Adk98708 Human int
	91	65	9.8	761	10	ADK98706	Adk98706 Human int

92	65	9.8	762	2	AAV83207	Aav83207 Interleuk
93	65	9.8	762	3	AAA35201	Aaa35201 Human ade
94	65	9.8	762	3	AAF21323	Aaf21323 Human low
95	65	9.8	762	10	ABZ97017	Abz97017 Human nuc
96	65	9.8	762	11	ABD20866	Abd20866 Human pul
97	65	9.8	762	12	ADO07654	Ado07654 Human int
98	65	9.8	762	13	ADS88021	Ads88021 Tumour tr
99	65	9.8	762	14	ADV42511	Adv42511 Human psy
100	65	9.8	823	10	ACD26420	Acd26420 cDNA enco
101	65	9.8	856	2	AAQ12150	Aaq12150 Cytotoxic
102	65	9.8	856	2	AAT77850	Aat77850 35 kDa su
103	65	9.8	856	2	AAT97970	Aat97970 35 kDa su
104	65	9.8	856	2	AAV00402	Aav00402 35 kDa su
105	65	9.8	856	2	AAV37772	Aav37772 Cytotoxic
106	65	9.8	856	12	ADG39389	Adg39389 Human cyt
107	65	9.8	856	12	ADO03760	Ado03760 Human CLM
108	65	9.8	889	13	ADU04652	Adu04652 Human ext
109	65	9.8	1026	3	AAZ40020	Aaz40020 Human p35
110	65	9.8	1026	8	ACA61266	Aca61266 DNA encod
111	65	9.8	1026	11	ADI31715	Adi31715 Human cDN
112	65	9.8	1026	13	ADS83782	Ads83782 Human lym
113	65	9.8	1172	8	ACC42373	Acc42373 Human ext
114	65	9.8	1200	8	ACF64408	Acf64408 Human IL1
115	65	9.8	1287	4	AAF76882	Aaf76882 DNA encod
116	65	9.8	1289	8	ACC42375	Acc42375 Human ext
117	65	9.8	1316	2	AAT63621	Aat63621 Interleuk
118	65	9.8	1316	6	AAD41639	Aad41639 Human int
119	65	9.8	1364	2	AAT48099	Aat48099 Human int
120	65	9.8	1364	2	AAV42536	Aav42536 Human int
121	65	9.8	1364	2	AAV15228	Aav15228 Heterodim
122	65	9.8	1364	3	AAZ28863	Aaz28863 Human int
123	65	9.8	1364	4	AAF56281	Aaf56281 IL-12 vac
124	65	9.8	1384	15	AEF92723	Aef92723 Human int
125	65	9.8	1396	2	AAQ24371	Aaq24371 Natural k
126	65	9.8	1444	12	ACF57533	Acf57533 Human IL1
127	65	9.8	1444	12	ADJ62891	Adj62891 Human int
128	65	9.8	1444	12	ADN12152	Adn12152 Interleuk
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132	65	9.8	1494	12	ADQ59495	Adq59495 Human can
133	65	9.8	1526	12	ADQ59549	Adq59549 Human can
134	65	9.8	1532	13	ADQ38388	Adq38388 Human SNP
135	65	9.8	1532	14	ADZ13866	Adz13866 Human can
136	65	9.8	1607	13	ADQ38387	Adq38387 Human SNP
137	65	9.8	1607	14	ADZ13864	Adz13864 Human can
138	65	9.8	2300	3	AAA92406	Aaa92406 Human int
139	65	9.8	2336	14	AEE03207	Aee03207 Human int
140	65	9.8	2390	12	ADM29103	Adm29103 Human int
141	65	9.8	3205	14	AEB48820	Aeb48820 Monoclona
142	65	9.8	4521	3	AAA35204	Aaa35204 Human ade
143	65	9.8	4521	3	AAF21326	Aaf21326 Human low
144	65	9.8	4521	10	ABZ97020	Abz97020 Human nuc
145	65	9.8	4521	11	ABD20869	Abd20869 Human pul
146	65	9.8	5013	14	AEA40941	Aea40941 T-DNA reg
147	65	9.8	5686	2	AAZ40415	Aaz40415 Plasmid p
148	65	9.8	5686	12	ADF77239	Adf77239 Human IL-
149	65	9.8	6139	3	AAZ40023	Aaz40023 Interleuk
150	65	9.8	8578	6	AAD31546	Aad31546 pIRES-hB7
151	65	9.8	8578	6	AAD31545	Aad31545 pIRES-hB7
152	65	9.8	8608	6	AAD31548	Aad31548 pIRES-hB7
153	65	9.8	8623	6	AAD31547	Aad31547 pIRES-hB7
154	65	9.8	8629	6	AAD31552	Aad31552 pIRES-IL1
155	65	9.8	8638	6	AAD31549	Aad31549 pIRES-hB7
156	65	9.8	8644	6	AAD31551	Aad31551 pIRES-IL1
157	65	9.8	8659	6	AAD31550	Aad31550 pIRES-IL1
158	65	9.8	11441	6	AAL44225	Aal44225 Human int
159	65	9.8	11453	10	ADG25152	Adg25152 Vector pS
160	65	9.8	11569	10	ADG25150	Adg25150 Vector pA
161	65	9.8	27277	12	ADQ59494	Adq59494 Human can
162	65	9.8	27277	14	ADZ13863	Adz13863 Human can
163	62	9.3	683	4	AAF26096	Aaf26096 Human pG-
164	60	9.0	666	5	AAD15212	Aad15212 Modified
165	60	9.0	666	5	AAD15211	Aad15211 Modified
166	56	8.4	700	8	ACF64405	Acf64405 Human IL1
167	45	6.8	76	4	AAF26100	Aaf26100 Feline Il
c 168	45	6.8	76	4	AAF26093	Aaf26093 Feline IL
c 169	45	6.8	76	4	AAF26090	Aaf26090 Feline IL
170	43	6.5	79	2	AAV56639	Aav56639 Feline FL
171	41	6.2	703	3	AAA70708	Aaa70708 Bovine in
172	40	6.0	700	8	ACF64406	Acf64406 Human IL1
173	40	6.0	700	8	ACF64407	Acf64407 Human IL1
174	30	4.5	201	13	ADQ41830	Adq41830 Myocardia
175	30	4.5	201	13	ADQ41821	Adq41821 Myocardia
176	29	4.4	554	2	AAT50757	Aat50757 Partial s
177	27	4.1	39	6	ABK98991	Abk98991 Synthetic
178	27	4.1	39	14	ADV34741	Adv34741 Feline IL
179	27	4.1	79	2	AAX18181	Aax18181 Primer fo
180	27	4.1	582	4	AAF76877	Aaf76877 Mature mu
181	27	4.1	660	2	AAX78396	Aax78396 IL-12p35
182	27	4.1	660	2	AAX25946	Aax25946 Interleuk
183	27	4.1	713	2	AAT35199	Aat35199 Mouse int
184	27	4.1	1231	12	ADQ59492	Adq59492 Human can
185	27	4.1	1265	2	AAV28473	Aav28473 Murine in
186	27	4.1	1265	8	ACA61264	Aca61264 DNA encod
187	27	4.1	1273	14	ADZ13861	Adz13861 Murine ca
188	27	4.1	1278	4	AAF76881	Aaf76881 DNA encod
189	27	4.1	1569	4	AAF76888	Aaf76888 Single-ch
190	27	4.1	2013	4	AAF76887	Aaf76887 Murine p3
191	27	4.1	2334	14	AEE03206	Aee03206 Murine in
192	27	4.1	2438	12	ADO43004	Ado43004 DNA encod
193	27	4.1	2709	4	AAF76889	Aaf76889 Coding se
194	27	4.1	5252	12	ADO07652	Ado07652 Tricistro
195	27	4.1	5966	2	AAZ40417	Aaz40417 Plasmid p
196	27	4.1	5966	12	ADF77241	Adf77241 Mouse IL-
197	27	4.1	5985	12	ADQ82718	Adq82718 Anticance
198	27	4.1	6295	2	AAV02043	Aav02043 Plasmid p
199	27	4.1	7287	2	AAV02042	Aav02042 Plasmid p
200	27	4.1	9049	12	ADO07661	Ado07661 Viral vec

ALIGNMENTS

RESULT 1
ABK98947/c
ID ABK98947 standard; cDNA; 666 BP.
XX
AC ABK98947;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p35-666 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single

```
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 3; Page 56; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 666 BP; 160 A; 138 C; 179 G; 189 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 666;  DB 6;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  666;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 607

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 547

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 427

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 307

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 247

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 187

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 127

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 7

Qy        661 GCTTCC 666
              ||||||
Db          6 GCTTCC 1
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```
RESULT 2
ABK98946
ID   ABK98946 standard; cDNA; 666 BP.
XX
AC   ABK98946;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p35-666 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69304.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 54-55; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 666 BP; 189 A; 179 C; 138 G; 160 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 666;  DB 6;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  666;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        661 GCTTCC 666
              ||||||
Db        661 GCTTCC 666


RESULT 3
ADV34685
ID   ADV34685 standard; cDNA; 666 BP.
XX
AC   ADV34685;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12p35 full-length cDNA, nFeIL-12p35 666.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .666
FT                   /*tag=  a
FT                   /product= "PFeIL-12p35 222 protein "
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34686.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 23; SEQ ID NO 32; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12p35 subunit protein
CC   encoding full-length cDNA.
XX
SQ   Sequence 666 BP; 189 A; 179 C; 138 G; 160 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 666;  DB 14;  Length 666;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  666;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        661 GCTTCC 666
              ||||||
Db        661 GCTTCC 666


RESULT 4
ADV34687/c
```

```
ID   ADV34687 standard; DNA; 666 BP.
XX
AC   ADV34687;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12p35 complementary DNA, nFeIL-12p35 666.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 34; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12p35 subunit full-length
CC   complementary DNA.
XX
SQ   Sequence 666 BP; 160 A; 138 C; 179 G; 189 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 666;  DB 14;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  666;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 607

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 547

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 427

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 307

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 247

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 187

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 127

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 7

Qy        661 GCTTCC 666
              ||||||
Db          6 GCTTCC 1


RESULT 5
AAV56628
ID   AAV56628 standard; cDNA; 1441 BP.
XX
AC   AAV56628;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp35 cDNA.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             133. .811
FT                   /*tag=  a
FT   sig_peptide     133. .217
FT                   /*tag=  b
FT   mat_peptide     218. .808
FT                   /*tag=  c
FT                   /product= "FLAFp35"
FT                   /note= "feline cytokine"
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP001824.
XX
PR   04-JUN-1996;   96JP-00165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76175.
XX
PT   Novel feline cytokine protein - useful for treating feline auto:immune
PT   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS   Claim 22; Page 57-58; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine protein, FLAFp35. This
CC   protein can be used in the production of a FLAFp35/FLAFp40 heterodimer
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CC   which can potentiate the cytotoxic activity of feline cytotoxic T
CC   lymphocyte cells. Such proteins are used for treatment of feline
CC   autoimmune diseases e.g. as caused by feline herpes virus or feline
CC   calcivirus
XX
SQ   Sequence 1441 BP; 451 A; 325 C; 258 G; 407 T; 0 U; 0 Other;

  Query Match             90.4%;  Score 602;  DB 2;  Length 1441;
  Best Local Similarity   99.8%;  Pred. No. 2.7e-295;
  Matches  652;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTA 653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTA 795


RESULT 6
ABK99001
ID   ABK99001 standard; cDNA; 561 BP.
XX
AC   ABK99001;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p35-N561 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69315.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Disclosure; Page 92-93; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 561 BP; 167 A; 134 C; 120 G; 140 T; 0 U; 0 Other;

  Query Match             83.8%;  Score 558;  DB 6;  Length 561;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-273;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483
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Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543

Qy        649 AGCTATCTGAATGCTTCC 666
              ||||||||||||||||||
Db        544 AGCTATCTGAATGCTTCC 561


RESULT 7
ABK99002/c
ID   ABK99002 standard; cDNA; 561 BP.
XX
AC   ABK99002;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12nFeIL-12p35-N561 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Disclosure; Page 94; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 561 BP; 140 A; 120 C; 134 G; 167 T; 0 U; 0 Other;

  Query Match             83.8%;  Score 558;  DB 6;  Length 561;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-273;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        649 AGCTATCTGAATGCTTCC 666
              ||||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1


RESULT 8
ADV34751
ID   ADV34751 standard; cDNA; 561 BP.
XX
AC   ADV34751;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline N-terminal single chain IL-12p35 cDNA, nFeIL-12p35-N561.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .561
FT                   /*tag=  a
FT                   /product= "PFeIL-12p35-N187 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34752.
XX
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PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 23; SEQ ID NO 101; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline N-terminal single chain IL-12p35 subunit
CC   protein encoding cDNA.
XX
SQ   Sequence 561 BP; 167 A; 134 C; 120 G; 140 T; 0 U; 0 Other;

  Query Match             83.8%;  Score 558;  DB 14;  Length 561;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-273;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543

Qy        649 AGCTATCTGAATGCTTCC 666
              |||||||||||||||||
Db        544 AGCTATCTGAATGCTTCC 561


RESULT 9
ADV34753/c
ID   ADV34753 standard; cDNA; 561 BP.
XX
AC   ADV34753;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline N-terminal IL-12p35 complementary DNA, nFeIL-12p35-N561.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Disclosure; SEQ ID NO 103; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline N-terminal single chain IL-12p35 subunit
CC   protein complementary DNA.
XX
SQ   Sequence 561 BP; 140 A; 120 C; 134 G; 167 T; 0 U; 0 Other;

  Query Match             83.8%;  Score 558;  DB 14;  Length 561;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-273;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 79
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```
Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        649 AGCTATCTGAATGCTTCC 666
              |||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1
```

RESULT 10
ABK98948
ID ABK98948 standard; cDNA; 591 BP.
XX
AC ABK98948;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p35-591 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69305.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 1; Page 56-57; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 591 BP; 178 A; 149 C; 122 G; 142 T; 0 U; 0 Other;

  Query Match   81.1%; Score 540; DB 6; Length 591;
  Best Local Similarity 99.8%; Pred. No. 8.8e-264;
  Matches 590; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

```
Qy         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
```

RESULT 11
ABK98949/c
ID ABK98949 standard; cDNA; 591 BP.
XX
AC ABK98949;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p35-591 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Disclosure; Page 58; 106pp; English.
XX

```
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 591 BP; 142 A; 122 C; 149 G; 178 T; 0 U; 0 Other;

  Query Match             81.1%;  Score 540;  DB 6;  Length 591;
  Best Local Similarity   99.8%;  Pred. No. 8.8e-264;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy         376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy         436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy         496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy         556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy         616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1


RESULT 12
ADV34688
ID   ADV34688 standard; cDNA; 591 BP.
XX
AC   ADV34688;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain mature IL-12p35 protein cDNA, nFeIL-12p35 591.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .591
FT                   /*tag=  a
FT                   /product= "PFeIL-12p35 197 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34689.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 23; SEQ ID NO 35; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain mature IL-12p35 subunit
CC   protein encoding cDNA.
XX
SQ   Sequence 591 BP; 178 A; 149 C; 122 G; 142 T; 0 U; 0 Other;

  Query Match             81.1%;  Score 540;  DB 14;  Length 591;
  Best Local Similarity   99.8%;  Pred. No. 8.8e-264;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy         196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy         256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy         316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy         376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy         436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591


RESULT 13
ADV34690/c
ID   ADV34690 standard; DNA; 591 BP.
XX
AC   ADV34690;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain mature IL-12p35 complementary DNA, nFeIL-12p35 591.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 37; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain mature IL-12p35 subunit
CC   complementary DNA.
XX
SQ   Sequence 591 BP; 142 A; 122 C; 149 G; 178 T; 0 U; 0 Other;

  Query Match            81.1%;  Score 540;  DB 14;  Length 591;
  Best Local Similarity  99.8%;  Pred. No. 8.8e-264;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1


RESULT 14
AAV56629
ID   AAV56629 standard; cDNA; 591 BP.
XX
AC   AAV56629;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp35 cDNA mature transcript.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP001824.
XX
PR   04-JUN-1996;   96JP-00165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76176.
XX
PT   Novel feline cytokine protein - useful for treating feline auto:immune
PT   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS   Claim 23; Page 59; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine mature protein, FLAFp35.
CC   This protein can be used in the production of a FLAFp35/FLAFp40
CC   heterodimer which can potentiate the cytotoxic activity of feline
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CC   cytotoxic T lymphocyte cells. Such proteins are used for treatment of
CC   feline autoimmune diseases e.g. as caused by feline herpes virus or
CC   feline calcivirus
XX
SQ   Sequence 591 BP; 179 A; 151 C; 120 G; 141 T; 0 U; 0 Other;

  Query Match             79.1%;  Score 527;  DB 2;  Length 591;
  Best Local Similarity   99.8%;  Pred. No. 3.6e-257;
  Matches  577;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTA 653
              |||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTA 578


RESULT 15
ABK98954/c
ID   ABK98954 standard; cDNA; 1533 BP.
XX
AC   ABK98954;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1533 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS , Felis çatus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 66-67; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

  Query Match             76.1%;  Score 507;  DB 6;  Length 1533;
  Best Local Similarity   99.8%;  Pred. No. 5.3e-247;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        649 AGCTATCTGAATGCTTCC 666
              ||||||||||||||||||
```

```
Db         18 AGCTATCTGAATGCTTCC 1


RESULT 16
ABK98953
ID   ABK98953 standard; cDNA; 1533 BP.
XX
AC   ABK98953;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1533 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69307.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 63-64; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

  Query Match            76.1%;  Score 507;  DB 6;  Length 1533;
  Best Local Similarity  99.8%;  Pred. No. 5.3e-247;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        976 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 1035

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1036 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 1095

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1096 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 1155

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1156 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 1215

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1216 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 1275

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1276 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 1335

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1336 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 1395

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1396 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 1455

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1456 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 1515

Qy        649 AGCTATCTGAATGCTTCC 666
              ||||||||||||||||||
Db       1516 AGCTATCTGAATGCTTCC 1533


RESULT 17
ADV34697/c
ID   ADV34697 standard; DNA; 1533 BP.
XX
AC   ADV34697;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 complementary DNA, nFeIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 45; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 complementary DNA.
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XX
SQ   Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

  Query Match             76.1%;  Score 507;  DB 14;  Length 1533;
  Best Local Similarity   99.8%;  Pred. No. 5.3e-247;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        649 AGCTATCTGAATGCTTCC 666
              |||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1


RESULT 18
ADV34695
ID   ADV34695 standard; cDNA; 1533 BP.
XX
AC   ADV34695;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1533
FT                   /*tag=  a
FT                   /product= "PFeIL-12 511 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34696.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 43; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

  Query Match             76.1%;  Score 507;  DB 14;  Length 1533;
  Best Local Similarity   99.8%;  Pred. No. 5.3e-247;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        976 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 1035

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1036 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 1095

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1096 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 1155

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1156 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 1215

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1216 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 1275

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1276 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 1335

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1336 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 1395

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1396 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 1455

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1456 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 1515

Qy        649 AGCTATCTGAATGCTTCC 666
              |||||||||||||||||
Db       1516 AGCTATCTGAATGCTTCC 1533
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RESULT 19
ABK98950
ID   ABK98950 standard; cDNA; 1599 BP.
XX
AC   ABK98950;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1599 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69306.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 58-60; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

  Query Match             76.1%;  Score 507;  DB 6;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 5.3e-247;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1042 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 1101

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1102 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 1161

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1162 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 1221

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1222 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 1281

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1282 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 1341

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1342 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 1401

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1402 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 1461

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db       1462 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 1521

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1522 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 1581

Qy        649 AGCTATCTGAATGCTTCC 666
              ||||||||||||||||||
Db       1582 AGCTATCTGAATGCTTCC 1599


RESULT 20
ABK98951/c
ID   ABK98951 standard; cDNA; 1599 BP.
XX
AC   ABK98951;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1599 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 61-62; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
```

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CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

  Query Match             76.1%;  Score 507;  DB 6;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 5.3e-247;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        649 AGCTATCTGAATGCTTCC 666
              ||||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1


RESULT 21
ADV34691
ID   ADV34691 standard; cDNA; 1599 BP.
XX
AC   ADV34691;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1599
FT                   /*tag=  a
FT                   /product= "PFeIL-12p533 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34692.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 38; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

  Query Match             76.1%;  Score 507;  DB 14;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 5.3e-247;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1042 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 1101

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1102 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 1161

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1162 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 1221

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1222 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 1281

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1282 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 1341

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1342 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 1401

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1402 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 1461

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1462 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 1521

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1522 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 1581

Qy        649 AGCTATCTGAATGCTTCC 666
              ||||||||||||||||||
Db       1582 AGCTATCTGAATGCTTCC 1599


RESULT 22
ADV34693/c
ID   ADV34693 standard; DNA; 1599 BP.
XX
AC   ADV34693;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 complementary DNA, nFeIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 40; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 complementary DNA.
XX
SQ   Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

  Query Match           76.1%;  Score 507;  DB 14;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 5.3e-247;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        649 AGCTATCTGAATGCTTCC 666
              ||||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1


RESULT 23
AAF26097
ID   AAF26097 standard; DNA; 679 BP.
XX
AC   AAF26097;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline fil12p35a DNA.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS   Felis sp.
XX
PN   WO200104155-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002263.
XX
PR   08-JUL-1999;   99CH-00001259.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Lutz H,  Leutenegger C,  Pedersen N,  Schroff M,  Wittig B;
XX
DR   WPI; 2001-147178/15.
XX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs.
XX
PS   Disclosure; Fig 2; 35pp; German.
XX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
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CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
CC   following: (i) as immunostimulant, for preventative or therapeutic use;
CC   and (ii) treating tumors and autoimmune diseases, or diseases associated
CC   with a Th1 defect, especially pre-existing infections by feline immune
CC   deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ   Sequence 679 BP; 196 A; 180 C; 140 G; 163 T; 0 U; 0 Other;

  Query Match            67.0%;  Score 446;  DB 4;  Length 679;
  Best Local Similarity  99.6%;  Pred. No. 5.5e-216;
  Matches  546;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGGCTGGCCTCCAGAAAGACCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAA 548
              ||||||||
Db        541 CCACAGAA 548


RESULT 24
AAF26083
ID   AAF26083 standard; DNA; 669 BP.
XX
AC   AAF26083;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p35 encoding DNA SEQ ID 4.
XX
KW   Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW   interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS   Felis sp.
XX
PN   WO200104280-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002262.
XX
PR   08-JUL-1999;   99CH-00001258.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
XX
PI   Leutenegger C,  Schroff M,  Wittig B,  Lutz H;
XX
DR   WPI; 2001-147190/15.
XX
PT   Vaccine for treating or preventing lentivirus infection in cats, contains
PT   nucleic acid sequence encoding viral protein under control of eukaryotic
PT   promoter.
XX
PS   Claim 14; Page 37; 37pp; German.
XX
CC   This invention describes a novel vaccine (A) for prevention or treatment
CC   of lentivirus infection in felines which comprises an immunizing nucleic
CC   acid sequence (I) that contains, or comprises, at least part of a gene
CC   encoding a protein (II) of the virus, under control of a eukaryotic
CC   promoter functional in the relevant animal. (II) is especially the
CC   envelope (env) protein. The invention also describes (1) vaccine (A)
CC   containing an immunizing protein, or fragment, from a lentivirus plus at
CC   least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC   lentivirus protein, or fragment, especially derived from feline immune
CC   deficiency virus (FIV), by expressing the corresponding nucleic acid
CC   sequence in a host cell. The products of the invention have antiviral
CC   activity. The vaccine (A) and related protein-based vaccines, are
CC   particularly used to treat or prevent lentivirus infections in domestic
CC   cats, especially feline immune deficiency virus (FIV). Vaccination with
CC   (A) allows differentiation between vaccinated and infected animals, from
CC   the antibody status. The vaccines may be formulated with an adjuvant
CC   (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC   immune response, particularly a Th1 response
XX
SQ   Sequence 669 BP; 189 A; 179 C; 140 G; 161 T; 0 U; 0 Other;

  Query Match            45.5%;  Score 303;  DB 4;  Length 669;
  Best Local Similarity  99.2%;  Pred. No. 2.8e-143;
  Matches  503;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              |||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTG 507
                |||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTG 507


RESULT 25
AAF26086
ID   AAF26086 standard; DNA; 669 BP.
XX
AC   AAF26086;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p35 encoding DNA.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS   Felis sp.
XX
PN   WO200104155-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002263.
XX
PR   08-JUL-1999;   99CH-00001259.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Lutz H,  Leutenegger C,  Pedersen N,  Schroff M,  Wittig B;
XX
DR   WPI; 2001-147178/15.
XX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs.
XX
PS   Claim 3; Page 31; 35pp; German.
XX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
CC   following: (i) as immunostimulant, for preventative or therapeutic use;
CC   and (ii) treating tumors and autoimmune diseases, or diseases associated
CC   with a Th1 defect, especially pre-existing infections by feline immune
CC   deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ   Sequence 669 BP; 189 A; 179 C; 140 G; 161 T; 0 U; 0 Other;

  Query Match             45.5%;  Score 303;  DB 4;  Length 669;
  Best Local Similarity   99.2%;  Pred. No. 2.8e-143;
  Matches  503;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
                |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
                |||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTG 507
                |||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTG 507


RESULT 26
AAF26077
ID   AAF26077 standard; DNA; 4201 BP.
XX
AC   AAF26077;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p35 encoding DNA SEQ ID 3.
XX
KW   Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW   interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS   Felis sp.
XX
PN   WO200104280-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002262.
XX
PR   08-JUL-1999;   99CH-00001258.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
XX
PI   Leutenegger C,  Schroff M,  Wittig B,  Lutz H;
XX
DR   WPI; 2001-147190/15.
XX
PT   Vaccine for treating or preventing lentivirus infection in cats, contains
```

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PT   nucleic acid sequence encoding viral protein under control of eukaryotic
PT   promoter.
XX
PS   Disclosure; Page 31-33; 37pp; German.
XX
CC   This invention describes a novel vaccine (A) for prevention or treatment
CC   of lentivirus infection in felines which comprises an immunizing nucleic
CC   acid sequence (I) that contains, or comprises, at least part of a gene
CC   encoding a protein (II) of the virus, under control of a eukaryotic
CC   promoter functional in the relevant animal. (II) is especially the
CC   envelope (env) protein. The invention also describes (1) vaccine (A)
CC   containing an immunizing protein, or fragment, from a lentivirus plus at
CC   least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC   lentivirus protein, or fragment, especially derived from feline immune
CC   deficiency virus (FIV), by expressing the corresponding nucleic acid
CC   sequence in a host cell. The products of the invention have antiviral
CC   activity. The vaccine (A) and related protein-based vaccines, are
CC   particularly used to treat or prevent lentivirus infections in domestic
CC   cats, especially feline immune deficiency virus (FIV). Vaccination with
CC   (A) allows differentiation between vaccinated and infected animals, from
CC   the antibody status. The vaccines may be formulated with an adjuvant
CC   (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC   immune response, particularly a Th1 response
XX
SQ   Sequence 4201 BP; 1086 A; 1055 C; 999 G; 1061 T; 0 U; 0 Other;

  Query Match             45.5%;  Score 303;  DB 4;  Length 4201;
  Best Local Similarity   99.2%;  Pred. No. 2.8e-143;
  Matches  503;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3047 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 3106

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3107 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 3166

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3167 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 3226

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       3227 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 3286

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       3287 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTG 3346

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              |||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db       3347 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCT 3406

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3407 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 3466

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3467 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 3526

Qy        481 AACATGCTGACAGCTATTGATGAGCTG 507
              |||||||||||||||||||||||||||
Db       3527 AACATGCTGACAGCTATTGATGAGCTG 3553


RESULT 27
AAV56641
ID   AAV56641 standard; DNA; 689 BP.
XX
AC   AAV56641;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp35 DNA fragment.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ss.
XX
OS   Felis catus.
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP001824.
XX
PR   04-JUN-1996;   96JP-00165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
XX
PT   Novel feline cytokine protein - useful for treating feline auto:immune
PT   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS   Claim 24; Page 67; 94pp; Japanese.
XX
CC   This sequence encodes a fragment of a novel feline cytokine protein,
CC   FLAFp35. This protein can be used in the production of a FLAFp35/FLAFp40
CC   heterodimer which can potentiate the cytotoxic activity of feline
CC   cytotoxic T lymphocyte cells. Such proteins are used for treatment of
CC   feline autoimmune diseases e.g. as caused by feline herpes virus or
CC   feline calcivirus
XX
SQ   Sequence 689 BP; 192 A; 193 C; 145 G; 159 T; 0 U; 0 Other;

  Query Match             37.2%;  Score 248;  DB 2;  Length 689;
  Best Local Similarity   98.8%;  Pred. No. 2.5e-115;
  Matches  598;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         49 AACCACCTGGACCACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGA 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         55 AACCACCTGGACCACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGA 114

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 174

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 234

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              |||||||||||||||||||||||||||||||||| | ||||||||| | |||||||||
Db        235 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATGAAT 294

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 354

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 414

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              |||||||||||||||||||||||||||||||| | ||||||||||||||||||||||
Db        415 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATC 474

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 534
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Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        535 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATC 594

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 654

Qy        649 AGCTA 653
              |||||
Db        655 AGCTA 659
```

RESULT 28
AAF26098
ID AAF26098 standard; DNA; 639 BP.
XX
AC AAF26098;
XX
DT 24-APR-2001 (first entry)
XX
DE Plasmid pMOL-fIL12 p35 DNA.
XX
KW Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS Synthetic.
XX
PN WO200104155-A2.
XX
PD 18-JAN-2001.
XX
PF 08-JUL-2000; 2000WO-DE002263.
XX
PR 08-JUL-1999; 99CH-00001259.
XX
PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA (UYZU-) UNIV ZUERICH.
PA (REGC) UNIV CALIFORNIA.
XX
PI Lutz H, Leutenegger C, Pedersen N, Schroff M, Wittig B;
XX
DR WPI; 2001-147178/15.
XX
PT Recombinant feline interleukin-12, useful as immunostimulant and for
PT treating e.g. viral infections in cats, and related nucleic acid
PT constructs.
XX
PS Disclosure; Fig 2; 35pp; German.
XX
CC This invention describes a novel feline interleukin-12 (fIL-12)
CC polypeptide (I) that is expressed, by recombinant gene expression in
CC eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC of subunits p35 and p40. These proteins are formed so that, in equimolar
CC concentrations and in presence of an immunizing antigen, they can be
CC administered to carnivores, particularly domestic cats. The invention
CC also describes a nucleic acid construct (II) encoding fIL-12 containing
CC sequences at least 95% identical with the p40- and p35-encoding sequences
CC (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC as immunostimulants for immunization against infectious diseases and/or
CC for treating infections or tumors in felines, especially domestic cats.
CC The products of the invention have immunostimulatory, antiviral and
CC antitumor activity. Nucleic acid constructs that encode (II) are useful
CC as adjuvants for prophylactic immunization against viral diseases and for
CC treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC is useful for carnivores, and particularly domestic cats in the
CC following: (i) as immunostimulant, for preventative or therapeutic use;
CC and (ii) treating tumors and autoimmune diseases, or diseases associated
CC with a Th1 defect, especially pre-existing infections by feline immune
CC deficiency virus (FIV), feline leukemia virus and corona virus
XX

SQ Sequence 639 BP; 189 A; 166 C; 133 G; 151 T; 0 U; 0 Other;

Query Match 29.9%; Score 199; DB 4; Length 639;
Best Local Similarity 98.9%; Pred. No. 2.1e-90;
Matches 449; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy         54 CCTGGACCACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTT 113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCTGGACCACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTT 60

Qy        114 CCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGC 173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGC 120

Qy        174 CAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCAC 233
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        121 CAGACAAACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCAC 180

Qy        234 AAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAG 293
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        181 AAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAG 240

Qy        294 TTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAA 353
              |||||||||||||||||||||||||||||||||||||||||||| ||||  ||||||||
Db        241 TTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGGCTGGTGTCCAGAAA 300

Qy        354 GACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCA 413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCA 360

Qy        414 GGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCT 473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCT 420

Qy        474 GGATCAAAACATGCTGACAGCTATTGATGAGCTG 507
              |||||||||||||||||||||||||||||||||
Db        421 GGATCAAAACATGCTGACAGCTATTGATGAGCTG 454
```

RESULT 29
AAD15214
ID AAD15214 standard; DNA; 660 BP.
XX
AC AAD15214;
XX
DT 01-NOV-2001 (first entry)
XX
DE Modified human cytokine p35 encoding DNA from clone R2-631.
XX
KW Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW p35; mutant; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1. .660
FT /*tag= a
FT /product= "Modified p35 protein precursor"
FT sig_peptide 1. .66
FT /*tag= b
FT mat_peptide 67. .657
FT /*tag= c
FT /product= "Mature modified p35 protein"
XX
PN WO200140257-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000WO-US032664.
XX
PR 02-DEC-1999; 99US-0169035P.

```
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08607.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 87; Page 139; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein encoding
CC   DNA
XX
SQ   Sequence 660 BP; 182 A; 178 C; 142 G; 158 T; 0 U; 0 Other;

  Query Match             26.7%;  Score 178;  DB 5;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 9.9e-80;
  Matches  178;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        312 GATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGAC 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 GATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGAC 362

Qy        372 CCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCAT 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 CCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCAT 422

Qy        432 GAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 489
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 GAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480


RESULT 30
AAD15215
ID   AAD15215 standard; DNA; 660 BP.
XX
AC   AAD15215;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 encoding DNA from clone R2-613.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p35; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "Modified p35 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .657
FT                   /*tag=  c
FT                   /product= "Mature modified p35 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08608.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 87; Page 139-140; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein encoding
CC   DNA
XX
SQ   Sequence 660 BP; 190 A; 171 C; 137 G; 162 T; 0 U; 0 Other;

  Query Match             18.0%;  Score 120;  DB 5;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 3e-50;
  Matches  120;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        370 ACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCC 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCC 420

Qy        430 ATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 489
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480


RESULT 31
AAD15213
ID   AAD15213 standard; DNA; 660 BP.
XX
AC   AAD15213;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 encoding DNA from clone R2-796.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p35; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "Modified p35 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .657
FT                   /*tag=  c
FT                   /product= "Mature modified p35 protein"
```

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XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08606.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 87; Page 139; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein encoding
CC   DNA
XX
SQ   Sequence 660 BP; 189 A; 172 C; 136 G; 163 T; 0 U; 0 Other;

  Query Match            17.3%;  Score 115;  DB 5;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-47;
  Matches  115;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        166 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 216

Qy        226 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAA 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        217 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAA 271


RESULT 32
AAD15220
ID   AAD15220 standard; DNA; 660 BP.
XX
AC   AAD15220;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 encoding DNA from clone R1-4-87.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p35; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "Modified p35 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .657
FT                   /*tag=  c
FT                   /product= "Mature modified p35 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08613.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 87; Page 140-141; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein encoding
CC   DNA
XX
SQ   Sequence 660 BP; 189 A; 172 C; 136 G; 163 T; 0 U; 0 Other;

  Query Match            17.3%;  Score 115;  DB 5;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-47;
  Matches  115;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        166 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 216

Qy        226 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAA 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        217 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAA 271


RESULT 33
AAD15218
ID   AAD15218 standard; DNA; 660 BP.
XX
AC   AAD15218;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 encoding DNA from clone R2-162.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p35; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "Modified p35 protein precursor"
FT   sig_peptide     1. .66
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FT                   /*tag=  b
FT   mat_peptide     67. .657
FT                   /*tag=  c
FT                   /product= "Mature modified p35 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08611.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 87; Page 140; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein encoding
CC   DNA
XX
SQ   Sequence 660 BP; 182 A; 180 C; 144 G; 154 T; 0 U; 0 Other;

  Query Match             15.3%;  Score 102;  DB 5;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-41;
  Matches  102;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        388 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 438

Qy        448 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 489
              |||||||||||||||||||||||||||||||||||||||||||
Db        439 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480


RESULT 34
AAD15216
ID   AAD15216 standard; DNA; 660 BP.
XX
AC   AAD15216;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 encoding DNA from clone R2-571.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p35; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "Modified p35 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .657
FT                   /*tag=  c
FT                   /product= "Mature modified p35 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08609.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 87; Page 140; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein encoding
CC   DNA
XX
SQ   Sequence 660 BP; 184 A; 172 C; 141 G; 163 T; 0 U; 0 Other;

  Query Match             14.7%;  Score 98;  DB 5;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 4.7e-39;
  Matches   98;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        166 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 216

Qy        226 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 263
              |||||||||||||||||||||||||||||||||||||
Db        217 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 254


RESULT 35
AAD15219
ID   AAD15219 standard; DNA; 660 BP.
XX
AC   AAD15219;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 encoding DNA from clone R2-157.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p35; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
```

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FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "Modified p35 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .657
FT                   /*tag=  c
FT                   /product= "Mature modified p35 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08612.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 87; Page 140; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein encoding
CC   DNA
XX
SQ   Sequence 660 BP; 181 A; 178 C; 144 G; 157 T; 0 U; 0 Other;

  Query Match             12.6%;  Score 84;  DB 5;  Length 660;
  Best Local Similarity   99.3%;  Pred. No. 6.1e-32;
  Matches  134;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        312 GATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGAC 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 GATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGAC 362

Qy        372 CCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCAT 431
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        363 CCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCAT 422

Qy        432 GAATGCAAAGCTGTT 446
              |||||||||||||||
Db        423 GAATGCAAAGCTGTT 437


RESULT 36
AAX18179
ID   AAX18179 standard; cDNA; 591 BP.
XX
AC   AAX18179;
XX
DT   07-MAY-1999  (first entry)
XX
DE   Canine mature CLAF p35 subunit coding sequence.
XX
KW   CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW   viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW   canine infectious hepatitis; ds.
XX
OS   Canis sp.
XX
PN   WO9855511-A1.
XX
PD   10-DEC-1998.
XX
PF   26-MAY-1998;   98WO-JP002295.
XX
PR   03-JUN-1997;   97JP-00161936.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Tokiyoshi S,  Eda Y;
XX
DR   WPI; 1999-070260/06.
DR   P-PSDB; AAW74325.
XX
PT   Canine cytokine protein which activates canine cytotoxic T lymphocytes -
PT   is useful for treatment of viral and autoimmune diseases in dogs.
XX
PS   Claim 8; Page 34-35; 51pp; Japanese.
XX
CC   This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC   the invention. CLAF activates lymphocytes, especially canine cytotoxic T
CC   cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC   recognising it may be used in the treatment of viral diseases in dogs
CC   (such as canine distemper, canine parvovirus and canine infectious
CC   hepatitis). The antibodies may also be used in isolation of CLAF from
CC   culture of the transformant host cells by affinity chromatography. The
CC   p40 homodimer can be used for the treatment of autoimmune diseases in
CC   dogs
XX
SQ   Sequence 591 BP; 173 A; 146 C; 127 G; 145 T; 0 U; 0 Other;

  Query Match             12.2%;  Score 81;  DB 2;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        223 CTGGCTTCCAGAGAGATCTCT 243


RESULT 37
ABK98958/c
ID   ABK98958 standard; cDNA; 591 BP.
XX
AC   ABK98958;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p35-591 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
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```
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Disclosure; Page 70; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 591 BP; 145 A; 127 C; 146 G; 173 T; 0 U; 0 Other;

  Query Match             12.2%;  Score 81;  DB 6;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 38
ABK98957
ID   ABK98957 standard; cDNA; 591 BP.
XX
AC   ABK98957;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p35-591 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69309.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 69; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 591 BP; 173 A; 146 C; 127 G; 145 T; 0 U; 0 Other;

  Query Match             12.2%;  Score 81;  DB 6;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        223 CTGGCTTCCAGAGAGATCTCT 243


RESULT 39
ADV34701
ID   ADV34701 standard; cDNA; 591 BP.
XX
AC   ADV34701;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p35 protein cDNA, nCaIL-12p35 591.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .591
FT                   /*tag=  a
FT                   /product= "PCaIL-12P35 197 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
```

```
DR   P-PSDB; ADV34702.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 49; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p35 subunit protein
CC   encoding cDNA.
XX
SQ   Sequence 591 BP; 173 A; 146 C; 127 G; 145 T; 0 U; 0 Other;

  Query Match             12.2%;  Score 81;  DB 14;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        223 CTGGCTTCCAGAGAGATCTCT 243


RESULT 40
ADV34703/c
ID   ADV34703 standard; DNA; 591 BP.
XX
AC   ADV34703;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p35 complementary DNA, nCaIL-12p35 591.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 51; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p35 subunit
CC   complementary DNA.
XX
SQ   Sequence 591 BP; 145 A; 127 C; 146 G; 173 T; 0 U; 0 Other;

  Query Match             12.2%;  Score 81;  DB 14;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 41
ABK98955
ID   ABK98955 standard; cDNA; 666 BP.
XX
AC   ABK98955;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p35-666 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69308.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 67-68; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 666 BP; 182 A; 177 C; 145 G; 162 T; 0 U; 0 Other;
```

```
  Query Match             12.2%;  Score 81;  DB 6;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 42
ABK98956/c
ID   ABK98956 standard; cDNA; 666 BP.
XX
AC   ABK98956;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p35-66 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Disclosure; Page 68-69; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 666 BP; 162 A; 145 C; 177 G; 182 T; 0 U; 0 Other;

  Query Match             12.2%;  Score 81;  DB 6;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 43
ADV34700/c
ID   ADV34700 standard; DNA; 666 BP.
XX
AC   ADV34700;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p35 complementary DNA, nCaIL-12p35 666.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 48; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p35 subunit full-length
CC   complementary DNA.
XX
SQ   Sequence 666 BP; 162 A; 145 C; 177 G; 182 T; 0 U; 0 Other;

  Query Match             12.2%;  Score 81;  DB 14;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 44
ADV34698
ID   ADV34698 standard; cDNA; 666 BP.
XX
AC   ADV34698;
```

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XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p35 full-length cDNA, nCaIL-12p35 666.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .666
FT                   /*tag=  a
FT                   /product= "PCaIL-12p222 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34699.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 46; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p35 subunit protein
CC   encoding full-length cDNA.
XX
SQ   Sequence 666 BP; 182 A; 177 C; 145 G; 162 T; 0 U; 0 Other;

  Query Match             12.2%;  Score 81;  DB 14;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 45
AAV13818
ID   AAV13818 standard; cDNA to mRNA; 669 BP.
XX
AC   AAV13818;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P35 subunit cDNA.
XX
KW   Canine; interleukin-12 P35 subunit; IL-12 P35 subunit; antitumour;
KW   antiviral; vaccine adjuvant; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag=  a
FT                   /product= "interleukin-12_P35_subunit"
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-00296789.
XX
PR   08-NOV-1995;   95JP-00289729.
PR   23-MAY-1996;   96JP-00128104.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   P-PSDB; AAW41792.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected.
XX
PS   Claim 9; Page 9; 12pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin-12 (IL-12) P35 subunit.
CC   A canine IL-12 comprising a P40 and P35 subunit is capable of inducing an
CC   antiviral activating factor and the expression of class II MHC molecules
CC   in canine tumour cells, stimulating proliferation of canine blastogenic
CC   lymphocytes and activating canine leukocytes to inhibit canine tumour
CC   cells. The canine IL-12 can be used in veterinary medicines, e.g.
CC   antitumour, antivirus and vaccine adjuvant activities are expected
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 U; 0 Other;

  Query Match             12.2%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 46
AAV13819
ID   AAV13819 standard; cDNA to mRNA; 669 BP.
XX
AC   AAV13819;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P35 subunit cDNA.
XX
KW   Canine; interleukin-12 P35 subunit; IL-12 P35 subunit; antitumour;
KW   antiviral; vaccine adjuvant; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag=  a
FT                   /product= "interleukin-12_P35_subunit"
```

```
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-00296789.
XX
PR   08-NOV-1995;   95JP-00289729.
PR   23-MAY-1996;   96JP-00128104.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   P-PSDB; AAW41793.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected.
XX
PS   Claim 11; Page 11-12; 12pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin-12 (IL-12) P35 subunit.
CC   A canine IL-12 comprising a P40 and P35 subunit is capable of inducing an
CC   antiviral activating factor and the expression of class II MHC molecules
CC   in canine tumour cells, stimulating proliferation of canine blastogenic
CC   lymphocytes and activating canine leukocytes to inhibit canine tumour
CC   cells. The canine IL-12 can be used in veterinary medicines, e.g.
CC   antitumour, antivirus and vaccine adjuvant activities are expected
XX
SQ   Sequence 669 BP; 185 A; 177 C; 144 G; 163 T; 0 U; 0 Other;

  Query Match             12.2%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 47
AAX03163
ID   AAX03163 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX03163;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Nucleic acid encoding canine interleukin 12.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag=  a
FT                   /product= "interleukin_12"
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP002031.
XX
PR   16-MAY-1997;   97JP-00127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   P-PSDB; AAW84374.
XX
PT   New therapeutic and prophylactic agents - comprise genetically-engineered
PT   canine interleukin 12, used to treat, e.g. canine and feline
PT   immunological diseases.
XX
PS   Claim 1; Page 33-34; 45pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin 12 (IL-12) protein. The
CC   IL-12 protein can be used in therapeutic or prophylactic agents. The
CC   agents can be used to prevent and treat canine and feline immunological
CC   diseases including dog and cat tumours, skin diseases, viral infections
CC   and allergic diseases, especially tumours, breast tumour, oesinophilic
CC   granuloma, epidermoid tumour, skin tumour, lipoma, othematoma,
CC   pneumonoedema, skin soft pedicled soft tumour and anal tumour; skin
CC   diseases, otitis externa, dermatitis, eczema, fungal diseases of the
CC   skin, pyoderma, allergic dermatitis, nettle rash, traumatic dermatitis
CC   and hair loss; infections; dog Parvovirus infection and distemper virus,
CC   cat plaque virus infection and feline leukaemia, and allergic diseases,
CC   e.g. pollinosis
XX
SQ   Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 U; 0 Other;

  Query Match             12.2%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 48
AAX03153
ID   AAX03153 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX03153;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Nucleic acid encoding canine interleukin 12.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag=  a
FT                   /product= "interleukin_12"
XX
PN   WO9851327-A1.
```

```
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP002031.
XX
PR   16-MAY-1997;   97JP-00127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   P-PSDB; AAW84372.
XX
PT   New therapeutic and prophylactic agents - comprise genetically-engineered
PT   canine interleukin 12, used to treat, e.g. canine and feline
PT   immunological diseases.
XX
PS   Claim 1; Page 26-27; 45pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin 12 (IL-12) protein. The
CC   IL-12 protein can be used in therapeutic or prophylactic agents. The
CC   agents can be used to prevent and treat canine and feline immunological
CC   diseases including dog and cat tumours, skin diseases, viral infections
CC   and allergic diseases, especially tumours, breast tumour, oesinophilic
CC   granuloma, epidermoid tumour, skin tumour, lipoma, othematoma,
CC   pneumonoedema, skin soft pedicled soft tumour and anal tumour; skin
CC   diseases, otitis externa, dermatitis, eczema, fungal diseases of the
CC   skin, pyoderma, allergic dermatitis, nettle rash, traumatic dermatitis
CC   and hair loss; infections; dog Parvovirus infection and distemper virus,
CC   cat plaque virus infection and feline leukaemia, and allergic diseases,
CC   e.g. pollinosis
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 U; 0 Other;

  Query Match             12.2%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 49
AAX35616
ID   AAX35616 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX35616;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag=  a
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-00133345.
XX
PR   16-MAY-1997;   97JP-00127690.
PR   07-AUG-1997;   97JP-00213755.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   P-PSDB; AAY02340.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) - for
PT   prevention and treatment of dog and cat immune diseases.
XX
PS   Claim 1; Page 13; 16pp; Japanese.
XX
CC   The present sequence encodes canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment of dog
CC   and cat immune diseases. The treatment used an agent comprising dog IL-12
CC   (CaIL12) proteins to form a heterodimer. The agent is useful for
CC   preventing and treating dog and cat immune diseases, including tumours,
CC   skin diseases, infectious diseases and allergic diseases
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 U; 0 Other;

  Query Match             12.2%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 50
AAX35626
ID   AAX35626 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX35626;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag=  a
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-00133345.
XX
PR   16-MAY-1997;   97JP-00127690.
PR   07-AUG-1997;   97JP-00213755.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   P-PSDB; AAY02343.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) - for
PT   prevention and treatment of dog and cat immune diseases.
XX
PS   Claim 1; Page 15-16; 16pp; Japanese.
XX
```

```
CC   The present sequence encodes canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment of dog
CC   and cat immune diseases. The treatment used an agent comprising dog IL-12
CC   (CaIL12) proteins to form a heterodimer. The agent is useful for
CC   preventing and treating dog and cat immune diseases, including tumours,
CC   skin diseases, infectious diseases and allergic diseases
XX
SQ   Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 U; 0 Other;

  Query Match             12.2%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 51
AAI64389
ID   AAI64389 standard; DNA; 669 BP.
XX
AC   AAI64389;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine coding sequence #4.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag=  a
FT                   /product= "Canine protein #4"
FT   sig_peptide     1. .75
FT                   /*tag=  b
FT   mat_peptide     76. .666
FT                   /*tag=  c
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-00292946.
XX
PR   01-OCT-1999;   99JP-00281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   P-PSDB; AAG66483.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian.
XX
PS   Claim 6; Page 18; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention
XX
SQ   Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 U; 0 Other;

  Query Match             12.2%;  Score 81;  DB 4;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 52
AAI64379
ID   AAI64379 standard; DNA; 669 BP.
XX
AC   AAI64379;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine coding sequence #2.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag=  a
FT                   /product= "Canine protein #2"
FT   sig_peptide     1. .75
FT                   /*tag=  b
FT   mat_peptide     76. .666
FT                   /*tag=  c
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-00292946.
XX
PR   01-OCT-1999;   99JP-00281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   P-PSDB; AAG66481.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian.
XX
PS   Claim 6; Page 15; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 U; 0 Other;

  Query Match             12.2%;  Score 81;  DB 4;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
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                    ||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 53
ADZ25701
ID   ADZ25701 standard; cDNA; 669 BP.
XX
AC   ADZ25701;
XX
DT   16-JUN-2005  (first entry)
XX
DE   Canine interleukin 12 P35 encoding cDNA SEQ ID NO:6.
XX
KW   interleukin-12; antiviral; gene; ss.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag=  b
FT                   /product= "interleukin-12 P40"
FT   sig_peptide     1. .75
FT                   /*tag=  a
FT   mat_peptide     76. .666
FT                   /*tag=  c
FT                   /product= "interleukin-12 P40"
XX
PN   JP2003284585-A.
XX
PD   07-OCT-2003.
XX
PF   28-MAR-2002; 2002JP-00090161.
XX
PR   28-MAR-2002; 2002JP-00090161.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2003-885430/82.
DR   P-PSDB; ADZ25703.
XX
PT   Large scale production of interleukin-12 for pharmaceutical applications,
PT   comprises infecting an insect cell with a recombinant virus containing
PT   gene encoding IL-12, and producing IL-12 by carrying out spinner culture
PT   of insect cell.
XX
PS   Example; SEQ ID NO 6; 8pp; Japanese.
XX
CC   The invention related to the large scale production of interleukin-12 (IL
CC   -12), which involves infecting an insect cell with a recombinant virus
CC   containing a gene encoding IL-12, and producing IL-12 by carrying out
CC   spinner culture of insect cell. The method is useful for producing IL-12,
CC   preferably canine IL-12. IL-12 has pharmaceutical applications. The
CC   present sequence encodes canine IL-12 P35, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 U; 0 Other;

  Query Match             12.2%;  Score 81;  DB 11;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              ||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 54
ADT04852
ID   ADT04852 standard; DNA; 669 BP.
XX
AC   ADT04852;
XX
DT   13-JAN-2005  (first entry)
XX
DE   Canine interleukin-12 (IL-12) p35 DNA.
XX
KW   gene expression; insect; ds; interleukin-12; IL-12.
XX
OS   Canis familiaris.
XX
PN   JP2004290182-A.
XX
PD   21-OCT-2004.
XX
PF   06-FEB-2004; 2004JP-00030183.
XX
PR   10-MAR-2003; 2003JP-00062907.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2004-740760/73.
XX
PT   Novel gene vector for expression in insect useful for expression of
PT   foreign gene such as dog interleukin 12 gene, comprises two promoters.
XX
PS   Claim 4; SEQ ID NO 8; 13pp; Japanese.
XX
CC   The invention relates to a novel gene vector for expression in an insect
CC   comprising at least two promoters, particularly the polyhedrin promoter
CC   and p10 promoter. The vector contains at least two types of foreign
CC   protein expression gene and the gene product of the vector is produced
CC   using a gene recombinant baculovirus, particularly a recombinant silkworm
CC   nuclear polyhedrosis virus. The baculovirus is proliferated in a
CC   silkworm. The vector of the invention may be useful for expression of a
CC   foreign gene, such as canine interleukin 12. Within the vector, two types
CC   of foreign protein expression genes are integrated simultaneously for
CC   their simultaneous expression. The current sequence is that of the canine
CC   interleukin-12 (IL-12) p35 DNA of the invention.
XX
SQ   Sequence 669 BP; 183 A; 177 C; 145 G; 164 T; 0 U; 0 Other;

  Query Match             12.2%;  Score 81;  DB 13;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              ||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 55
AAX18178
ID   AAX18178 standard; cDNA; 1282 BP.
XX
AC   AAX18178;
XX
DT   07-MAY-1999  (first entry)
XX
DE   Canine full length CLAF p35 subunit coding sequence.
XX
KW   CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW   viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW   canine infectious hepatitis; ds.
XX
OS   Canis sp.
XX
PN   WO9855511-A1.
```

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XX
PD   10-DEC-1998.
XX
PF   26-MAY-1998;   98WO-JP002295.
XX
PR   03-JUN-1997;   97JP-00161936.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Tokiyoshi S,  Eda Y;
XX
DR   WPI; 1999-070260/06.
DR   P-PSDB; AAW74324.
XX
PT   Canine cytokine protein which activates canine cytotoxic T lymphocytes -
PT   is useful for treatment of viral and autoimmune diseases in dogs.
XX
PS   Claim 8; Page 33-34; 51pp; Japanese.
XX
CC   This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC   the invention. CLAF activates lymphocytes, especially canine cytotoxic T
CC   cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC   recognising it may be used in the treatment of viral diseases in dogs
CC   (such as canine distemper, canine parvovirus and canine infectious
CC   hepatitis). The antibodies may also be used in isolation of CLAF from
CC   culture of the transformant host cells by affinity chromatography. The
CC   p40 homodimer can be used for the treatment of autoimmune diseases in
CC   dogs
XX
SQ   Sequence 1282 BP; 391 A; 279 C; 257 G; 355 T; 0 U; 0 Other;

  Query Match             12.2%;  Score 81;  DB 2;  Length 1282;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 362

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        363 CTGGCTTCCAGAGAGATCTCT 383


RESULT 56
ABK99003
ID   ABK99003 standard; cDNA; 1455 BP.
XX
AC   ABK99003;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p35-1455 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69316.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 4; Page 94-95; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1455 BP; 437 A; 341 C; 304 G; 373 T; 0 U; 0 Other;

  Query Match             12.2%;  Score 81;  DB 6;  Length 1455;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 528

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        529 CTGGCTTCCAGAGAGATCTCT 549


RESULT 57
ABK99004/c
ID   ABK99004 standard; cDNA; 1455 BP.
XX
AC   ABK99004;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p35-1455 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
```

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XX
PS   Example 4; Page 96; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1455 BP; 373 A; 304 C; 341 G; 437 T; 0 U; 0 Other;

  Query Match            12.2%;  Score 81;  DB 6;  Length 1455;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 928

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        927 CTGGCTTCCAGAGAGATCTCT 907


RESULT 58
ADV34756/c
ID   ADV34756 standard; DNA; 1455 BP.
XX
AC   ADV34756;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p35 complementary DNA, nCaIL-12p35 1455.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 106; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p35 subunit
CC   complementary DNA.
XX
SQ   Sequence 1455 BP; 373 A; 304 C; 341 G; 437 T; 0 U; 0 Other;

  Query Match            12.2%;  Score 81;  DB 14;  Length 1455;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 928

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        927 CTGGCTTCCAGAGAGATCTCT 907


RESULT 59
ADV34754
ID   ADV34754 standard; cDNA; 1455 BP.
XX
AC   ADV34754;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p35 protein cDNA, nCaIL-12p35 1455.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             232. .900
FT                   /*tag= a
FT                   /product= "PCaIL-12p35 222 protein"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34755.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 104; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p35 subunit protein
CC   encoding cDNA.
XX
SQ   Sequence 1455 BP; 437 A; 341 C; 304 G; 373 T; 0 U; 0 Other;
```

```
  Query Match            12.2%;  Score 81;  DB 14;  Length 1455;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 528

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        529 CTGGCTTCCAGAGAGATCTCT 549


RESULT 60
ABK98967
ID   ABK98967 standard; cDNA; 1533 BP.
XX
AC   ABK98967;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1533 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69314.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 83-85; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 446 A; 368 C; 369 G; 350 T; 0 U; 0 Other;

  Query Match            12.2%;  Score 81;  DB 6;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1105 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1164

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db       1165 CTGGCTTCCAGAGAGATCTCT 1185


RESULT 61
ABK98968/c
ID   ABK98968 standard; cDNA; 1533 BP.
XX
AC   ABK98968;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1533 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 86-87; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

  Query Match            12.2%;  Score 81;  DB 6;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349
```

```
RESULT 62
ADV34718/c
ID   ADV34718 standard; DNA; 1533 BP.
XX
AC   ADV34718;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12 complementary DNA, nCaIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 68; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 complementary DNA.
XX
SQ   Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

  Query Match             12.2%;  Score 81;  DB 14;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 63
ADV34716
ID   ADV34716 standard; cDNA; 1533 BP.
XX
AC   ADV34716;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12 protein cDNA, nCaIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1533
FT                   /*tag=  a
FT                   /product= "PCaIL-12 511 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34717.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 66; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1533 BP; 446 A; 368 C; 369 G; 350 T; 0 U; 0 Other;

  Query Match             12.2%;  Score 81;  DB 14;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1105 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1164

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db       1165 CTGGCTTCCAGAGAGATCTCT 1185


RESULT 64
ABK98965
ID   ABK98965 standard; cDNA; 1599 BP.
XX
AC   ABK98965;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1599 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
```

PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69313.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 79-80; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1599 BP; 452 A; 392 C; 383 G; 372 T; 0 U; 0 Other;

Query Match 12.2%; Score 81; DB 6; Length 1599;
Best Local Similarity 100.0%; Pred. No. 2.1e-30;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1230

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db       1231 CTGGCTTCCAGAGAGATCTCT 1251
```

RESULT 65
ABK98966/c
ID ABK98966 standard; cDNA; 1599 BP.
XX
AC ABK98966;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12-1599 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 82-83; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1599 BP; 372 A; 383 C; 392 G; 452 T; 0 U; 0 Other;

Query Match 12.2%; Score 81; DB 6; Length 1599;
Best Local Similarity 100.0%; Pred. No. 2.1e-30;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349
```

RESULT 66
ADV34715/c
ID ADV34715 standard; DNA; 1599 BP.
XX
AC ADV34715;
XX
DT 24-FEB-2005 (first entry)
XX
DE Canine single chain IL-12 complementary DNA, nCaIL-12 1599.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Canis familiaris.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX

PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 4; SEQ ID NO 63; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the canine single chain IL-12 complementary DNA.
XX
SQ Sequence 1599 BP; 372 A; 383 C; 392 G; 452 T; 0 U; 0 Other;

Query Match 12.2%; Score 81; DB 14; Length 1599;
Best Local Similarity 100.0%; Pred. No. 2.1e-30;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy 298 CTGGCTTCCAGAGAGATCTCT 318
||||||||||||||||||||
Db 369 CTGGCTTCCAGAGAGATCTCT 349

RESULT 67
ADV34713
ID ADV34713 standard; cDNA; 1599 BP.
XX
AC ADV34713;
XX
DT 24-FEB-2005 (first entry)
XX
DE Canine single chain IL-12 protein cDNA, nCaIL-12 1599.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; gene; ss.
XX
OS Canis familiaris.
XX
FH Key Location/Qualifiers
FT CDS 1. .1599
FT /*tag= a
FT /product= "PCaIL-12 533 protein"
FT /partial
FT /note= "No stop codon"
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
DR P-PSDB; ADV34714.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 4; SEQ ID NO 61; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the canine single chain IL-12 protein encoding cDNA.
XX
SQ Sequence 1599 BP; 452 A; 392 C; 383 G; 372 T; 0 U; 0 Other;

Query Match 12.2%; Score 81; DB 14; Length 1599;
Best Local Similarity 100.0%; Pred. No. 2.1e-30;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1171 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1230

Qy 298 CTGGCTTCCAGAGAGATCTCT 318
||||||||||||||||||||
Db 1231 CTGGCTTCCAGAGAGATCTCT 1251

RESULT 68
AAF26092
ID AAF26092 standard; DNA; 71 BP.
XX
AC AAF26092;
XX
DT 24-APR-2001 (first entry)
XX
DE Feline IL-12p35 PCR primer SEQ ID 8.
XX
KW Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW Th1 defect; autoimmune disease; IL-12p40; IL-12p35; PCR primer; ss.
XX
OS Felis sp.
XX
PN WO200104155-A2.
XX
PD 18-JAN-2001.
XX
PF 08-JUL-2000; 2000WO-DE002263.
XX
PR 08-JUL-1999; 99CH-00001259.
XX
PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA (UYZU-) UNIV ZUERICH.
PA (REGC) UNIV CALIFORNIA.
XX
PI Lutz H, Leutenegger C, Pedersen N, Schroff M, Wittig B;
XX
DR WPI; 2001-147178/15.
XX
PT Recombinant feline interleukin-12, useful as immunostimulant and for
PT treating e.g. viral infections in cats, and related nucleic acid
PT constructs.
XX
PS Example 1b; Page 33; 35pp; German.
XX
CC This invention describes a novel feline interleukin-12 (fIL-12)
CC polypeptide (I) that is expressed, by recombinant gene expression in
CC eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC of subunits p35 and p40. These proteins are formed so that, in equimolar
CC concentrations and in presence of an immunizing antigen, they can be
CC administered to carnivores, particularly domestic cats. The invention
CC also describes a nucleic acid construct (II) encoding fIL-12 containing
CC sequences at least 95% identical with the p40- and p35-encoding sequences
CC (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC as immunostimulants for immunization against infectious diseases and/or
CC for treating infections or tumors in felines, especially domestic cats.

CC The products of the invention have immunostimulatory, antiviral and
CC antitumor activity. Nucleic acid constructs that encode (II) are useful
CC as adjuvants for prophylactic immunization against viral diseases and for
CC treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC is useful for carnivores, and particularly domestic cats in the
CC following: (i) as immunostimulant, for preventative or therapeutic use;
CC and (ii) treating tumors and autoimmune diseases, or diseases associated
CC with a Th1 defect, especially pre-existing infections by feline immune
CC deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ Sequence 71 BP; 17 A; 19 C; 17 G; 18 T; 0 U; 0 Other;

Query Match 10.7%; Score 71; DB 4; Length 71;
Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 485 TGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCAC 544
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 TGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCAC 60

Qy 545 AGAACTCCTCC 555
||||||||||||
Db 61 AGAACTCCTCC 71

RESULT 69
AAF26099
ID AAF26099 standard; DNA; 71 BP.
XX
AC AAF26099;
XX
DT 24-APR-2001 (first entry)
XX
DE Feline Il-12 associated DNA #1.
XX
KW Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS Unidentified.
XX
PN WO200104155-A2.
XX
PD 18-JAN-2001.
XX
PF 08-JUL-2000; 2000WO-DE002263.
XX
PR 08-JUL-1999; 99CH-00001259.
XX
PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA (UYZU-) UNIV ZUERICH.
PA (REGC) UNIV CALIFORNIA.
XX
PI Lutz H, Leutenegger C, Pedersen N, Schroff M, Wittig B;
XX
DR WPI; 2001-147178/15.
XX
PT Recombinant feline interleukin-12, useful as immunostimulant and for
PT treating e.g. viral infections in cats, and related nucleic acid
PT constructs.
XX
PS Disclosure; Fig 2; 35pp; German.
XX
CC This invention describes a novel feline interleukin-12 (fIL-12)
CC polypeptide (I) that is expressed, by recombinant gene expression in
CC eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC of subunits p35 and p40. These proteins are formed so that, in equimolar
CC concentrations and in presence of an immunizing antigen, they can be
CC administered to carnivores, particularly domestic cats. The invention
CC also describes a nucleic acid construct (II) encoding fIL-12 containing
CC sequences at least 95% identical with the p40- and p35-encoding sequences
CC (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC as immunostimulants for immunization against infectious diseases and/or
CC for treating infections or tumors in felines, especially domestic cats.
CC The products of the invention have immunostimulatory, antiviral and
CC antitumor activity. Nucleic acid constructs that encode (II) are useful
CC as adjuvants for prophylactic immunization against viral diseases and for
CC treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC is useful for carnivores, and particularly domestic cats in the
CC following: (i) as immunostimulant, for preventative or therapeutic use;
CC and (ii) treating tumors and autoimmune diseases, or diseases associated
CC with a Th1 defect, especially pre-existing infections by feline immune
CC deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ Sequence 71 BP; 17 A; 19 C; 17 G; 18 T; 0 U; 0 Other;

Query Match 10.7%; Score 71; DB 4; Length 71;
Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 485 TGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCAC 544
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 TGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCAC 60

Qy 545 AGAACTCCTCC 555
||||||||||||
Db 61 AGAACTCCTCC 71

RESULT 70
ADQ41825
ID ADQ41825 standard; DNA; 201 BP.
XX
AC ADQ41825;
XX
DT 18-NOV-2004 (first entry)
XX
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 3488.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human; ds.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JJ, Iakoubova O;
XX
DR WPI; 2004-533949/51.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 7; SEQ ID NO 3488; 145pp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least

CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a transcript-based context sequence
CC which flanks an SNP found in a human myocardial infarction-associated
CC gene of the invention. Note: This sequence was not shown in the
CC specification. The sequence has come from an electronic sequence listing
CC downloaded from the WIPO website.
XX
SQ Sequence 201 BP; 64 A; 39 C; 37 G; 60 T; 0 U; 1 Other;

Query Match 9.8%; Score 65; DB 13; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.8e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 21 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 80

Qy 619 ATTCG 623
|||||
Db 81 ATTCG 85

RESULT 71
ADQ41824
ID ADQ41824 standard; DNA; 201 BP.
XX
AC ADQ41824;
XX
DT 18-NOV-2004 (first entry)
XX
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 3487.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human; ds.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JJ, Iakoubova O;
XX
DR WPI; 2004-533949/51.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 7; SEQ ID NO 3487; 145pp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a transcript-based context sequence
CC which flanks an SNP found in a human myocardial infarction-associated
CC gene of the invention. Note: This sequence was not shown in the
CC specification. The sequence has come from an electronic sequence listing
CC downloaded from the WIPO website.
XX
SQ Sequence 201 BP; 65 A; 36 C; 38 G; 61 T; 0 U; 1 Other;

Query Match 9.8%; Score 65; DB 13; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.8e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 13 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 72

Qy 619 ATTCG 623
|||||
Db 73 ATTCG 77

RESULT 72
ADQ41835
ID ADQ41835 standard; DNA; 201 BP.
XX
AC ADQ41835;
XX
DT 18-NOV-2004 (first entry)
XX
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 3498.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human; ds.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.

XX
PI Cargill M, Devlin JJ, Iakoubova O;
XX
DR WPI; 2004-533949/51.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 7; SEQ ID NO 3498; 145pp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a transcript-based context sequence
CC which flanks an SNP found in a human myocardial infarction-associated
CC gene of the invention. Note: This sequence was not shown in the
CC specification. The sequence has come from an electronic sequence listing
CC downloaded from the WIPO website.
XX
SQ Sequence 201 BP; 64 A; 39 C; 37 G; 60 T; 0 U; 1 Other;

```
  Query Match             9.8%;  Score 65;  DB 13;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 80

Qy        619 ATTCG 623
              |||||
Db         81 ATTCG 85
```

RESULT 73
ADQ41829
ID ADQ41829 standard; DNA; 201 BP.
XX
AC ADQ41829;
XX
DT 18-NOV-2004 (first entry)
XX
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 3492.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW ' cardiant; gene therapy; human; ds.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JJ, Iakoubova O;
XX
DR WPI; 2004-533949/51.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 7; SEQ ID NO 3492; 145pp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a transcript-based context sequence
CC which flanks an SNP found in a human myocardial infarction-associated
CC gene of the invention. Note: This sequence was not shown in the
CC specification. The sequence has come from an electronic sequence listing
CC downloaded from the WIPO website.
XX
SQ Sequence 201 BP; 62 A; 42 C; 39 G; 57 T; 0 U; 1 Other;

```
  Query Match             9.8%;  Score 65;  DB 13;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 181

Qy        619 ATTCG 623
              |||||
Db        182 ATTCG 186
```

RESULT 74
ADQ41838
ID ADQ41838 standard; DNA; 201 BP.
XX
AC ADQ41838;
XX
DT 18-NOV-2004 (first entry)
XX
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 3501.

XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human; ds.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JJ, Iakoubova O;
XX
DR WPI; 2004-533949/51.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 7; SEQ ID NO 3501; 145pp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a transcript-based context sequence
CC which flanks an SNP found in a human myocardial infarction-associated
CC gene of the invention. Note: This sequence was not shown in the
CC specification. The sequence has come from an electronic sequence listing
CC downloaded from the WIPO website.
XX
SQ Sequence 201 BP; 62 A; 42 C; 39 G; 57 T; 0 U; 1 Other;

Query Match 9.8%; Score 65; DB 13; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.8e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 122 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 181

Qy 619 ATTCG 623
|||||
Db 182 ATTCG 186

RESULT 75
ADQ41833
ID ADQ41833 standard; DNA; 201 BP.
XX
AC ADQ41833;
XX
DT 18-NOV-2004 (first entry)
XX
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 3496.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human; ds.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JJ, Iakoubova O;
XX
DR WPI; 2004-533949/51.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 7; SEQ ID NO 3496; 145pp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a transcript-based context sequence
CC which flanks an SNP found in a human myocardial infarction-associated
CC gene of the invention. Note: This sequence was not shown in the
CC specification. The sequence has come from an electronic sequence listing
CC downloaded from the WIPO website.
XX
SQ Sequence 201 BP; 65 A; 36 C; 38 G; 61 T; 0 U; 1 Other;

Query Match 9.8%; Score 65; DB 13; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.8e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 72

Qy        619 ATTCG 623
              |||||
Db         73 ATTCG 77
```

```
RESULT 76
ADG39431
ID   ADG39431 standard; DNA; 657 BP.
XX
AC   ADG39431;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human CLMF 35 kDa subunit DNA.
XX
KW   human; cytotoxic lymphocyte maturation factor; CLMF;
KW   activated T-cell stimulator; natural killer cell stimulator;
KW   immunoenhancer; antitumour; tumour; cancer; ds; gene.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             67. .657
FT                   /*tag=  a
FT                   /partial
FT                   /product= "CLMF 35 kDa subunit"
FT                   /note= "No start or stop codon given"
XX
PN   US2003204059-A1.
XX
PD   30-OCT-2003.
XX
PF   08-OCT-2002; 2002US-00267565.
XX
PR   22-DEC-1989;   89US-00455708.
PR   09-MAY-1990;   90US-00520935.
PR   27-AUG-1990;   90US-00572284.
PR   24-MAR-1992;   92US-00857023.
PR   02-MAR-1994;   94US-00205011.
PR   02-JUN-1995;   95US-00459151.
PR   22-SEP-1999;   99US-00401839.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CIE SA F.
XX
PI   Gately MK,  Gubler UA,  Hulmes JD,  Podlaski FJ,  Stern AS;
PI   Chizzonite RA,  Pan YE;
XX
DR   WPI; 2004-010534/01.
DR   P-PSDB; ADG39428.
XX
PT   Novel protein comprising cytotoxic lymphocyte maturation factor in
PT   substantially pure form or protein which exhibits cytotoxic lymphocyte
PT   maturation factor activity, useful as antitumor and immunoenhancing
PT   agent.
XX
PS   Claim 20; Page 29; 74pp; English.
XX
CC   The invention relates to a protein which comprises a cytotoxic lymphocyte
CC   maturation factor (CLMF). The protein is useful for stimulating activated
CC   T-cells which involves treating T-cells with the protein. The method
CC   further involves treating the activated T-cells with IL2 or its
CC   biologically active fragment. The protein is useful for stimulating
CC   natural killer cells which involves treating the natural killer cells
CC   with the protein. The protein has immunoenhancing and antitumour effects
CC   when used as single therapeutic agent in vivo. The present sequence is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 657 BP; 186 A; 166 C; 139 G; 166 T; 0 U; 0 Other;
```

```
  Query Match             9.8%;  Score 65;  DB 12;  Length 657;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        619 ATTCG 623
              |||||
Db        610 ATTCG 614
```

```
RESULT 77
AAQ97485
ID   AAQ97485 standard; cDNA; 660 BP.
XX
AC   AAQ97485;
XX
DT   25-MAR-2003  (revised)
DT   22-DEC-1995  (first entry)
XX
DE   Human interleukin-12 35 kD subunit.
XX
KW   Interleukin-12; IL-12; cytokine; gamma-interferon; T cell;
KW   natural killer cell; graft vs. host disease; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
XX
PN   WO9519786-A1.
XX
PD   27-JUL-1995.
XX
PF   20-JAN-1995;   95WO-US000879.
XX
PR   21-JAN-1994;   94US-00186529.
XX
PA   (GEMY ) GENETICS INST INC.
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Wolf SF,  Sykes M;
XX
DR   WPI; 1995-269273/35.
DR   P-PSDB; AAR79187.
XX
PT   Control of graft versus host disease using interleukin 12 - partic.
PT   admin. at the time of bone marrow transplant.
XX
PS   Disclosure; Page 23-24; 32pp; English.
XX
CC   AAQ97484 and AAQ97485 are from human lymphoblast cell line RMPI 8866. IL-
CC   12 is a heterodimeric cytokine which was originally identified as a
CC   factor which induces gamma-interferon from T cells and natural killer
CC   cells as set forth in PCT/US91/06332, published April 2 1992, and
CC   incorporated by reference. EP 433827, published June 26 1991, disclosed
CC   IL-12 as a cytotoxin lymphocyte maturation factor. In the patent, IL-12
CC   is defined as a heterodimeric glycoprotein comprised of two covalently
CC   linked subunits having mol. wts of about 40 kD and 35 kD. The two
CC   subunits may be disulfide-bonded. IL-12 is administered to prevent or
CC   ameliorate GVHD. Dosage is 1 ng-0.1 mg (esp. 1.0 ng-1 microg)/kg daily
CC   for 3 days, the first dose given 1 hr. after transplant. IL-12 can be
CC   used as the native heterodimer or as subunits. (Updated on 25-MAR-2003 to
CC   correct PN field.)
XX
SQ   Sequence 660 BP; 188 A; 164 C; 139 G; 169 T; 0 U; 0 Other;
```

```
  Query Match             9.8%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        619 ATTCG 623
              |||||
Db        610 ATTCG 614


RESULT 78
AAV07274
ID   AAV07274 standard; cDNA; 660 BP.
XX
AC   AAV07274;
XX
DT   25-SEP-1998  (first entry)
XX
DE   Human Interleukin-12 p35 gene.
XX
KW   IL-12 subunit; expression construct; treatment; asthma;
KW   microbial infection; viral infection; cancer; Human; Interleukin; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "IL-12 p35"
FT                   /transl_except= (pos:58. .60,aa:Ser)
XX
PN   WO9817689-A2.
XX
PD   30-APR-1998.
XX
PF   10-OCT-1997;   97WO-US018779.
XX
PR   18-OCT-1996;   96US-0028676P.
XX
PA   (GENE-) GENEMEDICINE INC.
XX
PI   Nordstrom J,  Freimark B,  Deshpande D;
XX
DR   WPI; 1998-261428/23.
DR   P-PSDB; AAV07274.
XX
PT   Constructs for expression of interleukin-12 sub-units - are used for
PT   delivery of IL-12 sub-units for treating e.g. asthma, microbial or viral
PT   infections and certain cancers.
XX
PS   Claim 1; Page 34-35; 80pp; English.
XX
CC   The IL-12 subunits AAV07273 and AAV07274 can be expressed using an
CC   appropriate expression construct engineered into a plasmid. The plasmids
CC   can provide for efficient expression of IL-12 subunits. The products can
CC   be used for the treatment of asthma, microbial and viral infections and
CC   certain cancers
XX
SQ   Sequence 660 BP; 188 A; 167 C; 138 G; 167 T; 0 U; 0 Other;

  Query Match             9.8%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        619 ATTCG 623
              |||||
Db        610 ATTCG 614


RESULT 79
AAV07218
ID   AAV07218 standard; DNA; 660 BP.
XX
AC   AAV07218;
XX
DT   12-AUG-1998  (first entry)
XX
DE   DNA encoding human interleukin-12 35kDa subunit.
XX
KW   Interleukin-12; IL-12; graft-versus-host disease;
KW   GVHD. bone marrow transplantation; graft-versus-leukemia; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "Interleukin-12_35kDa_subunit"
XX
PN   US5756085-A.
XX
PD   26-MAY-1998.
XX
PF   30-APR-1996;   96US-00640386.
XX
PR   21-JAN-1994;   94US-00186529.
XX
PA   (GEMY ) GENETICS INST INC.
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Sykes M,  Wolf SF;
XX
DR   WPI; 1998-321459/28.
DR   P-PSDB; AAW51222.
XX
PT   Therapy of graft-versus-host disease - by administration of interleukin-
PT   12 to maintain and/or promote graft-versus-leukaemia effects.
XX
PS   Disclosure; Col 23-24; 20pp; English.
XX
CC   The invention relates to a method for the treatment or prevention of
CC   graft-versus-host disease (GVHD) which comprises the administration of
CC   interleukin-12 (IL-12) at the time of bone-marrow transplantation to
CC   maintain or promote graft-versus-leukaemia effects. Preferably, dosage is
CC   0.001-100 (preferably 1-100) mu g/kg for 3 days starting on the day of
CC   the bone marrow transplant. IL-12 is administered daily until there is an
CC   improvement in the condition. Administration is oral, cutaneous,
CC   subcutaneous, intravenous or by inhalation preferably subcutaneous, or
CC   intravenous. The present sequence encodes the human interleukin-12 35kDa
CC   subunit
XX
SQ   Sequence 660 BP; 188 A; 164 C; 139 G; 169 T; 0 U; 0 Other;

  Query Match             9.8%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        619 ATTCG 623
              |||||
Db        610 ATTCG 614


RESULT 80
AAZ40407
ID   AAZ40407 standard; DNA; 660 BP.
XX
AC   AAZ40407;
XX
```

DT 15-FEB-2000 (first entry)
XX
DE Human interleukin 12 p35 subunit wild type coding sequence.
XX
KW Wild type; human; interferon-alpha; plasmid; cytomegalovirus; CMV;
KW promoter; growth hormone; untranslated region; UTR; mammal; disease;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO9947678-A2.
XX
PD 23-SEP-1999.
XX
PF 12-MAR-1999; 99WO-US005394.
XX
PR 19-MAR-1998; 98US-0078654P.
XX
PA (GENE-) GENEMEDICINE INC.
XX
PI Nordstrom J, Pericle F, Rolland A, Ralston R;
XX
DR WPI; 1999-562116/47.
DR P-PSDB; AAY42488.
XX
PT New plasmids containing an interferon-alpha coding sequence, used for the
PT treatment of a mammalian condition or disease, particularly cancer.
XX
PS Claim 11; Page 38-39; 137pp; English.
XX
CC This sequence represents the wild type coding region for the human
CC interleukin 12 p35 subunit. The invention relates to a novel plasmid
CC comprising a cytomegalovirus (CMV) promoter transcriptionally linked with
CC an interferon alpha (IFN-alpha) coding sequence, and a growth hormone 3'-
CC untranslated region (UTR). The plasmids can be used for treating a
CC mammalian condition or disease, particularly cancer
XX
SQ Sequence 660 BP; 188 A; 167 C; 138 G; 167 T; 0 U; 0 Other;

Query Match 9.8%; Score 65; DB 2; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.8e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        619 ATTCG 623
              |||||
Db        610 ATTCG 614
```

RESULT 81
AAD15217
ID AAD15217 standard; DNA; 660 BP.
XX
AC AAD15217;
XX
DT 01-NOV-2001 (first entry)
XX
DE Modified human cytokine p35 encoding DNA from clone R2-555.
XX
KW Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW p35; mutant; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX

FH	Key	Location/Qualifiers
FT	CDS	1. .660
FT		/*tag= a
FT		/product= "Modified p35 protein precursor"
FT	sig_peptide	1. .66
FT		/*tag= b
FT	mat_peptide	67. .657
FT		/*tag= c
FT		/product= "Mature modified p35 protein"

XX
PN WO200140257-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000WO-US032664.
XX
PR 02-DEC-1999; 99US-0169035P.
PR 28-NOV-2000; 2000US-00725324.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Leong SR, Punnonen J;
XX
DR WPI; 2001-502381/55.
DR P-PSDB; AAE08610.
XX
PT Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT retinopathy and cancer.
XX
PS Claim 87; Page 140; 223pp; English.
XX
CC The invention relates to nucleic acids encoding modified cytokine
CC polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC gamma induction activities. The polypeptides and polynucleotides of the
CC invention are useful for treating various diseases e.g. bacterial
CC infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC vaccinated host's cell-mediated immunity for protective response to a
CC pathogen. The present sequence is a modified human p35 protein encoding
CC DNA
XX
SQ Sequence 660 BP; 189 A; 173 C; 136 G; 162 T; 0 U; 0 Other;

Query Match 9.8%; Score 65; DB 5; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.8e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        216 TGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGA 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 TGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGA 266

Qy        276 ATTAA 280
              |||||
Db        267 ATTAA 271
```

RESULT 82
AAD15221
ID AAD15221 standard; DNA; 660 BP.
XX
AC AAD15221;
XX
DT 01-NOV-2001 (first entry)
XX
DE Human cytokine p35 DNA.
XX
KW Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW p35; ds.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	CDS	1. .660
FT		/*tag= a

```
FT                   /product= "p35 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .657
FT                   /*tag=  c
FT                   /product= "Mature p35 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08614.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 91; Page 142; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is human p35 protein encoding DNA
XX
SQ   Sequence 660 BP; 188 A; 166 C; 139 G; 167 T; 0 U; 0 Other;

  Query Match             9.8%;  Score 65;  DB 5;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        619 ATTCG 623
              |||||
Db        610 ATTCG 614


RESULT 83
AAL44226
ID   AAL44226 standard; DNA; 660 BP.
XX
AC   AAL44226;
XX
DT   08-NOV-2002  (first entry)
XX
DE   Human interleukin 12A (IL-12A) coding sequence.
XX
KW   Human; gene; ds; interleukin 12A; IL-12A; drug screening; AIDS; malaria;
KW   tuberculosis; cancer; haplotyping; genotyping; transgenic animal.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "Human interleukin 12A (IL-12A)"
FT   variation       replace(142, A)
FT                   /*tag=  b
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   WO200229115-A1.
XX
PD   11-APR-2002.
XX
PF   05-OCT-2001; 2001WO-US031656.
XX
PR   06-OCT-2000; 2000US-0238693P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Armstrong B,  Cappola G,  Choi JY,  Gilson CR,  Kliem SE,  Koshy B;
PI   Parks KE;
XX
DR   WPI; 2002-315865/35.
DR   P-PSDB; AAO15506.
XX
PT   New interleukin 12A (IL-12A) gene polymorphic variants, for studying the
PT   expression and function of IL-12A and screening candidate drugs for
PT   treating AIDS and cancer.
XX
PS   Claim 28; Fig 2; 72pp; English.
XX
CC   The invention comprises the amino acid and coding sequence of the human
CC   interleukin 12A (IL-12A) protein. Specifically the invention relates to
CC   the identification of polymorphisms within the human (IL-12A) gene
CC   sequence. The polymorphisms identified in the human IL-12A gene sequence
CC   are useful in studying the expression and function of IL-12A, and in
CC   screening drugs for the treatment of disorders such as AIDS, malaria,
CC   tuberculosis and cancer. The IL-12A polymorphisms may be used to
CC   haplotype and genotype the IL-12A gene of an individual. The IL-12A DNA
CC   sequences of the invention can be used to create transgenic animals for
CC   studying expression of the IL-12A isogenes in vivo. The present DNA
CC   sequence represents the coding sequence of the human interleukin 12A (IL-
CC   12A) gene
XX
SQ   Sequence 660 BP; 188 A; 166 C; 139 G; 167 T; 0 U; 0 Other;

  Query Match             9.8%;  Score 65;  DB 6;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        619 ATTCG 623
              |||||
Db        610 ATTCG 614


RESULT 84
ACC47589
ID   ACC47589 standard; DNA; 660 BP.
XX
AC   ACC47589;
XX
DT   12-JUN-2003  (first entry)
XX
DE   Human interleukin 12 (hIL-12) P35 subunit gene.
XX
KW   Human; interleukin 12; hIL-12; baculovirus vector;
KW   recombinant production; AcNPV-hIL12;
KW   Autographa california nuclear polyhedrosis virus; tumour; cancer;
KW   infection; bacterial; viral; cytostatic; P35 subunit; gene; ds.
XX
OS   Homo sapiens.
XX
PN   CN1357622-A.
XX
```

PD 10-JUL-2002.
XX
PF 02-NOV-2001; 2001CN-00133631.
XX
PR 02-NOV-2001; 2001CN-00133631.
XX
PA (UYWU-) UNIV WUHAN.
XX
PI Meng X, Xu J, Yu Z;
XX
DR WPI; 2002-741792/81.
XX
PT Human interleukin-12 recombinant insect virus strain and its preparation.
XX
PS Claim 4; Fig 6; 17pp; Chinese.
XX
CC The invention relates to a recombinant baculovirus comprising DNA
CC encoding human interleukin 12 (hIL-12) and methods for its preparation.
CC The recombinant baculovirus strain is designated Autographa california
CC nuclear polyhedrosis virus AcNPV-hIL12 (CCTCC No. 2 V200108). This strain
CC contains two human IL-12 subunit genes, the IL-12 P35 subunit gene
CC (ACC47589) and the IL-12 P40 subunit gene (ACC47592) which are
CC respectively under the control of the viral polyhedrin and P10 promoters.
CC The baculovirus can be used in the recombinant production of human IL-12
CC which is suitable for treating tumours and bacterial, viral and other
CC infections. The present sequence represents the human IL-12 P35 subunit
CC gene used in construction of the baculovirus vector of the invention
XX
SQ Sequence 660 BP; 188 A; 166 C; 139 G; 167 T; 0 U; 0 Other;

Query Match 9.8%; Score 65; DB 6; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.8e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy 619 ATTCG 623
|||||
Db 610 ATTCG 614

RESULT 85
ADF77244
ID ADF77244 standard; DNA; 660 BP.
XX
AC ADF77244;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human IL-12 p35 subunit DNA.
XX
KW ds; human; interferon alpha expression plasmid; tumour; IL-12.
XX
OS Homo sapiens.
XX
PN US2003181405-A1.
XX
PD 25-SEP-2003.
XX
PF 29-APR-2002; 2002US-00136837.
XX
PR 12-MAR-1999; 99US-00268135.
XX
PA (NORD/) NORDSTROM J L.
PA (PERI/) PERICLE F.
PA (ROLL/) ROLLAND A.
PA (RALS/) RALSTON R O.
XX
PI Nordstrom JL, Pericle F, Rolland A, Ralston RO;
XX
DR WPI; 2004-020834/02.
XX
PT A mammalian interferon alpha expression plasmid is useful in gene therapy
PT to deliver interferon alpha to cells to modulate tumor activity in the
PT treatment of cancer.
XX
PS Disclosure; SEQ ID NO 6; 65pp; English.
XX
CC The invention relates to a mammalian interferon alpha expression plasmid,
CC comprising a promoter and a synthetic 5' intron transcriptionally linked
CC with an interferon alpha coding sequence and a 3' untranslated region.
CC The mammalian interferon alpha expression plasmid is useful for treating
CC tumour growth. The present sequence is used in the exemplification of the
CC present invention.
XX
SQ Sequence 660 BP; 188 A; 167 C; 138 G; 167 T; 0 U; 0 Other;

Query Match 9.8%; Score 65; DB 12; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.8e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy 619 ATTCG 623
|||||
Db 610 ATTCG 614

RESULT 86
ADP88401
ID ADP88401 standard; cDNA; 702 BP.
XX
AC ADP88401;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human interleukin-12 alpha chain coding sequence.
XX
KW antiinflammatory; antiasthmatic; antiallergic; immunosuppressive;
KW antibacterial; protozoacide; gene therapy; expression vector;
KW interleukin; ecdysone-inducible promoter; ss; gene; interleukin-12;
KW human.
XX
OS Homo sapiens.
XX
PN WO2004052929-A2.
XX
PD 24-JUN-2004.
XX
PF 08-DEC-2003; 2003WO-IB006404.
XX
PR 06-DEC-2002; 2002GB-00028465.
XX
PA (UYBE-) UNIV QUEENS BELFAST.
XX
PI Vandenbroeck K, Alloza I;
XX
DR WPI; 2004-487887/46.
XX
PT New expression vector comprising DNA encoding a subunit of a dimeric form
PT of interleukin under transcriptional control of an ecdysone-inducible
PT promoter, useful in preparing a composition for treating e.g.,
PT inflammatory disease.
XX
PS Disclosure; Page 85-86; 87pp; English.
XX
CC The present invention relates to an expression vector comprising DNA
CC encoding a subunit of a dimeric form of interleukin under transcriptional
CC control of an ecdysone-inducible promoter. The expression vector is
CC useful in preparing a composition for treating a disease having a
CC pathogenesis which includes endogenous production of cytokine IL-12, IL-
CC 23 or IL-27, e.g., infectious diseases, bacterial, protozoal or virus-

```
CC   induced inflammation, epithelial airway inflammation such as asthma,
CC   allergic disease, or autoimmune disease such as multiple sclerosis or
CC   inflammatory bowel disease. The present sequence is the coding sequence
CC   of the human interleukin-12 alpha chain used in the exemplification of
CC   the invention.
XX
SQ   Sequence 702 BP; 199 A; 184 C; 147 G; 172 T; 0 U; 0 Other;

  Query Match             9.8%;  Score 65;  DB 12;  Length 702;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 624

Qy        619 ATTCG 623
              |||||
Db        625 ATTCG 629


RESULT 87
AAQ67880
ID   AAQ67880 standard; DNA; 721 BP.
XX
AC   AAQ67880;
XX
DT   25-MAR-2003  (revised)
DT   23-MAR-1995  (first entry)
XX
DE   EPV 42 kD promoter/Human IL-12 p35 subunit expression cassette.
XX
KW   Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant;
KW   murine; interleukin-2; IL-2; pRW825; pmut-1; pBS-SK; pMM151; TK vector;
KW   plasmid; vaccinia; H6 promoter; amplify; primer; antigenic response;
KW   polymerase chain reaction; poxvirus; pSD542; immunological response;
KW   pathogen; human; interferon; IFN; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   promoter        1. .61
FT                   /*tag=  a
FT                   /note= "Vaccinia E3L promoter"
FT   CDS             32. .1018
FT                   /*tag=  b
FT                   /product= "Human IL-12 p35"
XX
PN   WO9416716-A1.
XX
PD   04-AUG-1994.
XX
PF   21-JAN-1994;   94WO-US000888.
XX
PR   21-JAN-1993;   93US-00007115.
PR   19-JAN-1994;   94US-00184009.
XX
PA   (VIRO-) VIROGENETICS CORP.
XX
PI   Paoletti E,  Tartaglia J,  Cox WI;
XX
DR   WPI; 1994-263767/32.
XX
PT   Attenuated recombinant virus used for cancer therapy - comprises DNA
PT   encoding cytokine and/or tumour associated antigen.
XX
PS   Example 27; Fig 34; 232pp; English.
XX
CC   The sequences given in AAQ67879-80 are expression cassettes which contain
CC   the p40 and p35 subunits of human interleukin-12 (IL-12) under the
CC   control of the entomopox virus (EPV) promoter and the vaccinia E3L
CC   promoter, respectively. These sequences were used in the construction of
CC   an ALVAC-based recombinant virus containing the genes for the two
CC   subunits of human IL-12. The p40 subunit was amplified using primers
CC   JP202 and JP189 and placed under the control of the entomopox virus (EPV)
CC   42 kD promoter in plasmid PBSHIL12p40II. The p35 subunit was amplified
CC   using primers JP186 and JP201 and placed under the control of the
CC   vaccinia E3L promoter using primers JP218 and JP220. The expression
CC   cassette was isolated and ligated with pBSSK+ generating plasmid
CC   PBSHIL12p35II. The p35 and p40 expression cassettes were excised and
CC   assembled in pBSSK+ to give PBSHIL12 in which the two expression
CC   cassettes are orientated head-to-head relative to each other. The
CC   combination casette containing the poxvirus promoted genes for both IL-12
CC   subunits was excised from PBSHIL12 and cloned in to ALVAC C6 vector
CC   plasmid pC6L to give pC6HIL12. Recombination between this donor plasmid
CC   and ALVAC rescuing virus produced recombinant virus ALVAC+IL12, which
CC   contains both the human IL-12 genes in the C6 locus. The resulting virus
CC   may be used in a composition for inducing an antigenic or immunological
CC   response, ie. for immunisation against pathogens. (Updated on 25-MAR-2003
CC   to correct PN field.)
XX
SQ   Sequence 721 BP; 209 A; 171 C; 151 G; 190 T; 0 U; 0 Other;

  Query Match             9.8%;  Score 65;  DB 2;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy        619 ATTCG 623
              |||||
Db        671 ATTCG 675


RESULT 88
AAZ08515
ID   AAZ08515 standard; DNA; 721 BP.
XX
AC   AAZ08515;
XX
DT   19-OCT-1999  (first entry)
XX
DE   Vaccinia E3L/human IL-12 P35 expression cassette.
XX
KW   Attenuated recombinant virus; cytokine; tumour associated antigen;
KW   NYVAC recombinant virus; ALVAC recombinant virus; gene therapy; rabies;
KW   cancer; tumour necrosis factor; nuclear phosphoprotein; p53; IL-2; GMCSF;
KW   interleukin; interferon; IFN-gamma; IL-4; melanoma associated antigen;
KW   carcinoembryonic antigen; immunisation; antigenic; poxvirus; influenza;
KW   immunological response; immunotherapy; vaccine; Newcastle Disease; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
OS   Vaccinia virus.
XX
PN   US5942235-A.
XX
PD   24-AUG-1999.
XX
PF   02-JUN-1995;   95US-00458356.
XX
PR   24-DEC-1981;   81US-00334456.
PR   08-DEC-1982;   82US-00446824.
PR   19-JUN-1984;   84US-00622135.
PR   27-AUG-1987;   87US-00090209.
PR   28-AUG-1987;   87US-00090711.
PR   20-OCT-1987;   87US-00110335.
PR   25-APR-1988;   88US-00186054.
PR   23-AUG-1988;   88US-00234390.
PR   14-JUN-1990;   90US-00537882.
PR   14-JUN-1990;   90US-00537890.
PR   16-DEC-1991;   91US-00805567.
PR   03-MAR-1992;   92US-00847977.
PR   06-MAR-1992;   92US-00847951.
```

PR 04-MAY-1992; 92US-00881995.
PR 22-JUL-1992; 92US-00918278.
PR 20-JAN-1993; 93US-00007115.
PR 19-JAN-1994; 94US-00184009.
PR 14-APR-1994; 94US-00228926.
PR 13-SEP-1994; 94US-00306259.
XX
PA (HEAL-) HEALTH RES INC.
XX
PI Paoletti E;
XX
DR WPI; 1999-493494/41.
XX
PT Recombinant poxviruses comprising exogenous DNA encoding antigenic
PT determinants useful in immunotherapy to immunize against cancers and
PT other diseases such as influenza, Newcastle Disease and rabies.
XX
PS Example 27; Fig 34; 163pp; English.
XX
CC The present invention describes a recombinant poxvirus (I), comprising
CC exogenous DNA encoding an antigenic determinant of a pathogen which is
CC then expressed in vivo in infected host cells after administration to a
CC patient and therefore induces an immunological response. (I) may be used
CC to vaccinate patients against a wide range of diseases and disorders
CC depending on the type of antigen encoded by the exogenous DNA. (I) may be
CC used to vaccinate against diseases such as rabies, influenza and
CC Newcastle Disease. It is particularly useful for immunising against
CC cancers. The poxvirus (I) also provides a means of manipulating
CC lymphocytes and tumour cells for use in cell-based immunotherapeutic
CC modalities for cancer. (I) also have enhanced safety compared to
CC unattenuated viruses (attenuation reduces the virulence of the viruses)
CC and known recombinant poxvirus vaccines. This increased level of safety
CC reduces the possibility of a 'runaway' infection in the host and reduces
CC the chance of transmission from vaccinated to unvaccinated individuals
CC and contamination of the environment. The present sequence represents a
CC Vaccinia E3L/human IL-12 P35 expression cassette used in the
CC exemplification of the present invention
XX
SQ Sequence 721 BP; 209 A; 171 C; 151 G; 190 T; 0 U; 0 Other;

Query Match 9.8%; Score 65; DB 2; Length 721;
Best Local Similarity 100.0%; Pred. No. 2.8e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy 619 ATTCG 623
|||||
Db 671 ATTCG 675

RESULT 89
ADR21891
ID ADR21891 standard; DNA; 721 BP.
XX
AC ADR21891;
XX
DT 04-NOV-2004 (first entry)
XX
DE Vaccinia E3L/human IL-12 expression cassette.
XX
KW Cytostatic; Vaccine; recombinant poxvirus; nonessential region;
KW attenuated avipox Virus; carcinoembryonic antigen; B7 protein;
KW cancer therapy; ds; human; IL-12; interleukin-12; E3L;
KW expression cassette.
XX
OS Vaccinia virus.
OS Homo sapiens.
OS Synthetic.
XX
PN US6780407-B1.
XX
PD 24-AUG-2004.
XX
PF 15-SEP-2000; 2000US-00663667.
XX
PR 08-MAR-1989; 89US-00320471.
PR 14-FEB-1990; 90US-00478179.
PR 07-JAN-1991; 91US-00638080.
PR 07-MAR-1991; 91US-00666056.
PR 11-JUN-1991; 91US-00713967.
PR 16-DEC-1991; 91US-00805567.
PR 03-MAR-1992; 92US-00847977.
PR 06-MAR-1992; 92US-00847951.
PR 21-JAN-1993; 93US-00007115.
PR 19-JAN-1994; 94US-00184009.
PR 30-AUG-1995; 95US-00521016.
XX
PA (AVET) AVENTIS PASTEUR.
XX
PI Paoletti E, Tartaglia J, Cox WI;
XX
DR WPI; 2004-601998/58.
XX
PT New recombinant poxvirus which is an attenuated avipox Virus that
PT expresses an exogenous DNA encoding carcinoembryonic antigen and an
PT exogenous DNA encoding B7 protein, useful for cancer therapy.
XX
PS Example 27; SEQ ID NO 199; 181pp; English.
XX
CC The invention describes a recombinant poxvirus containing exogenous DNA
CC in a nonessential region of the poxvirus, where the poxvirus is an
CC attenuated avipox Virus that expresses an exogenous DNA encoding
CC carcinoembryonic antigen and an exogenous DNA encoding B7 protein. Also
CC described are: a composition comprising a poxvirus above in admixture
CC with a carrier; and expressing carcinoembryonic antigen and B7 protein in
CC vivo comprising administering to a mammal the composition above.
CC Disclosed are: making recombinant poxvirus defined above; recombinant
CC poxvirus vaccine having an increased level of safety compared to known
CC recombinant poxvirus vaccines; and a modified vector for expressing a
CC gene product in a host. The recombinant poxvirus is useful for providing
CC a recombinant poxvirus vaccine having an increased level of safety
CC compared to known recombinant poxvirus vaccines. The recombinant poxvirus
CC is useful for cancer therapy. This sequence represents a human IL-12
CC expression cassette used in the creation of NYVAC rescue virus and
CC canarypox virus vector ALVAC comprising the human IL-12 gene.
XX
SQ Sequence 721 BP; 209 A; 171 C; 151 G; 190 T; 0 U; 0 Other;

Query Match 9.8%; Score 65; DB 13; Length 721;
Best Local Similarity 100.0%; Pred. No. 2.8e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy 619 ATTCG 623
|||||
Db 671 ATTCG 675

RESULT 90
ADK98708
ID ADK98708 standard; DNA; 761 BP.
XX
AC ADK98708;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human interleukin-12 (IL-12) P35 subunit DNA seqid 3.
XX
KW human; recombinant interleukin-12; IL-12; P35 subunit; P40 subunit; ds.
XX

OS Homo sapiens.
XX
PN CN1408727-A.
XX
PD 09-APR-2003.
XX
PF 29-SEP-2001; 2001CN-00126923.
XX
PR 29-SEP-2001; 2001CN-00126923.
XX
PA (ZHON-) ZHONGXIN GUOJIAN PHARM CO LTD SHANGHAI.
XX
PI Wan G, Li C;
XX
DR WPI; 2003-664076/63.
XX
PT Method for efficiently expressing recombinant human interleukin 12 in
PT eukaryotic cell.
XX
PS Claim 6; SEQ ID NO 3; 14pp; Chinese.
XX
CC The invention describes the process of producing human recombinant
CC interleukin-12 (IL-12) includes: providing a nucleotide sequence
CC corresponding to the P35 subunit with the first signal peptide and a
CC nucleotide sequence corresponding to the P40 subunit; inserting the
CC nucleotide sequences into an expression vector; converting the eukaryotic
CC cell with the expression vector; and culturing the transfected eukaryotic
CC cell in condition suitable for recombinant human IL-12 expression. The
CC process balances the expression amount of both P35 and P40 subunits and
CC thus raises the expression amount of IL-12 with bioactivity via raising
CC the expression strength of P35 subunit. This sequence represents the
CC human interleukin-12 (IL-12) P35 subunit polynucleotide.
XX
SQ Sequence 761 BP; 205 A; 204 C; 164 G; 187 T; 0 U; 1 Other;

Query Match 9.8%; Score 65; DB 10; Length 761;
Best Local Similarity 100.0%; Pred. No. 2.8e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 651 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 710

Qy 619 ATTCG 623
|||||
Db 711 ATTCG 715

RESULT 91
ADK98706
ID ADK98706 standard; DNA; 761 BP.
XX
AC ADK98706;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human interleukin-12 (IL-12) P35 subunit DNA seqid 1.
XX
KW human; recombinant interleukin-12; IL-12; P35 subunit; P40 subunit; ds.
XX
OS Homo sapiens.
XX
PN CN1408727-A.
XX
PD 09-APR-2003.
XX
PF 29-SEP-2001; 2001CN-00126923.
XX
PR 29-SEP-2001; 2001CN-00126923.
XX
PA (ZHON-) ZHONGXIN GUOJIAN PHARM CO LTD SHANGHAI.
XX
PI Wan G, Li C;
XX
DR WPI; 2003-664076/63.
XX
PT Method for efficiently expressing recombinant human interleukin 12 in
PT eukaryotic cell.
XX
PS Claim 4; SEQ ID NO 1; 14pp; Chinese.
XX
CC The invention describes the process of producing human recombinant
CC interleukin-12 (IL-12) includes: providing a nucleotide sequence
CC corresponding to the P35 subunit with the first signal peptide and a
CC nucleotide sequence corresponding to the P40 subunit; inserting the
CC nucleotide sequences into an expression vector; converting the eukaryotic
CC cell with the expression vector; and culturing the transfected eukaryotic
CC cell in condition suitable for recombinant human IL-12 expression. The
CC process balances the expression amount of both P35 and P40 subunits and
CC thus raises the expression amount of IL-12 with bioactivity via raising
CC the expression strength of P35 subunit. This sequence represents the
CC human interleukin-12 (IL-12) P35 subunit polynucleotide.
XX
SQ Sequence 761 BP; 199 A; 209 C; 167 G; 185 T; 0 U; 1 Other;

Query Match 9.8%; Score 65; DB 10; Length 761;
Best Local Similarity 100.0%; Pred. No. 2.8e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 651 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 710

Qy 619 ATTCG 623
|||||
Db 711 ATTCG 715

RESULT 92
AAV83207
ID AAV83207 standard; cDNA; 762 BP.
XX
AC AAV83207;
XX
DT 02-MAR-1999 (first entry)
XX
DE Interleukin (IL)-12A cDNA.
XX
KW Mouse; immunodeficient; pathogen; tumour; lymphocyte; antigen;
KW immunomodulator; vector; vaccine; cancer; HIV; Leishmania; Mycobacterium;
KW Listeria; Plasmodium; retrovirus; evaluation;
KW human immunodeficiency virus; ds.
XX
OS Homo sapiens.
XX
PN WO9844788-A2.
XX
PD 15-OCT-1998.
XX
PF 09-APR-1998; 98WO-US006944.
XX
PR 09-APR-1997; 97US-00838702.
PR 01-MAY-1997; 97US-00848760..
PR 09-DEC-1997; 97US-0069163P.
XX
PA (CHAN/) CHANG L.
XX
PI Chang L;
XX
DR WPI; 1999-024005/02.
XX
PT Use of immunodeficient mice comprising human cells - particularly
PT SCTD/beige mice comprising human immune cells for evaluating vaccines
PT against cancers or human pathogens, e.g. HIV.
XX
PS Example 10(c)(i); Page 108-109; 154pp; English.

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XX
CC   Immunodeficient mice comprising human cells can be used for exposure to
CC   human pathogens and/or their components or human tumour cells and human
CC   peripheral blood lymphocytes. Also claimed is a vaccine comprising a cell
CC   modified to express an antigen and an immune-modulating protein, this is
CC   preferably an expression vector comprising a polynucleotide sequence that
CC   encodes the antigen and immune-modulating protein. Such vectors can be
CC   used to treat a subject having a tumour by transferring the expression
CC   vector into the tumour so that the antigen and the immune-modulator are
CC   expressed by at least the tumour. The methods can be used for producing
CC   and evaluating vaccines including cancer vaccines and vaccines directed
CC   against human pathogens, e.g. HIV, Leishmania, Mycobacterium, Listeria or
CC   Plasmodium. Two primers (AAV83197, AAV83198) were used to amplify the IL-
CC   12B for insertion into expression vectors of the invention
XX
SQ   Sequence 762 BP; 199 A; 211 C; 166 G; 186 T; 0 U; 0 Other;

  Query Match             9.8%;  Score 65;  DB 2;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        619 ATTCG 623
              |||||
Db        712 ATTCG 716


RESULT 93
AAA35201
ID   AAA35201 standard; DNA; 762 BP.
XX
AC   AAA35201;
XX
DT   28-JUL-2000  (first entry)
XX
DE   Human adenosine receptor related polynucleotide 2nd SEQ ID NO:75.
XX
KW   Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW   phosphorothioate; impaired respiration; inflammation; allergy;
KW   allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW   antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW   lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW   respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW   pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW   cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200009525-A2.
XX
PD   24-FEB-2000.
XX
PF   03-AUG-1999;   99WO-US017712.
XX
PR   03-AUG-1998;   98US-0095212P.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-205971/18.
XX
PT   New antisense oligonucleotides useful for treating e.g. pulmonary
PT   vasoconstruction, inflammation, allergies, asthma, hypertension,
PT   bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT   cancers.
XX
PS   Disclosure; Page 1242; 1343pp; English.
XX
CC   The present invention describes a new composition comprising an antisense
CC   oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC   nucleic acids involved in bronchoconstriction, allergies, and/or
CC   inflammation. The ON can have antiinflammatory, antiallergic,
CC   antiasthmatic, cytostatic and analgesic activities. The compositions are
CC   useful for the treatment of diseases associated with inflammation,
CC   impaired airways, including lung disease and diseases whose secondary
CC   effects afflict the lungs of a subject. They can be used for treating
CC   e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC   impeded respiration, respiratory distress syndrome, pain, cystic
CC   fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC   carcinomas, and cancers which may metastasise to the lungs, including
CC   breast and prostate cancer. The reduction of the adenosine content of the
CC   ONs reduces side effects. The A-containing ONs break down with the
CC   release of deoxyadenosine which activates adenosine receptors causing
CC   bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC   nucleotide sequences given in the sequence listing from the present
CC   invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC   sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC   from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC   AAA33992) are specifically claimed ONs from the present invention. N.B.
CC   Sequences given in the disclosure of the present invention do not match
CC   up with their corresponding SEQ ID NO: sequences given in the sequence
CC   listing
XX
SQ   Sequence 762 BP; 199 A; 210 C; 167 G; 186 T; 0 U; 0 Other;

  Query Match             9.8%;  Score 65;  DB 3;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        619 ATTCG 623
              |||||
Db        712 ATTCG 716


RESULT 94
AAF21323
ID   AAF21323 standard; DNA; 762 BP.
XX
AC   AAF21323;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human low adenosine antisense oligonucleotide related sequence #2890.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW   chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200062736-A2.
XX
PD   26-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US008020.
XX
PR   06-APR-1999;   99US-0127958P.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
PA   (NYCE/) NYCE J W.
```

```
XX
PI   Nyce JW;
XX
DR   WPI; 2000-679539/66.
XX
PT   Low adenosine (A) content antisense oligonucleotides which do not trigger
PT   adenosine receptors during metabolism, useful e.g. for treating cancers
PT   and respiratory obstructions.
XX
PS   Disclosure; Page 1326; 1592pp; English.
XX
CC   The present invention describes low adenosine (A) content antisense
CC   oligonucleotides and compositions (I) comprising them. In the antisense
CC   oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC   (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC   immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC   The antisense oligonucleotides and (I) can be used to down-regulate the
CC   expression and or activity of target polypeptides associated with
CC   lung/respiratory disorders and malignancies, such as stimulating and
CC   activating peptide factors and transmitters, transcription factors,
CC   immunoglobulins and antibodies, antibody receptors, cytokines and
CC   chemokines, endogenously produced specific and non-specific enzymes,
CC   binding proteins, adhesion molecules and their receptors, cytokine and
CC   chemokine receptors, adenosine receptors, bradykinin receptors, central
CC   nervous system (CNS) and peripheral nervous and non-nervous system
CC   receptors, CNS and peripheral nervous and non-nervous system peptide
CC   transmitters, defensins, growth factors, vasoactive peptides and
CC   receptors, binding proteins and malignancy associated proteins. The
CC   antisense oligonucleotides may be used in this way to treat disorders
CC   including respiratory obstruction (especially pulmonary obstruction
CC   and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC   surfactant hypoproduction which are associated with a disease or
CC   condition selected from pulmonary vasoconstriction, inflammation,
CC   allergies, asthma, impeded respiration, respiratory distress syndrome
CC   (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC   hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC   pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC   and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC   fragments and antisense oligonucleotides used in the exemplification of
CC   the present invention
XX
SQ   Sequence 762 BP; 199 A; 210 C; 167 G; 186 T; 0 U; 0 Other;

  Query Match             9.8%;  Score 65;  DB 3;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        619 ATTCG 623
              |||||
Db        712 ATTCG 716


RESULT 95
ABZ97017
ID   ABZ97017 standard; DNA; 762 BP.
XX
AC   ABZ97017;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human nucleic acid sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 12259; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 762 BP; 199 A; 210 C; 167 G; 186 T; 0 U; 0 Other;

  Query Match             9.8%;  Score 65;  DB 10;  Length 762;
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  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        619 ATTCG 623
              |||||
Db        712 ATTCG 716


RESULT 96
ABD20866
ID   ABD20866 standard; DNA; 762 BP.
XX
AC   ABD20866;
XX
DT   29-JUL-2004  (first entry)
XX
DE   Human pulmonary and inflammatory target DNA #477.
XX
KW   Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW   respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW   surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
```

KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ds.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 12259; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 762 BP; 199 A; 210 C; 167 G; 186 T; 0 U; 0 Other;

```
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  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        619 ATTCG 623
              |||||
Db        712 ATTCG 716
```

RESULT 97
ADO07654
ID ADO07654 standard; DNA; 762 BP.
XX
AC ADO07654;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human interleukin-12 35kDa coding sequence.
XX
KW cytostatic; virucide; anti-HIV; hepatotropic; neuroprotective;
KW immunostimulant; expression cassette; viral vector; interleukin-12;
KW co-stimulatory protein; cancer; infection; ds; gene; human.
XX
OS Homo sapiens.
XX
PN WO2004035799-A2.
XX
PD 29-APR-2004.
XX
PF 10-OCT-2003; 2003WO-EP011252.
XX
PR 11-OCT-2002; 2002DE-01048141.
XX
PA (UYHA-) UNIV HAMBURG-EPPENDORF KLINIKUM.
XX
PI Waehler R, Schnieders F;
XX
DR WPI; 2004-357221/33.
XX
PT Viral vector that expresses single-chain interleukin-12 and costimulator,
PT useful for treatment of tumors, viral infections, e.g. human
PT immunodeficiency virus, and prion diseases.
XX
PS Claim 4; Fig 20; 129pp; German.
XX
CC The present invention relates to a viral vector that includes a nucleic
CC acid encoding a single-chain interleukin-12 (IL-12) and a co-stimulatory
CC protein. Viral vectors and virus particles derived from them are useful
CC for treatment of tumours, infectious diseases (e.g. HIV, hepatitis A, B
CC or C, cytomegalovirus or human papilloma virus), or prion diseases. The
CC present sequence is a human interleukin-12 coding sequence used in the
CC exemplification of the invention.
XX
SQ Sequence 762 BP; 199 A; 210 C; 167 G; 186 T; 0 U; 0 Other;

```
  Query Match             9.8%;  Score 65;  DB 12;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        619 ATTCG 623
              |||||
Db        712 ATTCG 716
```

RESULT 98
ADS88021
ID ADS88021 standard; DNA; 762 BP.
XX
AC ADS88021;
XX
DT 18-NOV-2004 (first entry)
XX
DE Tumour treatment-related human gene sequence SeqID57.
XX
KW tumour inhibition; tumour treatment; metastasis; infectious lesion;

KW antigen presenting cell; immunostimulatory cytokine; cytostatic;
KW vulnerary; immunomodulator; melanoma; hepatoma; adenocarcinoma;
KW colorectal cancer; basal cell cancer; oral cancer; nasopharyngeal cancer;
KW laryngeal cancer; bladder cancer; head cancer; neck cancer;
KW renal cell cancer; pancreatic cancer; pulmonary cancer; cervical cancer;
KW ovarian cancer; oesophageal cancer; gastric cancer; prostrate cancer;
KW testicular cancer; breast cancer; gene; ds; human.
XX
OS Homo sapiens.
XX
PN WO2004034995-A2.
XX
PD 29-APR-2004.
XX
PF 15-OCT-2003; 2003WO-US032827.
XX
PR 15-OCT-2002; 2002US-0418865P.
XX
PA (UYPI-) UNIV PITTSBURGH.
XX
PI Lotze MT, Tahara H;
XX
DR WPI; 2004-365083/34.
DR P-PSDB; ADS88022.
XX
PT Inhibiting or treating a tumor, metastasis or infectious lesion comprises
PT administering into or near site of a tumor or infectious lesion an
PT antigen presenting cell and an immunostimulatory cytokine or a nucleic
PT acid encoding the cytokine.
XX
PS Disclosure; SEQ ID NO 57; 169pp; English.
XX
CC This invention relates to a novel method of inhibiting or treating a
CC tumour, metastasis or infectious lesion in a subject which comprises
CC administering into or near a site of a tumour or infectious lesion in a
CC subject an antigen presenting cell and an immunostimulatory cytokine or a
CC nucleic acid encoding the cytokine. The invention may be useful for the
CC production of compounds with a cytostatic or vulnerary activity acting as
CC immunomodulators. The method is useful in inhibiting or treating a
CC tumour, metastasis or infectious lesion in a subject, where the size of
CC the tumour, metastasis (where number is also decreased) or infectious
CC lesion is decreased. The tumour is selected from melanoma, hepatoma,
CC adenocarcinoma, colorectal cancer, basal cell cancer, oral cancer,
CC nasopharyngeal cancer, laryngeal cancer, bladder cancer, head and neck
CC cancer, renal cell cancer, pancreatic cancer, pulmonary cancer, cervical
CC cancer, ovarian cancer, oesophageal cancer, gastric cancer, prostrate
CC cancer, testicular cancer and breast cancer. The present sequence is that
CC of a gene which is related to the invention.
XX
SQ Sequence 762 BP; 199 A; 210 C; 167 G; 186 T; 0 U; 0 Other;

Query Match 9.8%; Score 65; DB 13; Length 762;
Best Local Similarity 100.0%; Pred. No. 2.8e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy 619 ATTCG 623
|||||
Db 712 ATTCG 716

RESULT 99
ADV42511
ID ADV42511 standard; cDNA; 762 BP.
XX
AC ADV42511;
XX
DT 10-MAR-2005 (first entry)
XX
DE Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 139.
XX
KW microarray; psychoneuroendocrinimmune; chronic fatigue;
KW non-insulin dependent diabetes; allergy; immune disorder; inflammation;
KW cancer; neoplasm; infection; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO2004108899-A2.
XX
PD 16-DEC-2004.
XX
PF 04-JUN-2004; 2004WO-US017686.
XX
PR 04-JUN-2003; 2003US-0475915P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Nicholson A, Vernon SD;
XX
DR WPI; 2005-031682/03.
XX
PT New microarray comprising probes for genes involved in
PT psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a
PT condition associated with PNI activity, e.g., inflammatory or infectious
PT diseases.
XX
PS Claim 1; SEQ ID NO 139; 254pp; English.
XX
CC The invention relates to a new microarray which comprises probes for
CC genes involved in psychoneuroendocrinimmune (PNI) activity. The
CC microarray is useful in diagnosing a condition associated with PNI
CC activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
CC cancer and infection. The present sequence represents a
CC psychoneuroendocrinimmune gene expressed sequence tag. Note the
CC specificatio mentions SEQ ID NO of up to 3314 but only sequences up to
CC SEQ ID NO 1829 are provided.
XX
SQ Sequence 762 BP; 199 A; 210 C; 167 G; 186 T; 0 U; 0 Other;

Query Match 9.8%; Score 65; DB 14; Length 762;
Best Local Similarity 100.0%; Pred. No. 2.8e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy 619 ATTCG 623
|||||
Db 712 ATTCG 716

RESULT 100
ACD26420
ID ACD26420 standard; cDNA; 823 BP.
XX
AC ACD26420;
XX
DT 15-SEP-2003 (first entry)
XX
DE cDNA encoding interleukin-12 (IL-12) P35 subunit.
XX
KW Interleukin-12; IL-12; P35 subunit; tumour; virus infection;
KW fungal infection; parasite infection; gene; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 60. .821
FT /*tag= a
FT /product= "Interleukin-12 P35 subunit"
XX
PN CN1373221-A.

XX
PD 09-OCT-2002.
XX
PF 04-FEB-2002; 2002CN-00100866.
XX
PR 04-FEB-2002; 2002CN-00100866.
XX
PA (VIRO-) INST VIROLOGY CHINESE ACAD PREVENTIVE ME.
XX
PI Jiao H, Zhan M;
XX
DR WPI; 2003-141476/14.
DR P-PSDB; ABU62768.
XX
PT Recombinant Chinese interleukin-12 with bio-activity and its preparation
PT process.
XX
PS Claim 1; Page 1-2; 20pp; Chinese.
XX
CC The invention describes a recombinant Chinese interleukin (IL)-12 with
CC bioactivity for resisting tumour, virus, fungus and parasites. This
CC sequence encodes the interleukin-12 (IL-12) P35 subunit
XX
SQ Sequence 823 BP; 222 A; 225 C; 183 G; 193 T; 0 U; 0 Other;

Query Match 9.8%; Score 65; DB 10; Length 823;
Best Local Similarity 100.0%; Pred. No. 2.8e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        711 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 770

Qy        619 ATTCG 623
              |||||
Db        771 ATTCG 775
```

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Job time : 527.581 secs

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OM nucleic - nucleic search, using sw model

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Searched: 5244920 seqs, 3486124231 residues

Word size : 1

Total number of hits satisfying chosen parameters: 10489196

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Maximum DB seq length: 2000000000

Post-processing: Listing first 200 summaries

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5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
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13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1		591	100.0	591	6	ABK98948	Abk98948 Feline in
2	c	591	100.0	591	6	ABK98949	Abk98949 Feline in
3		591	100.0	591	14	ADV34688	Adv34688 Feline si
4	c	591	100.0	591	14	ADV34690	Adv34690 Feline si
5	c	558	94.4	1533	6	ABK98954	Abk98954 Feline in
6		558	94.4	1533	6	ABK98953	Abk98953 Feline in
7	c	558	94.4	1533	14	ADV34697	Adv34697 Feline si
8		558	94.4	1533	14	ADV34695	Adv34695 Feline si
9		558	94.4	1599	6	ABK98950	Abk98950 Feline in
10	c	558	94.4	1599	6	ABK98951	Abk98951 Feline in
11		558	94.4	1599	14	ADV34691	Adv34691 Feline si
12	c	558	94.4	1599	14	ADV34693	Adv34693 Feline si
13	c	540	91.4	666	6	ABK98947	Abk98947 Feline in
14		540	91.4	666	6	ABK98946	Abk98946 Feline in
15		540	91.4	666	14	ADV34685	Adv34685 Feline si
16	c	540	91.4	666	14	ADV34687	Adv34687 Feline si
17		507	85.8	561	6	ABK99001	Abk99001 Feline in
18	c	507	85.8	561	6	ABK99002	Abk99002 Feline in
19		507	85.8	561	14	ADV34751	Adv34751 Feline N-
20	c	507	85.8	561	14	ADV34753	Adv34753 Feline N-
21		480	81.2	591	2	AAV56629	Aav56629 Feline FL
22		480	81.2	1441	2	AAV56628	Aav56628 Feline FL
23		371	62.8	679	4	AAF26097	Aaf26097 Feline fi
24		228	38.6	669	4	AAF26083	Aaf26083 Feline IL
25		228	38.6	669	4	AAF26086	Aaf26086 Feline IL
26		228	38.6	4201	4	AAF26077	Aaf26077 Feline IL
27		189	32.0	689	2	AAV56641	Aav56641 Feline FL
28		178	30.1	660	5	AAD15214	Aad15214 Modified
29		177	29.9	639	4	AAF26098	Aaf26098 Plasmid p
30		120	20.3	660	5	AAD15215	Aad15215 Modified
31		115	19.5	660	5	AAD15213	Aad15213 Modified
32		115	19.5	660	5	AAD15220	Aad15220 Modified
33		102	17.3	660	5	AAD15218	Aad15218 Modified
34		98	16.6	660	5	AAD15216	Aad15216 Modified
35		84	14.2	660	5	AAD15219	Aad15219 Modified
36		81	13.7	591	2	AAX18179	Aax18179 Canine ma
37	c	81	13.7	591	6	ABK98958	Abk98958 Canine in
38		81	13.7	591	6	ABK98957	Abk98957 Canine in
39		81	13.7	591	14	ADV34701	Adv34701 Canine si
40	c	81	13.7	591	14	ADV34703	Adv34703 Canine si
41		81	13.7	666	6	ABK98955	Abk98955 Canine in
42	c	81	13.7	666	6	ABK98956	Abk98956 Canine in
43	c	81	13.7	666	14	ADV34700	Adv34700 Canine si
44		81	13.7	666	14	ADV34698	Adv34698 Canine si
45		81	13.7	669	2	AAV13818	Aav13818 Canine IL
46		81	13.7	669	2	AAV13819	Aav13819 Canine IL
47		81	13.7	669	2	AAX03163	Aax03163 Nucleic a
48		81	13.7	669	2	AAX03153	Aax03153 Nucleic a
49		81	13.7	669	2	AAX35616	Aax35616 Nucleic a
50		81	13.7	669	2	AAX35626	Aax35626 Nucleic a
51		81	13.7	669	4	AAI64389	Aai64389 Canine co
52		81	13.7	669	4	AAI64379	Aai64379 Canine co
53		81	13.7	669	11	ADZ25701	Adz25701 Canine in
54		81	13.7	669	13	ADT04852	Adt04852 Canine in
55		81	13.7	1282	2	AAX18178	Aax18178 Canine fu
56		81	13.7	1455	6	ABK99003	Abk99003 Canine in
57	c	81	13.7	1455	6	ABK99004	Abk99004 Canine in
58	c	81	13.7	1455	14	ADV34756	Adv34756 Canine si
59		81	13.7	1455	14	ADV34754	Adv34754 Canine si
60		81	13.7	1533	6	ABK98967	Abk98967 Canine in
61	c	81	13.7	1533	6	ABK98968	Abk98968 Canine in
62	c	81	13.7	1533	14	ADV34718	Adv34718 Canine si
63		81	13.7	1533	14	ADV34716	Adv34716 Canine si
64		81	13.7	1599	6	ABK98965	Abk98965 Canine in
65	c	81	13.7	1599	6	ABK98966	Abk98966 Canine in
66	c	81	13.7	1599	14	ADV34715	Adv34715 Canine si
67		81	13.7	1599	14	ADV34713	Adv34713 Canine si
68		71	12.0	71	4	AAF26092	Aaf26092 Feline IL
69		71	12.0	71	4	AAF26099	Aaf26099 Feline Il
70		65	11.0	201	13	ADQ41825	Adq41825 Myocardia
71		65	11.0	201	13	ADQ41824	Adq41824 Myocardia
72		65	11.0	201	13	ADQ41835	Adq41835 Myocardia
73		65	11.0	201	13	ADQ41829	Adq41829 Myocardia
74		65	11.0	201	13	ADQ41838	Adq41838 Myocardia
75		65	11.0	201	13	ADQ41833	Adq41833 Myocardia
76		65	11.0	657	12	ADG39431	Adg39431 Human CLM
77		65	11.0	660	2	AAQ97485	Aaq97485 Human int
78		65	11.0	660	2	AAV07274	Aav07274 Human Int
79		65	11.0	660	2	AAV07218	Aav07218 DNA encod
80		65	11.0	660	2	AAZ40407	Aaz40407 Human int
81		65	11.0	660	5	AAD15217	Aad15217 Modified
82		65	11.0	660	5	AAD15221	Aad15221 Human cyt
83		65	11.0	660	6	AAL44226	Aal44226 Human int
84		65	11.0	660	6	ACC47589	Acc47589 Human int
85		65	11.0	660	12	ADF77244	Adf77244 Human IL-
86		65	11.0	702	12	ADP88401	Adp88401 Human int
87		65	11.0	721	2	AAQ67880	Aaq67880 EPV 42 kD
88		65	11.0	721	2	AAZ08515	Aaz08515 Vaccinia
89		65	11.0	721	13	ADR21891	Adr21891 Vaccinia
90		65	11.0	761	10	ADK98708	Adk98708 Human int
91		65	11.0	761	10	ADK98706	Adk98706 Human int

92	65	11.0	762	2	AAV83207	Aav83207 Interleuk
93	65	11.0	762	3	AAA35201	Aaa35201 Human ade
94	65	11.0	762	3	AAF21323	Aaf21323 Human low
95	65	11.0	762	10	ABZ97017	Abz97017 Human nuc
96	65	11.0	762	11	ABD20866	Abd20866 Human pul
97	65	11.0	762	12	ADO07654	Ado07654 Human int
98	65	11.0	762	13	ADS88021	Ads88021 Tumour tr
99	65	11.0	762	14	ADV42511	Adv42511 Human psy
100	65	11.0	823	10	ACD26420	Acd26420 cDNA enco
101	65	11.0	856	2	AAQ12150	Aaq12150 Cytotoxic
102	65	11.0	856	2	AAT77850	Aat77850 35 kDa su
103	65	11.0	856	2	AAT97970	Aat97970 35 kDa su
104	65	11.0	856	2	AAV00402	Aav00402 35 kDa su
105	65	11.0	856	2	AAV37772	Aav37772 Cytotoxic
106	65	11.0	856	12	ADG39389	Adg39389 Human cyt
107	65	11.0	856	12	ADO03760	Ado03760 Human CLM
108	65	11.0	889	13	ADU04652	Adu04652 Human ext
109	65	11.0	1026	3	AAZ40020	Aaz40020 Human p35
110	65	11.0	1026	8	ACA61266	Aca61266 DNA encod
111	65	11.0	1026	11	ADI31715	Adi31715 Human cDN
112	65	11.0	1026	13	ADS83782	Ads83782 Human lym
113	65	11.0	1172	8	ACC42373	Acc42373 Human ext
114	65	11.0	1200	8	ACF64408	Acf64408 Human IL1
115	65	11.0	1287	4	AAF76882	Aaf76882 DNA encod
116	65	11.0	1289	8	ACC42375	Acc42375 Human ext
117	65	11.0	1316	2	AAT63621	Aat63621 Interleuk
118	65	11.0	1316	6	AAD41639	Aad41639 Human int
119	65	11.0	1364	2	AAT48099	Aat48099 Human int
120	65	11.0	1364	2	AAV42536	Aav42536 Human int
121	65	11.0	1364	2	AAV15228	Aav15228 Heterodim
122	65	11.0	1364	3	AAZ28863	Aaz28863 Human int
123	65	11.0	1364	4	AAF56281	Aaf56281 IL-12 vac
124	65	11.0	1384	15	AEF92723	Aef92723 Human int
125	65	11.0	1396	2	AAQ24371	Aaq24371 Natural k
126	65	11.0	1444	12	ACF57533	Acf57533 Human IL1
127	65	11.0	1444	12	ADJ62891	Adj62891 Human int
128	65	11.0	1444	12	ADN12152	Adn12152 Interleuk
129	65	11.0	1444	14	ADY15785	Ady15785 DNA encod
130	65	11.0	1444	14	ADZ26544	Adz26544 Human IL1
131	65	11.0	1444	14	AEB56478	Aeb56478 Radiochem
132	65	11.0	1494	12	ADQ59495	Adq59495 Human can
133	65	11.0	1526	12	ADQ59549	Adq59549 Human can
134	65	11.0	1532	13	ADQ38388	Adq38388 Human SNP
135	65	11.0	1532	14	ADZ13866	Adz13866 Human can
136	65	11.0	1607	13	ADQ38387	Adq38387 Human SNP
137	65	11.0	1607	14	ADZ13864	Adz13864 Human can
138	65	11.0	2300	3	AAA92406	Aaa92406 Human int
139	65	11.0	2336	14	AEE03207	Aee03207 Human int
140	65	11.0	2390	12	ADM29103	Adm29103 Human int
141	65	11.0	3205	14	AEB48820	Aeb48820 Monoclona
142	65	11.0	4521	3	AAA35204	Aaa35204 Human ade
143	65	11.0	4521	3	AAF21326	Aaf21326 Human low
144	65	11.0	4521	10	ABZ97020	Abz97020 Human nuc
145	65	11.0	4521	11	ABD20869	Abd20869 Human pul
146	65	11.0	5013	14	AEA40941	Aea40941 T-DNA reg
147	65	11.0	5686	2	AAZ40415	Aaz40415 Plasmid p
148	65	11.0	5686	12	ADF77239	Adf77239 Human IL-
149	65	11.0	6139	3	AAZ40023	Aaz40023 Interleuk
150	65	11.0	8578	6	AAD31546	Aad31546 pIRES-hB7
151	65	11.0	8578	6	AAD31545	Aad31545 pIRES-hB7
152	65	11.0	8608	6	AAD31548	Aad31548 pIRES-hB7
153	65	11.0	8623	6	AAD31547	Aad31547 pIRES-hB7
154	65	11.0	8629	6	AAD31552	Aad31552 pIRES-IL1
155	65	11.0	8638	6	AAD31549	Aad31549 pIRES-hB7
156	65	11.0	8644	6	AAD31551	Aad31551 pIRES-IL1
157	65	11.0	8659	6	AAD31550	Aad31550 pIRES-IL1
158	65	11.0	11441	6	AAL44225	Aal44225 Human int
159	65	11.0	11453	10	ADG25152	Adg25152 Vector pS
160	65	11.0	11569	10	ADG25150	Adg25150 Vector pA
161	65	11.0	27277	12	ADQ59494	Adq59494 Human can
162	65	11.0	27277	14	ADZ13863	Adz13863 Human can
163	62	10.5	683	4	AAF26096	Aaf26096 Human pG-
164	60	10.2	666	5	AAD15212	Aad15212 Modified
165	60	10.2	666	5	AAD15211	Aad15211 Modified
166	56	9.5	700	8	ACF64405	Acf64405 Human IL1
167	45	7.6	76	4	AAF26100	Aaf26100 Feline Il
c 168	45	7.6	76	4	AAF26093	Aaf26093 Feline IL
c 169	45	7.6	76	4	AAF26090	Aaf26090 Feline IL
170	43	7.3	79	2	AAV56639	Aav56639 Feline FL
171	41	6.9	703	3	AAA70708	Aaa70708 Bovine in
172	40	6.8	700	8	ACF64406	Acf64406 Human IL1
173	40	6.8	700	8	ACF64407	Acf64407 Human IL1
174	30	5.1	201	13	ADQ41830	Adq41830 Myocardia
175	30	5.1	201	13	ADQ41821	Adq41821 Myocardia
176	29	4.9	554	2	AAT50757	Aat50757 Partial s
177	27	4.6	39	6	ABK98991	Abk98991 Synthetic
178	27	4.6	39	14	ADV34741	Adv34741 Feline IL
179	27	4.6	79	2	AAX18181	Aax18181 Primer fo
180	27	4.6	582	4	AAF76877	Aaf76877 Mature mu
181	27	4.6	660	2	AAX78396	Aax78396 IL-12p35
182	27	4.6	660	2	AAX25946	Aax25946 Interleuk
183	27	4.6	713	2	AAT35199	Aat35199 Mouse int
184	27	4.6	1231	12	ADQ59492	Adq59492 Human can
185	27	4.6	1265	2	AAV28473	Aav28473 Murine in
186	27	4.6	1265	8	ACA61264	Aca61264 DNA encod
187	27	4.6	1273	14	ADZ13861	Adz13861 Murine ca
188	27	4.6	1278	4	AAF76881	Aaf76881 DNA encod
189	27	4.6	1569	4	AAF76888	Aaf76888 Single-ch
190	27	4.6	2013	4	AAF76887	Aaf76887 Murine p3
191	27	4.6	2334	14	AEE03206	Aee03206 Murine in
192	27	4.6	2438	12	ADO43004	Ado43004 DNA encod
193	27	4.6	2709	4	AAF76889	Aaf76889 Coding se
194	27	4.6	5252	12	ADO07652	Ado07652 Tricistro
195	27	4.6	5966	2	AAZ40417	Aaz40417 Plasmid p
196	27	4.6	5966	12	ADF77241	Adf77241 Mouse IL-
197	27	4.6	5985	12	ADQ82718	Adq82718 Anticance
198	27	4.6	6295	2	AAV02043	Aav02043 Plasmid p
199	27	4.6	7287	2	AAV02042	Aav02042 Plasmid p
200	27	4.6	9049	12	ADO07661	Ado07661 Viral vec

ALIGNMENTS

RESULT 1
ABK98948
ID ABK98948 standard; cDNA; 591 BP.
XX
AC ABK98948;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p35-591 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69305.
XX

PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 1; Page 56-57; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 591 BP; 178 A; 149 C; 122 G; 142 T; 0 U; 0 Other;

Query Match 100.0%; Score 591; DB 6; Length 591;
Best Local Similarity 100.0%; Pred. No. 3.3e-290;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
```

RESULT 2
ABK98949/c
ID ABK98949 standard; cDNA; 591 BP.
XX
AC ABK98949;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p35-591 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Disclosure; Page 58; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 591 BP; 142 A; 122 C; 149 G; 178 T; 0 U; 0 Other;

Query Match 100.0%; Score 591; DB 6; Length 591;
Best Local Similarity 100.0%; Pred. No. 3.3e-290;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1


RESULT 3
ADV34688
ID   ADV34688 standard; cDNA; 591 BP.
XX
AC   ADV34688;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain mature IL-12p35 protein cDNA, nFeIL-12p35 591.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .591
FT                   /*tag=  a
FT                   /product= "PFeIL-12p35 197 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34689.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 23; SEQ ID NO 35; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain mature IL-12p35 subunit
CC   protein encoding cDNA.
XX
SQ   Sequence 591 BP; 178 A; 149 C; 122 G; 142 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 591;  DB 14;  Length 591;
  Best Local Similarity  100.0%;  Pred. No. 3.3e-290;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591


RESULT 4
ADV34690/c
ID   ADV34690 standard; DNA; 591 BP.
XX
AC   ADV34690;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain mature IL-12p35 complementary DNA, nFeIL-12p35 591.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
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```
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 37; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain mature IL-12p35 subunit
CC   complementary DNA.
XX
SQ   Sequence 591 BP; 142 A; 122 C; 149 G; 178 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 591;  DB 14;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-290;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1


RESULT 5
ABK98954/c
ID   ABK98954 standard; cDNA; 1533 BP.
XX
AC   ABK98954;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1533 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 66-67; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

  Query Match             94.4%;  Score 558;  DB 6;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-273;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        574 AGCTATCTGAATGCTTCC 591
              ||||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1


RESULT 6
ABK98953
ID   ABK98953 standard; cDNA; 1533 BP.
XX
AC   ABK98953;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1533 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69307.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 63-64; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

  Query Match            94.4%;  Score 558;  DB 6;  Length 1533;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-273;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        976 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 1035

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1036 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 1095

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1096 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 1155

Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1156 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 1215

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1216 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 1275

Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1276 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 1335

Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1336 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 1395

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1396 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 1455

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1456 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 1515

Qy        574 AGCTATCTGAATGCTTCC 591
              ||||||||||||||||||
Db       1516 AGCTATCTGAATGCTTCC 1533


RESULT 7
ADV34697/c
ID   ADV34697 standard; DNA; 1533 BP.
XX
AC   ADV34697;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 complementary DNA, nFeIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
```

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XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 45; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 complementary DNA.
XX
SQ   Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

  Query Match             94.4%;  Score 558;  DB 14;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-273;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        574 AGCTATCTGAATGCTTCC 591
              |||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1


RESULT 8
ADV34695
ID   ADV34695 standard; cDNA; 1533 BP.
XX
AC   ADV34695;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1533
FT                   /*tag=  a
FT                   /product= "PFeIL-12 511 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34696.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 43; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

  Query Match             94.4%;  Score 558;  DB 14;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-273;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        976 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 1035

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1036 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 1095

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1096 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 1155

Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1156 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 1215

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1216 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 1275

Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1276 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 1335
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Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1336 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 1395

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1396 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 1455

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1456 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 1515

Qy        574 AGCTATCTGAATGCTTCC 591
              ||||||||||||||||||
Db       1516 AGCTATCTGAATGCTTCC 1533
```

RESULT 9
ABK98950
ID ABK98950 standard; cDNA; 1599 BP.
XX
AC ABK98950;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12-1599 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69306.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 58-60; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

Query Match 94.4%; Score 558; DB 6; Length 1599;
Best Local Similarity 100.0%; Pred. No. 2.1e-273;
Matches 558; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1042 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 1101

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1102 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 1161

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1162 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 1221

Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1222 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 1281

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1282 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 1341

Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1342 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 1401

Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1402 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 1461

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1462 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 1521

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1522 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 1581

Qy        574 AGCTATCTGAATGCTTCC 591
              ||||||||||||||||||
Db       1582 AGCTATCTGAATGCTTCC 1599
```

RESULT 10
ABK98951/c
ID ABK98951 standard; cDNA; 1599 BP.
XX
AC ABK98951;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12-1599 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX

```
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 61-62; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

  Query Match             94.4%;  Score 558;  DB 6;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-273;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        574 AGCTATCTGAATGCTTCC 591
              ||||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1


RESULT 11
ADV34691
ID   ADV34691 standard; cDNA; 1599 BP.
XX
AC   ADV34691;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1599
FT                   /*tag=  a
FT                   /product= "PFeIL-12p533 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34692.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 38; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

  Query Match             94.4%;  Score 558;  DB 14;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-273;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1042 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 1101

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1102 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 1161

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1162 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 1221

Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1222 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 1281

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1282 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 1341

Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1342 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 1401

Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1402 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 1461

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1462 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 1521

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1522 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 1581

Qy        574 AGCTATCTGAATGCTTCC 591
              ||||||||||||||||||
Db       1582 AGCTATCTGAATGCTTCC 1599
```

RESULT 12
ADV34693/c
ID ADV34693 standard; DNA; 1599 BP.
XX
AC ADV34693;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain IL-12 complementary DNA, nFeIL-12 1599.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Felis catus.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 3; SEQ ID NO 40; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain IL-12 complementary DNA.
XX
SQ Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

  Query Match   94.4%; Score 558; DB 14; Length 1599;
  Best Local Similarity 100.0%; Pred. No. 2.1e-273;
  Matches 558; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        574 AGCTATCTGAATGCTTCC 591
              ||||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1
```

RESULT 13
ABK98947/c
ID ABK98947 standard; cDNA; 666 BP.
XX
AC ABK98947;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p35-666 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX

```
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 3; Page 56; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 666 BP; 160 A; 138 C; 179 G; 189 T; 0 U; 0 Other;

  Query Match             91.4%;  Score 540;  DB 6;  Length 666;
  Best Local Similarity   99.8%;  Pred. No. 3.1e-264;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1


RESULT 14
ABK98946
ID   ABK98946 standard; cDNA; 666 BP.
XX
AC   ABK98946;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p35-666 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69304.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 54-55; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 666 BP; 189 A; 179 C; 138 G; 160 T; 0 U; 0 Other;

  Query Match             91.4%;  Score 540;  DB 6;  Length 666;
  Best Local Similarity   99.8%;  Pred. No. 3.1e-264;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
                |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666


RESULT 15
ADV34685
ID   ADV34685 standard; cDNA; 666 BP.
XX
AC   ADV34685;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12p35 full-length cDNA, nFeIL-12p35 666.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .666
FT                   /*tag=  a
FT                   /product= "PFeIL-12p35 222 protein "
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34686.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 23; SEQ ID NO 32; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12p35 subunit protein
CC   encoding full-length cDNA.
XX
SQ   Sequence 666 BP; 189 A; 179 C; 138 G; 160 T; 0 U; 0 Other;

  Query Match           91.4%;  Score 540;  DB 14;  Length 666;
  Best Local Similarity   99.8%;  Pred. No. 3.1e-264;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
                |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666


RESULT 16
ADV34687/c
ID   ADV34687 standard; DNA; 666 BP.
XX
AC   ADV34687;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12p35 complementary DNA, nFeIL-12p35 666.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
```

PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 3; SEQ ID NO 34; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain IL-12p35 subunit full-length
CC complementary DNA.
XX
SQ Sequence 666 BP; 160 A; 138 C; 179 G; 189 T; 0 U; 0 Other;

Query Match 91.4%; Score 540; DB 14; Length 666;
Best Local Similarity 99.8%; Pred. No. 3.1e-264;
Matches 590; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
```

RESULT 17
ABK99001
ID ABK99001 standard; cDNA; 561 BP.
XX
AC ABK99001;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p35-N561 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69315.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Disclosure; Page 92-93; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 561 BP; 167 A; 134 C; 120 G; 140 T; 0 U; 0 Other;

Query Match 85.8%; Score 507; DB 6; Length 561;
Best Local Similarity 99.8%; Pred. No. 2e-247;
Matches 557; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183

Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303
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```
Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363

Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543

Qy        574 AGCTATCTGAATGCTTCC 591
              ||||||||||||||||||
Db        544 AGCTATCTGAATGCTTCC 561
```

RESULT 18
ABK99002/c
ID ABK99002 standard; cDNA; 561 BP.
XX
AC ABK99002;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12nFeIL-12p35-N561 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Disclosure; Page 94; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 561 BP; 140 A; 120 C; 134 G; 167 T; 0 U; 0 Other;

Query Match 85.8%; Score 507; DB 6; Length 561;
Best Local Similarity 99.8%; Pred. No. 2e-247;
Matches 557; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
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Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
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Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
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Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        574 AGCTATCTGAATGCTTCC 591
              ||||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1
```

RESULT 19
ADV34751
ID ADV34751 standard; cDNA; 561 BP.
XX
AC ADV34751;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline N-terminal single chain IL-12p35 cDNA, nFeIL-12p35-N561.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; gene; ss.
XX
OS Felis catus.
XX
FH Key Location/Qualifiers
FT CDS 1. .561
FT /*tag= a
FT /product= "PFeIL-12p35-N187 protein"
FT /partial
FT /note= "No start and stop codon"
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.

```
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34752.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 23; SEQ ID NO 101; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline N-terminal single chain IL-12p35 subunit
CC   protein encoding cDNA.
XX
SQ   Sequence 561 BP; 167 A; 134 C; 120 G; 140 T; 0 U; 0 Other;

  Query Match             85.8%;  Score 507;  DB 14;  Length 561;
  Best Local Similarity   99.8%;  Pred. No. 2e-247;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183

Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303

Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363

Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543

Qy        574 AGCTATCTGAATGCTTCC 591
              ||||||||||||||||||
Db        544 AGCTATCTGAATGCTTCC 561
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RESULT 20
ADV34753/c
ID   ADV34753 standard; cDNA; 561 BP.
XX
AC   ADV34753;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline N-terminal IL-12p35 complementary DNA, nFeIL-12p35-N561.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Disclosure; SEQ ID NO 103; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline N-terminal single chain IL-12p35 subunit
CC   protein complementary DNA.
XX
SQ   Sequence 561 BP; 140 A; 120 C; 134 G; 167 T; 0 U; 0 Other;

  Query Match             85.8%;  Score 507;  DB 14;  Length 561;
  Best Local Similarity   99.8%;  Pred. No. 2e-247;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259
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Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        574 AGCTATCTGAATGCTTCC 591
              ||||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1
```

RESULT 21
AAV56629
ID AAV56629 standard; cDNA; 591 BP.
XX
AC AAV56629;
XX
DT 23-NOV-1998 (first entry)
XX
DE Feline FLAFp35 cDNA mature transcript.
XX
KW Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW T lymphocyte cell; autoimmune disease; ds.
XX
OS Felis catus.
XX
PN WO9746583-A1.
XX
PD 11-DEC-1997.
XX
PF 29-MAY-1997; 97WO-JP001824.
XX
PR 04-JUN-1996; 96JP-00165249.
XX
PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI Imamura T, Maeda H, Fujiyasu T, Imagawa Y, Tokiyoshi S;
XX
DR WPI; 1998-042118/04.
DR P-PSDB; AAW76176.
XX
PT Novel feline cytokine protein - useful for treating feline auto:immune
PT diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS Claim 23; Page 59; 94pp; Japanese.
XX
CC This sequence encodes a novel feline cytokine mature protein, FLAFp35.
CC This protein can be used in the production of a FLAFp35/FLAFp40
CC heterodimer which can potentiate the cytotoxic activity of feline
CC cytotoxic T lymphocyte cells. Such proteins are used for treatment of
CC feline autoimmune diseases e.g. as caused by feline herpes virus or
CC feline calcivirus
XX
SQ Sequence 591 BP; 179 A; 151 C; 120 G; 141 T; 0 U; 0 Other;

Query Match 81.2%; Score 480; DB 2; Length 591;
Best Local Similarity 100.0%; Pred. No. 1.1e-233;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
```

RESULT 22
AAV56628
ID AAV56628 standard; cDNA; 1441 BP.
XX
AC AAV56628;
XX
DT 23-NOV-1998 (first entry)
XX
DE Feline FLAFp35 cDNA.
XX
KW Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW T lymphocyte cell; autoimmune disease; ds.
XX
OS Felis catus.
XX
FH Key Location/Qualifiers
FT CDS 133. .811
FT /*tag= a
FT sig_peptide 133. .217
FT /*tag= b
FT mat_peptide 218. .808
FT /*tag= c
FT /product= "FLAFp35"
FT /note= "feline cytokine"
XX
PN WO9746583-A1.
XX
PD 11-DEC-1997.
XX
PF 29-MAY-1997; 97WO-JP001824.
XX
PR 04-JUN-1996; 96JP-00165249.
XX
PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI Imamura T, Maeda H, Fujiyasu T, Imagawa Y, Tokiyoshi S;
XX
DR WPI; 1998-042118/04.
DR P-PSDB; AAW76175.
XX
PT Novel feline cytokine protein - useful for treating feline auto:immune
PT diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS Claim 22; Page 57-58; 94pp; Japanese.

```
XX
CC   This sequence encodes a novel feline cytokine protein, FLAFp35. This
CC   protein can be used in the production of a FLAFp35/FLAFp40 heterodimer
CC   which can potentiate the cytotoxic activity of feline cytotoxic T
CC   lymphocyte cells. Such proteins are used for treatment of feline
CC   autoimmune diseases e.g. as caused by feline herpes virus or feline
CC   calcivirus
XX
SQ   Sequence 1441 BP; 451 A; 325 C; 258 G; 407 T; 0 U; 0 Other;

  Query Match            81.2%;  Score 480;  DB 2;  Length 1441;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-233;
  Matches  480;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 277

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 337

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 397

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 457

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 517

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 577

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        578 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 637

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        638 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 697


RESULT 23
AAF26097
ID   AAF26097 standard; DNA; 679 BP.
XX
AC   AAF26097;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline fil12p35a DNA.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS   Felis sp.
XX
PN   WO200104155-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002263.
XX
PR   08-JUL-1999;   99CH-00001259.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Lutz H,  Leutenegger C,  Pedersen N,  Schroff M,  Wittig B;
XX
DR   WPI; 2001-147178/15.
XX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs.
XX
PS   Disclosure; Fig 2; 35pp; German.
XX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
CC   following: (i) as immunostimulant, for preventative or therapeutic use;
CC   and (ii) treating tumors and autoimmune diseases, or diseases associated
CC   with a Th1 defect, especially pre-existing infections by feline immune
CC   deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ   Sequence 679 BP; 196 A; 180 C; 140 G; 163 T; 0 U; 0 Other;

  Query Match            62.8%;  Score 371;  DB 4;  Length 679;
  Best Local Similarity  99.6%;  Pred. No. 3.5e-178;
  Matches  471;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        316 TCTCTGATAACTAATGGGAGTTGGCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAA 473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAA 548
```

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RESULT 24
AAF26083
ID   AAF26083 standard; DNA; 669 BP.
XX
AC   AAF26083;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p35 encoding DNA SEQ ID 4.
XX
KW   Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW   interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS   Felis sp.
XX
PN   WO200104280-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002262.
XX
PR   08-JUL-1999;   99CH-00001258.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
XX
PI   Leutenegger C,  Schroff M,  Wittig B,  Lutz H;
XX
DR   WPI; 2001-147190/15.
XX
PT   Vaccine for treating or preventing lentivirus infection in cats, contains
PT   nucleic acid sequence encoding viral protein under control of eukaryotic
PT   promoter.
XX
PS   Claim 14; Page 37; 37pp; German.
XX
CC   This invention describes a novel vaccine (A) for prevention or treatment
CC   of lentivirus infection in felines which comprises an immunizing nucleic
CC   acid sequence (I) that contains, or comprises, at least part of a gene
CC   encoding a protein (II) of the virus, under control of a eukaryotic
CC   promoter functional in the relevant animal. (II) is especially the
CC   envelope (env) protein. The invention also describes (1) vaccine (A)
CC   containing an immunizing protein, or fragment, from a lentivirus plus at
CC   least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC   lentivirus protein, or fragment, especially derived from feline immune
CC   deficiency virus (FIV), by expressing the corresponding nucleic acid
CC   sequence in a host cell. The products of the invention have antiviral
CC   activity. The vaccine (A) and related protein-based vaccines, are
CC   particularly used to treat or prevent lentivirus infections in domestic
CC   cats, especially feline immune deficiency virus (FIV). Vaccination with
CC   (A) allows differentiation between vaccinated and infected animals, from
CC   the antibody status. The vaccines may be formulated with an adjuvant
CC   (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC   immune response, particularly a Th1 response
XX
SQ   Sequence 669 BP; 189 A; 179 C; 140 G; 161 T; 0 U; 0 Other;

  Query Match             38.6%;  Score 228;  DB 4;  Length 669;
  Best Local Similarity   99.1%;  Pred. No. 2.2e-105;
  Matches  428;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              |||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATTGATGAGCTG 432
              ||||||||||||
Db        496 ATTGATGAGCTG 507


RESULT 25
AAF26086
ID   AAF26086 standard; DNA; 669 BP.
XX
AC   AAF26086;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p35 encoding DNA.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS   Felis sp.
XX
PN   WO200104155-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002263.
XX
PR   08-JUL-1999;   99CH-00001259.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Lutz H,  Leutenegger C,  Pedersen N,  Schroff M,  Wittig B;
XX
DR   WPI; 2001-147178/15.
XX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs.
XX
PS   Claim 3; Page 31; 35pp; German.
XX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
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CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
CC   following: (i) as immunostimulant, for preventative or therapeutic use;
CC   and (ii) treating tumors and autoimmune diseases, or diseases associated
CC   with a Th1 defect, especially pre-existing infections by feline immune
CC   deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ   Sequence 669 BP; 189 A; 179 C; 140 G; 161 T; 0 U; 0 Other;

  Query Match             38.6%;  Score 228;  DB 4;  Length 669;
  Best Local Similarity   99.1%;  Pred. No. 2.2e-105;
  Matches  428;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              |||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATTGATGAGCTG 432
              ||||||||||||
Db        496 ATTGATGAGCTG 507


RESULT 26
AAF26077
ID   AAF26077 standard; DNA; 4201 BP.
XX
AC   AAF26077;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p35 encoding DNA SEQ ID 3.
XX
KW   Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW   interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS   Felis sp.
XX
PN   WO200104280-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002262.
XX
PR   08-JUL-1999;   99CH-00001258.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
XX
PI   Leutenegger C,  Schroff M,  Wittig B,  Lutz H;
XX
DR   WPI; 2001-147190/15.
XX
PT   Vaccine for treating or preventing lentivirus infection in cats, contains
PT   nucleic acid sequence encoding viral protein under control of eukaryotic
PT   promoter.
XX
PS   Disclosure; Page 31-33; 37pp; German.
XX
CC   This invention describes a novel vaccine (A) for prevention or treatment
CC   of lentivirus infection in felines which comprises an immunizing nucleic
CC   acid sequence (I) that contains, or comprises, at least part of a gene
CC   encoding a protein (II) of the virus, under control of a eukaryotic
CC   promoter functional in the relevant animal. (II) is especially the
CC   envelope (env) protein. The invention also describes (1) vaccine (A)
CC   containing an immunizing protein, or fragment, from a lentivirus plus at
CC   least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC   lentivirus protein, or fragment, especially derived from feline immune
CC   deficiency virus (FIV), by expressing the corresponding nucleic acid
CC   sequence in a host cell. The products of the invention have antiviral
CC   activity. The vaccine (A) and related protein-based vaccines, are
CC   particularly used to treat or prevent lentivirus infections in domestic
CC   cats, especially feline immune deficiency virus (FIV). Vaccination with
CC   (A) allows differentiation between vaccinated and infected animals, from
CC   the antibody status. The vaccines may be formulated with an adjuvant
CC   (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC   immune response, particularly a Th1 response
XX
SQ   Sequence 4201 BP; 1086 A; 1055 C; 999 G; 1061 T; 0 U; 0 Other;

  Query Match             38.6%;  Score 228;  DB 4;  Length 4201;
  Best Local Similarity   99.1%;  Pred. No. 2.2e-105;
  Matches  428;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3122 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 3181

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3182 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 3241

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3242 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 3301

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       3302 GAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 3361

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              |||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db       3362 TCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCTTTTATGACGACCCTG 3421

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3422 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 3481

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3482 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 3541

Qy        421 ATTGATGAGCTG 432
              ||||||||||||
Db       3542 ATTGATGAGCTG 3553


RESULT 27
AAV56641
ID   AAV56641 standard; DNA; 689 BP.
XX
AC   AAV56641;
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XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp35 DNA fragment.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ss.
XX
OS   Felis catus.
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP001824.
XX
PR   04-JUN-1996;   96JP-00165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
XX
PT   Novel feline cytokine protein - useful for treating feline auto:immune
PT   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS   Claim 24; Page 67; 94pp; Japanese.
XX
CC   This sequence encodes a fragment of a novel feline cytokine protein,
CC   FLAFp35. This protein can be used in the production of a FLAFp35/FLAFp40
CC   heterodimer which can potentiate the cytotoxic activity of feline
CC   cytotoxic T lymphocyte cells. Such proteins are used for treatment of
CC   feline autoimmune diseases e.g. as caused by feline herpes virus or
CC   feline calcivirus
XX
SQ   Sequence 689 BP; 192 A; 193 C; 145 G; 159 T; 0 U; 0 Other;

  Query Match            32.0%;  Score 189;  DB 2;  Length 689;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-85;
  Matches  189;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 141

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 201

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 261

Qy        181 GAGGCCTGC 189
              |||||||||
Db        262 GAGGCCTGC 270


RESULT 28
AAD15214
ID   AAD15214 standard; DNA; 660 BP.
XX
AC   AAD15214;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 encoding DNA from clone R2-631.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p35; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "Modified p35 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .657
FT                   /*tag=  c
FT                   /product= "Mature modified p35 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08607.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 87; Page 139; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein encoding
CC   DNA
XX
SQ   Sequence 660 BP; 182 A; 178 C; 142 G; 158 T; 0 U; 0 Other;

  Query Match            30.1%;  Score 178;  DB 5;  Length 660;
  Best Local Similarity  100.0%;  Pred. No. 6.5e-80;
  Matches  178;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        237 GATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGAC 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 GATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGAC 362

Qy        297 CCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCAT 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 CCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCAT 422

Qy        357 GAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 GAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480


RESULT 29
AAF26098
ID   AAF26098 standard; DNA; 639 BP.
XX
AC   AAF26098;
XX
DT   24-APR-2001  (first entry)
XX
```

DE Plasmid pMOL-fIL12 p35 DNA.
XX
KW Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS Synthetic.
XX
PN WO200104155-A2.
XX
PD 18-JAN-2001.
XX
PF 08-JUL-2000; 2000WO-DE002263.
XX
PR 08-JUL-1999; 99CH-00001259.
XX
PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA (UYZU-) UNIV ZUERICH.
PA (REGC) UNIV CALIFORNIA.
XX
PI Lutz H, Leutenegger C, Pedersen N, Schroff M, Wittig B;
XX
DR WPI; 2001-147178/15.
XX
PT Recombinant feline interleukin-12, useful as immunostimulant and for
PT treating e.g. viral infections in cats, and related nucleic acid
PT constructs.
XX
PS Disclosure; Fig 2; 35pp; German.
XX
CC This invention describes a novel feline interleukin-12 (fIL-12)
CC polypeptide (I) that is expressed, by recombinant gene expression in
CC eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC of subunits p35 and p40. These proteins are formed so that, in equimolar
CC concentrations and in presence of an immunizing antigen, they can be
CC administered to carnivores, particularly domestic cats. The invention
CC also describes a nucleic acid construct (II) encoding fIL-12 containing
CC sequences at least 95% identical with the p40- and p35-encoding sequences
CC (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC as immunostimulants for immunization against infectious diseases and/or
CC for treating infections or tumors in felines, especially domestic cats.
CC The products of the invention have immunostimulatory, antiviral and
CC antitumor activity. Nucleic acid constructs that encode (II) are useful
CC as adjuvants for prophylactic immunization against viral diseases and for
CC treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC is useful for carnivores, and particularly domestic cats in the
CC following: (i) as immunostimulant, for preventative or therapeutic use;
CC and (ii) treating tumors and autoimmune diseases, or diseases associated
CC with a Th1 defect, especially pre-existing infections by feline immune
CC deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ Sequence 639 BP; 189 A; 166 C; 133 G; 151 T; 0 U; 0 Other;

Query Match 29.9%; Score 177; DB 4; Length 639;
Best Local Similarity 98.8%; Pred. No. 2.1e-79;
Matches 427; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 82

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 142

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 202

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 GAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 262

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||| ||||  ||||||||||||||||||||||||||||
Db        263 TCTCTGATAACTAATGGGAGTTGGCTGGTGTCCAGAAAGACCTCTTTTATGACGACCCTG 322

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 382

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 442

Qy        421 ATTGATGAGCTG 432
              ||||||||||||
Db        443 ATTGATGAGCTG 454
```

RESULT 30
AAD15215
ID AAD15215 standard; DNA; 660 BP.
XX
AC AAD15215;
XX
DT 01-NOV-2001 (first entry)
XX
DE Modified human cytokine p35 encoding DNA from clone R2-613.
XX
KW Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW p35; mutant; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1. .660
FT /*tag= a
FT /product= "Modified p35 protein precursor"
FT sig_peptide 1. .66
FT /*tag= b
FT mat_peptide 67. .657
FT /*tag= c
FT /product= "Mature modified p35 protein"
XX
PN WO200140257-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000WO-US032664.
XX
PR 02-DEC-1999; 99US-0169035P.
PR 28-NOV-2000; 2000US-00725324.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Leong SR, Punnonen J;
XX
DR WPI; 2001-502381/55.
DR P-PSDB; AAE08608.
XX
PT Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT retinopathy and cancer.
XX
PS Claim 87; Page 139-140; 223pp; English.
XX
CC The invention relates to nucleic acids encoding modified cytokine
CC polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC gamma induction activities. The polypeptides and polynucleotides of the
CC invention are useful for treating various diseases e.g. bacterial
CC infections, AIDS, diabetic retinopathy and cancer. The polypeptide and

```
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein encoding
CC   DNA
XX
SQ   Sequence 660 BP; 190 A; 171 C; 137 G; 162 T; 0 U; 0 Other;

  Query Match             20.3%;  Score 120;  DB 5;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-50;
  Matches  120;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        295 ACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCC 354
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCC 420

Qy        355 ATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480


RESULT 31
AAD15213
ID   AAD15213 standard; DNA; 660 BP.
XX
AC   AAD15213;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 encoding DNA from clone R2-796.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p35; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "Modified p35 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .657
FT                   /*tag=  c
FT                   /product= "Mature modified p35 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08606.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 87; Page 139; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein encoding
CC   DNA
XX
SQ   Sequence 660 BP; 189 A; 172 C; 136 G; 163 T; 0 U; 0 Other;

  Query Match             19.5%;  Score 115;  DB 5;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-48;
  Matches  115;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 216

Qy        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAA 205
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        217 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAA 271


RESULT 32
AAD15220
ID   AAD15220 standard; DNA; 660 BP.
XX
AC   AAD15220;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 encoding DNA from clone R1-4-87.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p35; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "Modified p35 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .657
FT                   /*tag=  c
FT                   /product= "Mature modified p35 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08613.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 87; Page 140-141; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
```

```
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein encoding
CC   DNA
XX
SQ   Sequence 660 BP; 189 A; 172 C; 136 G; 163 T; 0 U; 0 Other;

  Query Match             19.5%;  Score 115;  DB 5;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-48;
  Matches  115;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 216

Qy        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAA 205
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        217 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAA 271


RESULT 33
AAD15218
ID   AAD15218 standard; DNA; 660 BP.
XX
AC   AAD15218;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 encoding DNA from clone R2-162.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p35; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "Modified p35 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .657
FT                   /*tag=  c
FT                   /product= "Mature modified p35 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08611.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 87; Page 140; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein encoding
CC   DNA
XX
SQ   Sequence 660 BP; 182 A; 180 C; 144 G; 154 T; 0 U; 0 Other;

  Query Match             17.3%;  Score 102;  DB 5;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-41;
  Matches  102;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        313 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 438

Qy        373 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 414
              |||||||||||||||||||||||||||||||||||||||||||
Db        439 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480


RESULT 34
AAD15216
ID   AAD15216 standard; DNA; 660 BP.
XX
AC   AAD15216;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 encoding DNA from clone R2-571.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p35; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "Modified p35 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .657
FT                   /*tag=  c
FT                   /product= "Mature modified p35 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08609.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
```

```
PS   Claim 87; Page 140; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein encoding
CC   DNA
XX
SQ   Sequence 660 BP; 184 A; 172 C; 141 G; 163 T; 0 U; 0 Other;

  Query Match            16.6%;  Score 98;  DB 5;  Length 660;
  Best Local Similarity  100.0%;  Pred. No. 3.5e-39;
  Matches   98;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 216

Qy        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 188
              ||||||||||||||||||||||||||||||||||||
Db        217 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 254


RESULT 35
AAD15219
ID   AAD15219 standard; DNA; 660 BP.
XX
AC   AAD15219;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 encoding DNA from clone R2-157.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p35; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "Modified p35 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .657
FT                   /*tag=  c
FT                   /product= "Mature modified p35 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08612.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 87; Page 140; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein encoding
CC   DNA
XX
SQ   Sequence 660 BP; 181 A; 178 C; 144 G; 157 T; 0 U; 0 Other;

  Query Match            14.2%;  Score 84;  DB 5;  Length 660;
  Best Local Similarity  99.3%;  Pred. No. 4.7e-32;
  Matches  134;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        237 GATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGAC 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 GATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGAC 362

Qy        297 CCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCAT 356
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        363 CCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCAT 422

Qy        357 GAATGCAAAGCTGTT 371
              |||||||||||||||
Db        423 GAATGCAAAGCTGTT 437


RESULT 36
AAX18179
ID   AAX18179 standard; cDNA; 591 BP.
XX
AC   AAX18179;
XX
DT   07-MAY-1999  (first entry)
XX
DE   Canine mature CLAF p35 subunit coding sequence.
XX
KW   CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW   viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW   canine infectious hepatitis; ds.
XX
OS   Canis sp.
XX
PN   WO9855511-A1.
XX
PD   10-DEC-1998.
XX
PF   26-MAY-1998;   98WO-JP002295.
XX
PR   03-JUN-1997;   97JP-00161936.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Tokiyoshi S,  Eda Y;
XX
DR   WPI; 1999-070260/06.
DR   P-PSDB; AAW74325.
XX
PT   Canine cytokine protein which activates canine cytotoxic T lymphocytes -
PT   is useful for treatment of viral and autoimmune diseases in dogs.
XX
PS   Claim 8; Page 34-35; 51pp; Japanese.
XX
CC   This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC   the invention. CLAF activates lymphocytes, especially canine cytotoxic T
CC   cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
```

```
CC   recognising it may be used in the treatment of viral diseases in dogs
CC   (such as canine distemper, canine parvovirus and canine infectious
CC   hepatitis). The antibodies may also be used in isolation of CLAF from
CC   culture of the transformant host cells by affinity chromatography. The
CC   p40 homodimer can be used for the treatment of autoimmune diseases in
CC   dogs
XX
SQ   Sequence 591 BP; 173 A; 146 C; 127 G; 145 T; 0 U; 0 Other;

  Query Match             13.7%;  Score 81;  DB 2;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        223 CTGGCTTCCAGAGAGATCTCT 243


RESULT 37
ABK98958/c
ID   ABK98958 standard; cDNA; 591 BP.
XX
AC   ABK98958;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p35-591 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Disclosure; Page 70; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 591 BP; 145 A; 127 C; 146 G; 173 T; 0 U; 0 Other;

  Query Match             13.7%;  Score 81;  DB 6;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 38
ABK98957
ID   ABK98957 standard; cDNA; 591 BP.
XX
AC   ABK98957;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p35-591 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69309.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 69; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 591 BP; 173 A; 146 C; 127 G; 145 T; 0 U; 0 Other;

  Query Match             13.7%;  Score 81;  DB 6;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        223 CTGGCTTCCAGAGAGATCTCT 243


RESULT 39
ADV34701
ID   ADV34701 standard; cDNA; 591 BP.
XX
AC   ADV34701;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p35 protein cDNA, nCaIL-12p35 591.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .591
FT                   /*tag=  a
FT                   /product= "PCaIL-12P35 197 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34702.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 49; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p35 subunit protein
CC   encoding cDNA.
XX
SQ   Sequence 591 BP; 173 A; 146 C; 127 G; 145 T; 0 U; 0 Other;

  Query Match             13.7%;  Score 81;  DB 14;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        223 CTGGCTTCCAGAGAGATCTCT 243


RESULT 40
ADV34703/c
ID   ADV34703 standard; DNA; 591 BP.
XX
AC   ADV34703;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p35 complementary DNA, nCaIL-12p35 591.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 51; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p35 subunit
CC   complementary DNA.
XX
SQ   Sequence 591 BP; 145 A; 127 C; 146 G; 173 T; 0 U; 0 Other;

  Query Match             13.7%;  Score 81;  DB 14;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 41
ABK98955
ID   ABK98955 standard; cDNA; 666 BP.
XX
AC   ABK98955;
XX
DT   21-OCT-2002  (first entry)
```

XX
DE Canine interleukin-12 nCaIL-12p35-666 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69308.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 1; Page 67-68; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 666 BP; 182 A; 177 C; 145 G; 162 T; 0 U; 0 Other;

Query Match 13.7%; Score 81; DB 6; Length 666;
Best Local Similarity 100.0%; Pred. No. 1.6e-30;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy 223 CTGGCTTCCAGAGAGATCTCT 243
||||||||||||||||||||
Db 298 CTGGCTTCCAGAGAGATCTCT 318

RESULT 42
ABK98956/c
ID ABK98956 standard; cDNA; 666 BP.
XX
AC ABK98956;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12p35-66 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Disclosure; Page 68-69; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 666 BP; 162 A; 145 C; 177 G; 182 T; 0 U; 0 Other;

Query Match 13.7%; Score 81; DB 6; Length 666;
Best Local Similarity 100.0%; Pred. No. 1.6e-30;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy 223 CTGGCTTCCAGAGAGATCTCT 243
||||||||||||||||||||
Db 369 CTGGCTTCCAGAGAGATCTCT 349

RESULT 43
ADV34700/c
ID ADV34700 standard; DNA; 666 BP.
XX
AC ADV34700;
XX
DT 24-FEB-2005 (first entry)
XX
DE Canine single chain IL-12p35 complementary DNA, nCaIL-12p35 666.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Canis familiaris.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.

```
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 48; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p35 subunit full-length
CC   complementary DNA.
XX
SQ   Sequence 666 BP; 162 A; 145 C; 177 G; 182 T; 0 U; 0 Other;

  Query Match             13.7%;  Score 81;  DB 14;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 44
ADV34698
ID   ADV34698 standard; cDNA; 666 BP.
XX
AC   ADV34698;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p35 full-length cDNA, nCaIL-12p35 666.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .666
FT                   /*tag=  a
FT                   /product= "PCaIL-12p222 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34699.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 46; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p35 subunit protein
CC   encoding full-length cDNA.
XX
SQ   Sequence 666 BP; 182 A; 177 C; 145 G; 162 T; 0 U; 0 Other;

  Query Match             13.7%;  Score 81;  DB 14;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 45
AAV13818
ID   AAV13818 standard; cDNA to mRNA; 669 BP.
XX
AC   AAV13818;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P35 subunit cDNA.
XX
KW   Canine; interleukin-12 P35 subunit; IL-12 P35 subunit; antitumour;
KW   antiviral; vaccine adjuvant; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag=  a
FT                   /product= "interleukin-12_P35_subunit"
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-00296789.
XX
PR   08-NOV-1995;   95JP-00289729.
PR   23-MAY-1996;   96JP-00128104.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   P-PSDB; AAW41792.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
```

```
PT   activities are expected.
XX
PS   Claim 9; Page 9; 12pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin-12 (IL-12) P35 subunit.
CC   A canine IL-12 comprising a P40 and P35 subunit is capable of inducing an
CC   antiviral activating factor and the expression of class II MHC molecules
CC   in canine tumour cells, stimulating proliferation of canine blastogenic
CC   lymphocytes and activating canine leukocytes to inhibit canine tumour
CC   cells. The canine IL-12 can be used in veterinary medicines, e.g.
CC   antitumour, antivirus and vaccine adjuvant activities are expected
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 U; 0 Other;

  Query Match             13.7%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 46
AAV13819
ID   AAV13819 standard; cDNA to mRNA; 669 BP.
XX
AC   AAV13819;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P35 subunit cDNA.
XX
KW   Canine; interleukin-12 P35 subunit; IL-12 P35 subunit; antitumour;
KW   antiviral; vaccine adjuvant; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag=  a
FT                   /product= "interleukin-12_P35_subunit"
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-00296789.
XX
PR   08-NOV-1995;   95JP-00289729.
PR   23-MAY-1996;   96JP-00128104.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   P-PSDB; AAW41793.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected.
XX
PS   Claim 11; Page 11-12; 12pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin-12 (IL-12) P35 subunit.
CC   A canine IL-12 comprising a P40 and P35 subunit is capable of inducing an
CC   antiviral activating factor and the expression of class II MHC molecules
CC   in canine tumour cells, stimulating proliferation of canine blastogenic
CC   lymphocytes and activating canine leukocytes to inhibit canine tumour
CC   cells. The canine IL-12 can be used in veterinary medicines, e.g.
CC   antitumour, antivirus and vaccine adjuvant activities are expected
XX
SQ   Sequence 669 BP; 185 A; 177 C; 144 G; 163 T; 0 U; 0 Other;

  Query Match             13.7%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 47
AAX03163
ID   AAX03163 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX03163;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Nucleic acid encoding canine interleukin 12.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag=  a
FT                   /product= "interleukin_12"
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP002031.
XX
PR   16-MAY-1997;   97JP-00127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   P-PSDB; AAW84374.
XX
PT   New therapeutic and prophylactic agents - comprise genetically-engineered
PT   canine interleukin 12, used to treat, e.g. canine and feline
PT   immunological diseases.
XX
PS   Claim 1; Page 33-34; 45pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin 12 (IL-12) protein. The
CC   IL-12 protein can be used in therapeutic or prophylactic agents. The
CC   agents can be used to prevent and treat canine and feline immunological
CC   diseases including dog and cat tumours, skin diseases, viral infections
CC   and allergic diseases, especially tumours, breast tumour, oesinophilic
CC   granuloma, epidermoid tumour, skin tumour, lipoma, othematoma,
CC   pneumonoedema, skin soft pedicled soft tumour and anal tumour; skin
CC   diseases, otitis externa, dermatitis, eczema, fungal diseases of the
CC   skin, pyoderma, allergic dermatitis, nettle rash, traumatic dermatitis
```

```
CC   and hair loss; infections; dog Parvovirus infection and distemper virus,
CC   cat plaque virus infection and feline leukaemia, and allergic diseases,
CC   e.g. pollinosis
XX
SQ   Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 U; 0 Other;

  Query Match             13.7%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 48
AAX03153
ID   AAX03153 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX03153;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Nucleic acid encoding canine interleukin 12.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag=  a
FT                   /product= "interleukin_12"
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP002031.
XX
PR   16-MAY-1997;   97JP-00127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   P-PSDB; AAW84372.
XX
PT   New therapeutic and prophylactic agents - comprise genetically-engineered
PT   canine interleukin 12, used to treat, e.g. canine and feline
PT   immunological diseases.
XX
PS   Claim 1; Page 26-27; 45pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin 12 (IL-12) protein. The
CC   IL-12 protein can be used in therapeutic or prophylactic agents. The
CC   agents can be used to prevent and treat canine and feline immunological
CC   diseases including dog and cat tumours, skin diseases, viral infections
CC   and allergic diseases, especially tumours, breast tumour, oesinophilic
CC   granuloma, epidermoid tumour, skin tumour, lipoma, othematoma,
CC   pneumonoedema, skin soft pedicled soft tumour and anal tumour; skin
CC   diseases, otitis externa, dermatitis, eczema, fungal diseases of the
CC   skin, pyoderma, allergic dermatitis, nettle rash, traumatic dermatitis
CC   and hair loss; infections; dog Parvovirus infection and distemper virus,
CC   cat plaque virus infection and feline leukaemia, and allergic diseases,
CC   e.g. pollinosis
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 U; 0 Other;

  Query Match             13.7%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 49
AAX35616
ID   AAX35616 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX35616;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag=  a
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-00133345.
XX
PR   16-MAY-1997;   97JP-00127690.
PR   07-AUG-1997;   97JP-00213755.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   P-PSDB; AAY02340.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) - for
PT   prevention and treatment of dog and cat immune diseases.
XX
PS   Claim 1; Page 13; 16pp; Japanese.
XX
CC   The present sequence encodes canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment of dog
CC   and cat immune diseases. The treatment used an agent comprising dog IL-12
CC   (CaIL12) proteins to form a heterodimer. The agent is useful for
CC   preventing and treating dog and cat immune diseases, including tumours,
CC   skin diseases, infectious diseases and allergic diseases
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 U; 0 Other;

  Query Match             13.7%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
```

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 50
AAX35626
ID   AAX35626 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX35626;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag=  a
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-00133345.
XX
PR   16-MAY-1997;   97JP-00127690.
PR   07-AUG-1997;   97JP-00213755.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   P-PSDB; AAY02343.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) - for
PT   prevention and treatment of dog and cat immune diseases.
XX
PS   Claim 1; Page 15-16; 16pp; Japanese.
XX
CC   The present sequence encodes canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment of dog
CC   and cat immune diseases. The treatment used an agent comprising dog IL-12
CC   (CaIL12) proteins to form a heterodimer. The agent is useful for
CC   preventing and treating dog and cat immune diseases, including tumours,
CC   skin diseases, infectious diseases and allergic diseases
XX
SQ   Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 U; 0 Other;

  Query Match             13.7%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 51
AAI64389
ID   AAI64389 standard; DNA; 669 BP.
XX
AC   AAI64389;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine coding sequence #4.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag=  a
FT                   /product= "Canine protein #4"
FT   sig_peptide     1. .75
FT                   /*tag=  b
FT   mat_peptide     76. .666
FT                   /*tag=  c
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-00292946.
XX
PR   01-OCT-1999;   99JP-00281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   P-PSDB; AAG66483.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian.
XX
PS   Claim 6; Page 18; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention
XX
SQ   Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 U; 0 Other;

  Query Match             13.7%;  Score 81;  DB 4;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 52
AAI64379
ID   AAI64379 standard; DNA; 669 BP.
XX
AC   AAI64379;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine coding sequence #2.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
OS   Canis familiaris.
XX
```

```
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag= a
FT                   /product= "Canine protein #2"
FT   sig_peptide     1. .75
FT                   /*tag= b
FT   mat_peptide     76. .666
FT                   /*tag= c
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-00292946.
XX
PR   01-OCT-1999;   99JP-00281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   P-PSDB; AAG66481.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian.
XX
PS   Claim 6; Page 15; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 U; 0 Other;

  Query Match             13.7%;  Score 81;  DB 4;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 53
ADZ25701
ID   ADZ25701 standard; cDNA; 669 BP.
XX
AC   ADZ25701;
XX
DT   16-JUN-2005  (first entry)
XX
DE   Canine interleukin 12 P35 encoding cDNA SEQ ID NO:6.
XX
KW   interleukin-12; antiviral; gene; ss.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag= b
FT                   /product= "interleukin-12 P40"
FT   sig_peptide     1. .75
FT                   /*tag= a
FT   mat_peptide     76. .666
FT                   /*tag= c
FT                   /product= "interleukin-12 P40"
XX
PN   JP2003284585-A.
XX
PD   07-OCT-2003.
XX
PF   28-MAR-2002; 2002JP-00090161.
XX
PR   28-MAR-2002; 2002JP-00090161.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2003-885430/82.
DR   P-PSDB; ADZ25703.
XX
PT   Large scale production of interleukin-12 for pharmaceutical applications,
PT   comprises infecting an insect cell with a recombinant virus containing
PT   gene encoding IL-12, and producing IL-12 by carrying out spinner culture
PT   of insect cell.
XX
PS   Example; SEQ ID NO 6; 8pp; Japanese.
XX
CC   The invention related to the large scale production of interleukin-12 (IL
CC   -12), which involves infecting an insect cell with a recombinant virus
CC   containing a gene encoding IL-12, and producing IL-12 by carrying out
CC   spinner culture of insect cell. The method is useful for producing IL-12,
CC   preferably canine IL-12. IL-12 has pharmaceutical applications. The
CC   present sequence encodes canine IL-12 P35, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 U; 0 Other;

  Query Match             13.7%;  Score 81;  DB 11;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 54
ADT04852
ID   ADT04852 standard; DNA; 669 BP.
XX
AC   ADT04852;
XX
DT   13-JAN-2005  (first entry)
XX
DE   Canine interleukin-12 (IL-12) p35 DNA.
XX
KW   gene expression; insect; ds; interleukin-12; IL-12.
XX
OS   Canis familiaris.
XX
PN   JP2004290182-A.
XX
PD   21-OCT-2004.
XX
PF   06-FEB-2004; 2004JP-00030183.
XX
PR   10-MAR-2003; 2003JP-00062907.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2004-740760/73.
XX
PT   Novel gene vector for expression in insect useful for expression of
PT   foreign gene such as dog interleukin 12 gene, comprises two promoters.
XX
```

PS Claim 4; SEQ ID NO 8; 13pp; Japanese.
XX
CC The invention relates to a novel gene vector for expression in an insect
CC comprising at least two promoters, particularly the polyhedrin promoter
CC and p10 promoter. The vector contains at least two types of foreign
CC protein expression gene and the gene product of the vector is produced
CC using a gene recombinant baculovirus, particularly a recombinant silkworm
CC nuclear polyhedrosis virus. The baculovirus is proliferated in a
CC silkworm. The vector of the invention may be useful for expression of a
CC foreign gene, such as canine interleukin 12. Within the vector, two types
CC of foreign protein expression genes are integrated simultaneously for
CC their simultaneous expression. The current sequence is that of the canine
CC interleukin-12 (IL-12) p35 DNA of the invention.
XX
SQ Sequence 669 BP; 183 A; 177 C; 145 G; 164 T; 0 U; 0 Other;

Query Match 13.7%; Score 81; DB 13; Length 669;
Best Local Similarity 100.0%; Pred. No. 1.6e-30;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy 223 CTGGCTTCCAGAGAGATCTCT 243
||||||||||||||||||||
Db 298 CTGGCTTCCAGAGAGATCTCT 318

RESULT 55
AAX18178
ID AAX18178 standard; cDNA; 1282 BP.
XX
AC AAX18178;
XX
DT 07-MAY-1999 (first entry)
XX
DE Canine full length CLAF p35 subunit coding sequence.
XX
KW CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW canine infectious hepatitis; ds.
XX
OS Canis sp.
XX
PN WO9855511-A1.
XX
PD 10-DEC-1998.
XX
PF 26-MAY-1998; 98WO-JP002295.
XX
PR 03-JUN-1997; 97JP-00161936.
XX
PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI Imamura T, Maeda H, Tokiyoshi S, Eda Y;
XX
DR WPI; 1999-070260/06.
DR P-PSDB; AAW74324.
XX
PT Canine cytokine protein which activates canine cytotoxic T lymphocytes -
PT is useful for treatment of viral and autoimmune diseases in dogs.
XX
PS Claim 8; Page 33-34; 51pp; Japanese.
XX
CC This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC the invention. CLAF activates lymphocytes, especially canine cytotoxic T
CC cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC recognising it may be used in the treatment of viral diseases in dogs
CC (such as canine distemper, canine parvovirus and canine infectious
CC hepatitis). The antibodies may also be used in isolation of CLAF from
CC culture of the transformant host cells by affinity chromatography. The
CC p40 homodimer can be used for the treatment of autoimmune diseases in
CC dogs
XX
SQ Sequence 1282 BP; 391 A; 279 C; 257 G; 355 T; 0 U; 0 Other;

Query Match 13.7%; Score 81; DB 2; Length 1282;
Best Local Similarity 100.0%; Pred. No. 1.6e-30;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 303 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 362

Qy 223 CTGGCTTCCAGAGAGATCTCT 243
||||||||||||||||||||
Db 363 CTGGCTTCCAGAGAGATCTCT 383

RESULT 56
ABK99003
ID ABK99003 standard; cDNA; 1455 BP.
XX
AC ABK99003;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12p35-1455 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69316.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Example 4; Page 94-95; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1455 BP; 437 A; 341 C; 304 G; 373 T; 0 U; 0 Other;

Query Match 13.7%; Score 81; DB 6; Length 1455;
Best Local Similarity 100.0%; Pred. No. 1.6e-30;

```
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 528

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        529 CTGGCTTCCAGAGAGATCTCT 549


RESULT 57
ABK99004/c
ID   ABK99004 standard; cDNA; 1455 BP.
XX
AC   ABK99004;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p35-1455 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 4; Page 96; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1455 BP; 373 A; 304 C; 341 G; 437 T; 0 U; 0 Other;

  Query Match             13.7%;  Score 81;  DB 6;  Length 1455;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 928

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        927 CTGGCTTCCAGAGAGATCTCT 907


RESULT 58
ADV34756/c
ID   ADV34756 standard; DNA; 1455 BP.
XX
AC   ADV34756;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p35 complementary DNA, nCaIL-12p35 1455.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 106; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p35 subunit
CC   complementary DNA.
XX
SQ   Sequence 1455 BP; 373 A; 304 C; 341 G; 437 T; 0 U; 0 Other;

  Query Match             13.7%;  Score 81;  DB 14;  Length 1455;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 928

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        927 CTGGCTTCCAGAGAGATCTCT 907


RESULT 59
ADV34754
ID   ADV34754 standard; cDNA; 1455 BP.
XX
AC   ADV34754;
XX
DT   24-FEB-2005  (first entry)
XX
```

DE Canine single chain IL-12p35 protein cDNA, nCaIL-12p35 1455.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; gene; ss.
XX
OS Canis familiaris.
XX
FH Key Location/Qualifiers
FT CDS 232. .900
FT /*tag= a
FT /product= "PCaIL-12p35 222 protein"
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
DR P-PSDB; ADV34755.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 4; SEQ ID NO 104; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the canine single chain IL-12p35 subunit protein
CC encoding cDNA.
XX
SQ Sequence 1455 BP; 437 A; 341 C; 304 G; 373 T; 0 U; 0 Other;

Query Match 13.7%; Score 81; DB 14; Length 1455;
Best Local Similarity 100.0%; Pred. No. 1.6e-30;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 469 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 528

Qy 223 CTGGCTTCCAGAGAGATCTCT 243
||||||||||||||||||||
Db 529 CTGGCTTCCAGAGAGATCTCT 549

RESULT 60
ABK98967
ID ABK98967 standard; cDNA; 1533 BP.
XX
AC ABK98967;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12-1533 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69314.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 83-85; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1533 BP; 446 A; 368 C; 369 G; 350 T; 0 U; 0 Other;

Query Match 13.7%; Score 81; DB 6; Length 1533;
Best Local Similarity 100.0%; Pred. No. 1.6e-30;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1105 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1164

Qy 223 CTGGCTTCCAGAGAGATCTCT 243
||||||||||||||||||||
Db 1165 CTGGCTTCCAGAGAGATCTCT 1185

RESULT 61
ABK98968/c
ID ABK98968 standard; cDNA; 1533 BP.
XX
AC ABK98968;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12-1533 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX

```
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 86-87; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

  Query Match             13.7%;  Score 81;  DB 6;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 62
ADV34718/c
ID   ADV34718 standard; DNA; 1533 BP.
XX
AC   ADV34718;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12 complementary DNA, nCaIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 68; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 complementary DNA.
XX
SQ   Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

  Query Match             13.7%;  Score 81;  DB 14;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 63
ADV34716
ID   ADV34716 standard; cDNA; 1533 BP.
XX
AC   ADV34716;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12 protein cDNA, nCaIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1533
FT                   /*tag=  a
FT                   /product= "PCaIL-12 511 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34717.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
```

PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 4; SEQ ID NO 66; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the canine single chain IL-12 protein encoding cDNA.
XX
SQ Sequence 1533 BP; 446 A; 368 C; 369 G; 350 T; 0 U; 0 Other;

Query Match 13.7%; Score 81; DB 14; Length 1533;
Best Local Similarity 100.0%; Pred. No. 1.6e-30;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1105 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1164

Qy 223 CTGGCTTCCAGAGAGATCTCT 243
||||||||||||||||||||
Db 1165 CTGGCTTCCAGAGAGATCTCT 1185

RESULT 64
ABK98965
ID ABK98965 standard; cDNA; 1599 BP.
XX
AC ABK98965;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12-1599 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69313.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 79-80; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1599 BP; 452 A; 392 C; 383 G; 372 T; 0 U; 0 Other;

Query Match 13.7%; Score 81; DB 6; Length 1599;
Best Local Similarity 100.0%; Pred. No. 1.6e-30;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1171 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1230

Qy 223 CTGGCTTCCAGAGAGATCTCT 243
||||||||||||||||||||
Db 1231 CTGGCTTCCAGAGAGATCTCT 1251

RESULT 65
ABK98966/c
ID ABK98966 standard; cDNA; 1599 BP.
XX
AC ABK98966;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12-1599 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 82-83; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX

```
SQ   Sequence 1599 BP; 372 A; 383 C; 392 G; 452 T; 0 U; 0 Other;

  Query Match             13.7%;  Score 81;  DB 6;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 66
ADV34715/c
ID   ADV34715 standard; DNA; 1599 BP.
XX
AC   ADV34715;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12 complementary DNA, nCaIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 63; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 complementary DNA.
XX
SQ   Sequence 1599 BP; 372 A; 383 C; 392 G; 452 T; 0 U; 0 Other;

  Query Match             13.7%;  Score 81;  DB 14;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 67
ADV34713
ID   ADV34713 standard; cDNA; 1599 BP.
XX
AC   ADV34713;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12 protein cDNA, nCaIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1599
FT                   /*tag=  a
FT                   /product= "PCaIL-12 533 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34714.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 61; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1599 BP; 452 A; 392 C; 383 G; 372 T; 0 U; 0 Other;

  Query Match             13.7%;  Score 81;  DB 14;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1230

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db       1231 CTGGCTTCCAGAGAGATCTCT 1251


RESULT 68
AAF26092
ID   AAF26092 standard; DNA; 71 BP.
```

```
XX
AC   AAF26092;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p35 PCR primer SEQ ID 8.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; PCR primer; ss.
XX
OS   Felis sp.
XX
PN   WO200104155-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002263.
XX
PR   08-JUL-1999;   99CH-00001259.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Lutz H,  Leutenegger C,  Pedersen N,  Schroff M,  Wittig B;
XX
DR   WPI; 2001-147178/15.
XX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs.
XX
PS   Example 1b; Page 33; 35pp; German.
XX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
CC   following: (i) as immunostimulant, for preventative or therapeutic use;
CC   and (ii) treating tumors and autoimmune diseases, or diseases associated
CC   with a Th1 defect, especially pre-existing infections by feline immune
CC   deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ   Sequence 71 BP; 17 A; 19 C; 17 G; 18 T; 0 U; 0 Other;

  Query Match             12.0%;  Score 71;  DB 4;  Length 71;
  Best Local Similarity   100.0%;  Pred. No. 2e-25;
  Matches   71;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        410 TGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCAC 469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCAC 60

Qy        470 AGAACTCCTCC 480
              ||||||||||||
Db         61 AGAACTCCTCC 71


RESULT 69
AAF26099
ID   AAF26099 standard; DNA; 71 BP.
XX
AC   AAF26099;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline Il-12 associated DNA #1.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS   Unidentified.
XX
PN   WO200104155-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002263.
XX
PR   08-JUL-1999;   99CH-00001259.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Lutz H,  Leutenegger C,  Pedersen N,  Schroff M,  Wittig B;
XX
DR   WPI; 2001-147178/15.
XX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs.
XX
PS   Disclosure; Fig 2; 35pp; German.
XX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
CC   following: (i) as immunostimulant, for preventative or therapeutic use;
CC   and (ii) treating tumors and autoimmune diseases, or diseases associated
CC   with a Th1 defect, especially pre-existing infections by feline immune
CC   deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ   Sequence 71 BP; 17 A; 19 C; 17 G; 18 T; 0 U; 0 Other;

  Query Match             12.0%;  Score 71;  DB 4;  Length 71;
  Best Local Similarity   100.0%;  Pred. No. 2e-25;
  Matches   71;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        410 TGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCAC 469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCAC 60

Qy        470 AGAACTCCTCC 480
              ||||||||||||
Db         61 AGAACTCCTCC 71
```

RESULT 70
ADQ41825
ID ADQ41825 standard; DNA; 201 BP.
XX
AC ADQ41825;
XX
DT 18-NOV-2004 (first entry)
XX
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 3488.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human; ds.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JJ, Iakoubova O;
XX
DR WPI; 2004-533949/51.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 7; SEQ ID NO 3488; 145pp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a transcript-based context sequence
CC which flanks an SNP found in a human myocardial infarction-associated
CC gene of the invention. Note: This sequence was not shown in the
CC specification. The sequence has come from an electronic sequence listing
CC downloaded from the WIPO website.
XX
SQ Sequence 201 BP; 64 A; 39 C; 37 G; 60 T; 0 U; 1 Other;

Query Match 11.0%; Score 65; DB 13; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.2e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 21 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 80

Qy 544 ATTCG 548
|||||
Db 81 ATTCG 85

RESULT 71
ADQ41824
ID ADQ41824 standard; DNA; 201 BP.
XX
AC ADQ41824;
XX
DT 18-NOV-2004 (first entry)
XX
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 3487.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human; ds.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JJ, Iakoubova O;
XX
DR WPI; 2004-533949/51.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 7; SEQ ID NO 3487; 145pp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a transcript-based context sequence
CC which flanks an SNP found in a human myocardial infarction-associated

CC gene of the invention. Note: This sequence was not shown in the
CC specification. The sequence has come from an electronic sequence listing
CC downloaded from the WIPO website.
XX
SQ Sequence 201 BP; 65 A; 36 C; 38 G; 61 T; 0 U; 1 Other;

Query Match 11.0%; Score 65; DB 13; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.2e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 13 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 72

Qy 544 ATTCG 548
|||||
Db 73 ATTCG 77

RESULT 72
ADQ41835
ID ADQ41835 standard; DNA; 201 BP.
XX
AC ADQ41835;
XX
DT 18-NOV-2004 (first entry)
XX
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 3498.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human; ds.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JJ, Iakoubova O;
XX
DR WPI; 2004-533949/51.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 7; SEQ ID NO 3498; 145pp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a transcript-based context sequence
CC which flanks an SNP found in a human myocardial infarction-associated
CC gene of the invention. Note: This sequence was not shown in the
CC specification. The sequence has come from an electronic sequence listing
CC downloaded from the WIPO website.
XX
SQ Sequence 201 BP; 64 A; 39 C; 37 G; 60 T; 0 U; 1 Other;

Query Match 11.0%; Score 65; DB 13; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.2e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 21 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 80

Qy 544 ATTCG 548
|||||
Db 81 ATTCG 85

RESULT 73
ADQ41829
ID ADQ41829 standard; DNA; 201 BP.
XX
AC ADQ41829;
XX
DT 18-NOV-2004 (first entry)
XX
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 3492.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human; ds.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JJ, Iakoubova O;
XX
DR WPI; 2004-533949/51.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 7; SEQ ID NO 3492; 145pp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least

CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a transcript-based context sequence
CC which flanks an SNP found in a human myocardial infarction-associated
CC gene of the invention. Note: This sequence was not shown in the
CC specification. The sequence has come from an electronic sequence listing
CC downloaded from the WIPO website.
XX
SQ Sequence 201 BP; 62 A; 42 C; 39 G; 57 T; 0 U; 1 Other;

Query Match 11.0%; Score 65; DB 13; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.2e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 122 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 181

Qy 544 ATTCG 548
|||||
Db 182 ATTCG 186

RESULT 74
ADQ41838
ID ADQ41838 standard; DNA; 201 BP.
XX
AC ADQ41838;
XX
DT 18-NOV-2004 (first entry)
XX
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 3501.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human; ds.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JJ, Iakoubova O;
XX
DR WPI; 2004-533949/51.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 7; SEQ ID NO 3501; 145pp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a transcript-based context sequence
CC which flanks an SNP found in a human myocardial infarction-associated
CC gene of the invention. Note: This sequence was not shown in the
CC specification. The sequence has come from an electronic sequence listing
CC downloaded from the WIPO website.
XX
SQ Sequence 201 BP; 62 A; 42 C; 39 G; 57 T; 0 U; 1 Other;

Query Match 11.0%; Score 65; DB 13; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.2e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 122 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 181

Qy 544 ATTCG 548
|||||
Db 182 ATTCG 186

RESULT 75
ADQ41833
ID ADQ41833 standard; DNA; 201 BP.
XX
AC ADQ41833;
XX
DT 18-NOV-2004 (first entry)
XX
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 3496.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human; ds.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.

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XX
PI   Cargill M,  Devlin JJ,  Iakoubova O;
XX
DR   WPI; 2004-533949/51.
XX
PT   Identifying an individual who has an altered risk for developing
PT   myocardial infarction by detecting a single nucleotide polymorphism in
PT   the individual's nucleic acids.
XX
PS   Claim 7; SEQ ID NO 3496; 145pp; English.
XX
CC   The invention relates to a novel method for identifying an individual who
CC   has an altered risk for developing myocardial infarction. The method
CC   comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC   the nucleotide sequences given in the specification in the individual's
CC   nucleic acids, where the presence of the SNP is correlated with an
CC   altered risk for myocardial infarction in the individual. The invention
CC   further comprises: an isolated nucleic acid molecule comprising at least
CC   8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC   the specification or its complement and encoding any one of the amino
CC   acid sequences given in the specification; an isolated polypeptide
CC   comprising an amino acid sequence given in the specification; an antibody
CC   that specifically binds to the polypeptide or its antigen-binding
CC   fragment; an amplified polynucleotide containing an SNP given in the
CC   specification and which is between about 16 and 1000 nucleotides in
CC   length; a kit for detecting an SNP in a nucleic acid, comprising the
CC   polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC   nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC   method for identifying an agent useful in treating or preventing
CC   myocardial infarction. The novel detection method has cardiant activity.
CC   The nucleic acids of the invention may be used in gene therapy. The
CC   method is useful in identifying an individual who has an increased or
CC   decreased risk for developing myocardial infarction and for preparing a
CC   composition for treating or preventing myocardial infarction. This
CC   polynucleotide sequence represents a transcript-based context sequence
CC   which flanks an SNP found in a human myocardial infarction-associated
CC   gene of the invention. Note: This sequence was not shown in the
CC   specification. The sequence has come from an electronic sequence listing
CC   downloaded from the WIPO website.
XX
SQ   Sequence 201 BP; 65 A; 36 C; 38 G; 61 T; 0 U; 1 Other;

  Query Match           11.0%;  Score 65;  DB 13;  Length 201;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 72

Qy        544 ATTCG 548
              |||||
Db         73 ATTCG 77


RESULT 76
ADG39431
ID   ADG39431 standard; DNA; 657 BP.
XX
AC   ADG39431;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human CLMF 35 kDa subunit DNA.
XX
KW   human; cytotoxic lymphocyte maturation factor; CLMF;
KW   activated T-cell stimulator; natural killer cell stimulator;
KW   immunoenhancer; antitumour; tumour; cancer; ds; gene.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             67. .657
FT                   /*tag=  a
FT                   /partial
FT                   /product= "CLMF 35 kDa subunit"
FT                   /note= "No start or stop codon given"
XX
PN   US2003204059-A1.
XX
PD   30-OCT-2003.
XX
PF   08-OCT-2002; 2002US-00267565.
XX
PR   22-DEC-1989;   89US-00455708.
PR   09-MAY-1990;   90US-00520935.
PR   27-AUG-1990;   90US-00572284.
PR   24-MAR-1992;   92US-00857023.
PR   02-MAR-1994;   94US-00205011.
PR   02-JUN-1995;   95US-00459151.
PR   22-SEP-1999;   99US-00401839.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CIE SA F.
XX
PI   Gately MK,  Gubler UA,  Hulmes JD,  Podlaski FJ,  Stern AS;
PI   Chizzonite RA,  Pan YE;
XX
DR   WPI; 2004-010534/01.
DR   P-PSDB; ADG39428.
XX
PT   Novel protein comprising cytotoxic lymphocyte maturation factor in
PT   substantially pure form or protein which exhibits cytotoxic lymphocyte
PT   maturation factor activity, useful as antitumor and immunoenhancing
PT   agent.
XX
PS   Claim 20; Page 29; 74pp; English.
XX
CC   The invention relates to a protein which comprises a cytotoxic lymphocyte
CC   maturation factor (CLMF). The protein is useful for stimulating activated
CC   T-cells which involves treating T-cells with the protein. The method
CC   further involves treating the activated T-cells with IL2 or its
CC   biologically active fragment. The protein is useful for stimulating
CC   natural killer cells which involves treating the natural killer cells
CC   with the protein. The protein has immunoenhancing and antitumour effects
CC   when used as single therapeutic agent in vivo. The present sequence is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 657 BP; 186 A; 166 C; 139 G; 166 T; 0 U; 0 Other;

  Query Match           11.0%;  Score 65;  DB 12;  Length 657;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        544 ATTCG 548
              |||||
Db        610 ATTCG 614


RESULT 77
AAQ97485
ID   AAQ97485 standard; cDNA; 660 BP.
XX
AC   AAQ97485;
XX
DT   25-MAR-2003  (revised)
DT   22-DEC-1995  (first entry)
XX
DE   Human interleukin-12 35 kD subunit.
XX
KW   Interleukin-12; IL-12; cytokine; gamma-interferon; T cell;
KW   natural killer cell; graft vs. host disease; ss.
XX
```

```
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
XX
PN   WO9519786-A1.
XX
PD   27-JUL-1995.
XX
PF   20-JAN-1995;   95WO-US000879.
XX
PR   21-JAN-1994;   94US-00186529.
XX
PA   (GEMY ) GENETICS INST INC.
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Wolf SF,  Sykes M;
XX
DR   WPI; 1995-269273/35.
DR   P-PSDB; AAR79187.
XX
PT   Control of graft versus host disease using interleukin 12 - partic.
PT   admin. at the time of bone marrow transplant.
XX
PS   Disclosure; Page 23-24; 32pp; English.
XX
CC   AAQ97484 and AAQ97485 are from human lymphoblast cell line RMPI 8866. IL-
CC   12 is a heterodimeric cytokine which was originally identified as a
CC   factor which induces gamma-interferon from T cells and natural killer
CC   cells as set forth in PCT/US91/06332, published April 2 1992, and
CC   incorporated by reference. EP 433827, published June 26 1991, disclosed
CC   IL-12 as a cytotoxin lymphocyte maturation factor. In the patent, IL-12
CC   is defined as a heterodimeric glycoprotein comprised of two covalently
CC   linked subunits having mol. wts of about 40 kD and 35 kD. The two
CC   subunits may be disulfide-bonded. IL-12 is administered to prevent or
CC   ameliorate GVHD. Dosage is 1 ng-0.1 mg (esp. 1.0 ng-1 microg)/kg daily
CC   for 3 days, the first dose given 1 hr. after transplant. IL-12 can be
CC   used as the native heterodimer or as subunits. (Updated on 25-MAR-2003 to
CC   correct PN field.)
XX
SQ   Sequence 660 BP; 188 A; 164 C; 139 G; 169 T; 0 U; 0 Other;

  Query Match             11.0%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        544 ATTCG 548
              |||||
Db        610 ATTCG 614


RESULT 78
AAV07274
ID   AAV07274 standard; cDNA; 660 BP.
XX
AC   AAV07274;
XX
DT   25-SEP-1998  (first entry)
XX
DE   Human Interleukin-12 p35 gene.
XX
KW   IL-12 subunit; expression construct; treatment; asthma;
KW   microbial infection; viral infection; cancer; Human; Interleukin; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "IL-12 p35"
FT                   /transl_except= (pos:58. .60,aa:Ser)
XX
PN   WO9817689-A2.
XX
PD   30-APR-1998.
XX
PF   10-OCT-1997;   97WO-US018779.
XX
PR   18-OCT-1996;   96US-0028676P.
XX
PA   (GENE-) GENEMEDICINE INC.
XX
PI   Nordstrom J,  Freimark B,  Deshpande D;
XX
DR   WPI; 1998-261428/23.
DR   P-PSDB; AAV07274.
XX
PT   Constructs for expression of interleukin-12 sub-units - are used for
PT   delivery of IL-12 sub-units for treating e.g. asthma, microbial or viral
PT   infections and certain cancers.
XX
PS   Claim 1; Page 34-35; 80pp; English.
XX
CC   The IL-12 subunits AAV07273 and AAV07274 can be expressed using an
CC   appropriate expression construct engineered into a plasmid. The plasmids
CC   can provide for efficient expression of IL-12 subunits. The products can
CC   be used for the treatment of asthma, microbial and viral infections and
CC   certain cancers
XX
SQ   Sequence 660 BP; 188 A; 167 C; 138 G; 167 T; 0 U; 0 Other;

  Query Match             11.0%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        544 ATTCG 548
              |||||
Db        610 ATTCG 614


RESULT 79
AAV07218
ID   AAV07218 standard; DNA; 660 BP.
XX
AC   AAV07218;
XX
DT   12-AUG-1998  (first entry)
XX
DE   DNA encoding human interleukin-12 35kDa subunit.
XX
KW   Interleukin-12; IL-12; graft-versus-host disease;
KW   GVHD. bone marrow transplantation; graft-versus-leukemia; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "Interleukin-12_35kDa_subunit"
XX
PN   US5756085-A.
XX
PD   26-MAY-1998.
XX
PF   30-APR-1996;   96US-00640386.
XX
PR   21-JAN-1994;   94US-00186529.
```

```
XX
PA   (GEMY ) GENETICS INST INC.
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Sykes M,  Wolf SF;
XX
DR   WPI; 1998-321459/28.
DR   P-PSDB; AAW51222.
XX
PT   Therapy of graft-versus-host disease - by administration of interleukin-
PT   12 to maintain and/or promote graft-versus-leukaemia effects.
XX
PS   Disclosure; Col 23-24; 20pp; English.
XX
CC   The invention relates to a method for the treatment or prevention of
CC   graft-versus-host disease (GVHD) which comprises the administration of
CC   interleukin-12 (IL-12) at the time of bone-marrow transplantation to
CC   maintain or promote graft-versus-leukaemia effects. Preferably, dosage is
CC   0.001-100 (preferably 1-100) mu g/kg for 3 days starting on the day of
CC   the bone marrow transplant. IL-12 is administered daily until there is an
CC   improvement in the condition. Administration is oral, cutaneous,
CC   subcutaneous, intravenous or by inhalation preferably subcutaneous, or
CC   intravenous. The present sequence encodes the human interleukin-12 35kDa
CC   subunit
XX
SQ   Sequence 660 BP; 188 A; 164 C; 139 G; 169 T; 0 U; 0 Other;

  Query Match             11.0%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        544 ATTCG 548
              |||||
Db        610 ATTCG 614


RESULT 80
AAZ40407
ID   AAZ40407 standard; DNA; 660 BP.
XX
AC   AAZ40407;
XX
DT   15-FEB-2000  (first entry)
XX
DE   Human interleukin 12 p35 subunit wild type coding sequence.
XX
KW   Wild type; human; interferon-alpha; plasmid; cytomegalovirus; CMV;
KW   promoter; growth hormone; untranslated region; UTR; mammal; disease;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9947678-A2.
XX
PD   23-SEP-1999.
XX
PF   12-MAR-1999;   99WO-US005394.
XX
PR   19-MAR-1998;   98US-0078654P.
XX
PA   (GENE-) GENEMEDICINE INC.
XX
PI   Nordstrom J,  Pericle F,  Rolland A,  Ralston R;
XX
DR   WPI; 1999-562116/47.
DR   P-PSDB; AAY42488.
XX
PT   New plasmids containing an interferon-alpha coding sequence, used for the
PT   treatment of a mammalian condition or disease, particularly cancer.
XX
PS   Claim 11; Page 38-39; 137pp; English.
XX
CC   This sequence represents the wild type coding region for the human
CC   interleukin 12 p35 subunit. The invention relates to a novel plasmid
CC   comprising a cytomegalovirus (CMV) promoter transcriptionally linked with
CC   an interferon alpha (IFN-alpha) coding sequence, and a growth hormone 3'-
CC   untranslated region (UTR). The plasmids can be used for treating a
CC   mammalian condition or disease, particularly cancer
XX
SQ   Sequence 660 BP; 188 A; 167 C; 138 G; 167 T; 0 U; 0 Other;

  Query Match             11.0%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        544 ATTCG 548
              |||||
Db        610 ATTCG 614


RESULT 81
AAD15217
ID   AAD15217 standard; DNA; 660 BP.
XX
AC   AAD15217;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 encoding DNA from clone R2-555.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p35; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "Modified p35 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .657
FT                   /*tag=  c
FT                   /product= "Mature modified p35 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08610.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 87; Page 140; 223pp; English.
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XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein encoding
CC   DNA
XX
SQ   Sequence 660 BP; 189 A; 173 C; 136 G; 162 T; 0 U; 0 Other;

  Query Match            11.0%;  Score 65;  DB 5;  Length 660;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        141 TGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGA 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 TGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGA 266

Qy        201 ATTAA 205
              |||||
Db        267 ATTAA 271


RESULT 82
AAD15221
ID   AAD15221 standard; DNA; 660 BP.
XX
AC   AAD15221;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Human cytokine p35 DNA.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p35; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "p35 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .657
FT                   /*tag=  c
FT                   /product= "Mature p35 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08614.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 91; Page 142; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is human p35 protein encoding DNA
XX
SQ   Sequence 660 BP; 188 A; 166 C; 139 G; 167 T; 0 U; 0 Other;

  Query Match            11.0%;  Score 65;  DB 5;  Length 660;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        544 ATTCG 548
              |||||
Db        610 ATTCG 614


RESULT 83
AAL44226
ID   AAL44226 standard; DNA; 660 BP.
XX
AC   AAL44226;
XX
DT   08-NOV-2002  (first entry)
XX
DE   Human interleukin 12A (IL-12A) coding sequence.
XX
KW   Human; gene; ds; interleukin 12A; IL-12A; drug screening; AIDS; malaria;
KW   tuberculosis; cancer; haplotyping; genotyping; transgenic animal.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .660
FT                   /*tag=  a
FT                   /product= "Human interleukin 12A (IL-12A)"
FT   variation       replace(142, A)
FT                   /*tag=  b
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   WO200229115-A1.
XX
PD   11-APR-2002.
XX
PF   05-OCT-2001; 2001WO-US031656.
XX
PR   06-OCT-2000; 2000US-0238693P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Armstrong B,  Cappola G,  Choi JY,  Gilson CR,  Kliem SE,  Koshy B;
PI   Parks KE;
XX
DR   WPI; 2002-315865/35.
DR   P-PSDB; AAO15506.
XX
PT   New interleukin 12A (IL-12A) gene polymorphic variants, for studying the
PT   expression and function of IL-12A and screening candidate drugs for
PT   treating AIDS and cancer.
XX
PS   Claim 28; Fig 2; 72pp; English.
XX
CC   The invention comprises the amino acid and coding sequence of the human
```

```
CC   interleukin 12A (IL-12A) protein. Specifically the invention relates to
CC   the identification of polymorphisms within the human (IL-12A) gene
CC   sequence. The polymorphisms identified in the human IL-12A gene sequence
CC   are useful in studying the expression and function of IL-12A, and in
CC   screening drugs for the treatment of disorders such as AIDS, malaria,
CC   tuberculosis and cancer. The IL-12A polymorphisms may be used to
CC   haplotype and genotype the IL-12A gene of an individual. The IL-12A DNA
CC   sequences of the invention can be used to create transgenic animals for
CC   studying expression of the IL-12A isogenes in vivo. The present DNA
CC   sequence represents the coding sequence of the human interleukin 12A (IL-
CC   12A) gene
XX
SQ   Sequence 660 BP; 188 A; 166 C; 139 G; 167 T; 0 U; 0 Other;

  Query Match             11.0%;  Score 65;  DB 6;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        544 ATTCG 548
              |||||
Db        610 ATTCG 614


RESULT 84
ACC47589
ID   ACC47589 standard; DNA; 660 BP.
XX
AC   ACC47589;
XX
DT   12-JUN-2003  (first entry)
XX
DE   Human interleukin 12 (hIL-12) P35 subunit gene.
XX
KW   Human; interleukin 12; hIL-12; baculovirus vector;
KW   recombinant production; AcNPV-hIL12;
KW   Autographa california nuclear polyhedrosis virus; tumour; cancer;
KW   infection; bacterial; viral; cytostatic; P35 subunit; gene; ds.
XX
OS   Homo sapiens.
XX
PN   CN1357622-A.
XX
PD   10-JUL-2002.
XX
PF   02-NOV-2001; 2001CN-00133631.
XX
PR   02-NOV-2001; 2001CN-00133631.
XX
PA   (UYWU-) UNIV WUHAN.
XX
PI   Meng X,  Xu J,  Yu Z;
XX
DR   WPI; 2002-741792/81.
XX
PT   Human interleukin-12 recombinant insect virus strain and its preparation.
XX
PS   Claim 4; Fig 6; 17pp; Chinese.
XX
CC   The invention relates to a recombinant baculovirus comprising DNA
CC   encoding human interleukin 12 (hIL-12) and methods for its preparation.
CC   The recombinant baculovirus strain is designated Autographa california
CC   nuclear polyhedrosis virus AcNPV-hIL12 (CCTCC No. 2 V200108). This strain
CC   contains two human IL-12 subunit genes, the IL-12 P35 subunit gene
CC   (ACC47589) and the IL-12 P40 subunit gene (ACC47592) which are
CC   respectively under the control of the viral polyhedrin and P10 promoters.
CC   The baculovirus can be used in the recombinant production of human IL-12
CC   which is suitable for treating tumours and bacterial, viral and other
CC   infections. The present sequence represents the human IL-12 P35 subunit
CC   gene used in construction of the baculovirus vector of the invention
XX
SQ   Sequence 660 BP; 188 A; 166 C; 139 G; 167 T; 0 U; 0 Other;

  Query Match             11.0%;  Score 65;  DB 6;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        544 ATTCG 548
              |||||
Db        610 ATTCG 614


RESULT 85
ADF77244
ID   ADF77244 standard; DNA; 660 BP.
XX
AC   ADF77244;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human IL-12 p35 subunit DNA.
XX
KW   ds; human; interferon alpha expression plasmid; tumour; IL-12.
XX
OS   Homo sapiens.
XX
PN   US2003181405-A1.
XX
PD   25-SEP-2003.
XX
PF   29-APR-2002; 2002US-00136837.
XX
PR   12-MAR-1999;   99US-00268135.
XX
PA   (NORD/) NORDSTROM J L.
PA   (PERI/) PERICLE F.
PA   (ROLL/) ROLLAND A.
PA   (RALS/) RALSTON R O.
XX
PI   Nordstrom JL,  Pericle F,  Rolland A,  Ralston RO;
XX
DR   WPI; 2004-020834/02.
XX
PT   A mammalian interferon alpha expression plasmid is useful in gene therapy
PT   to deliver interferon alpha to cells to modulate tumor activity in the
PT   treatment of cancer.
XX
PS   Disclosure; SEQ ID NO 6; 65pp; English.
XX
CC   The invention relates to a mammalian interferon alpha expression plasmid,
CC   comprising a promoter and a synthetic 5' intron transcriptionally linked
CC   with an interferon alpha coding sequence and a 3' untranslated region.
CC   The mammalian interferon alpha expression plasmid is useful for treating
CC   tumour growth. The present sequence is used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 660 BP; 188 A; 167 C; 138 G; 167 T; 0 U; 0 Other;

  Query Match             11.0%;  Score 65;  DB 12;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        544 ATTCG 548
              |||||
Db        610 ATTCG 614
```

```
RESULT 86
ADP88401
ID   ADP88401 standard; cDNA; 702 BP.
XX
AC   ADP88401;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human interleukin-12 alpha chain coding sequence.
XX
KW   antiinflammatory; antiasthmatic; antiallergic; immunosuppressive;
KW   antibacterial; protozoacide; gene therapy; expression vector;
KW   interleukin; ecdysone-inducible promoter; ss; gene; interleukin-12;
KW   human.
XX
OS   Homo sapiens.
XX
PN   WO2004052929-A2.
XX
PD   24-JUN-2004.
XX
PF   08-DEC-2003; 2003WO-IB006404.
XX
PR   06-DEC-2002; 2002GB-00028465.
XX
PA   (UYBE-) UNIV QUEENS BELFAST.
XX
PI   Vandenbroeck K,  Alloza I;
XX
DR   WPI; 2004-487887/46.
XX
PT   New expression vector comprising DNA encoding a subunit of a dimeric form
PT   of interleukin under transcriptional control of an ecdysone-inducible
PT   promoter, useful in preparing a composition for treating e.g.,
PT   inflammatory disease.
XX
PS   Disclosure; Page 85-86; 87pp; English.
XX
CC   The present invention relates to an expression vector comprising DNA
CC   encoding a subunit of a dimeric form of interleukin under transcriptional
CC   control of an ecdysone-inducible promoter. The expression vector is
CC   useful in preparing a composition for treating a disease having a
CC   pathogenesis which includes endogenous production of cytokine IL-12, IL-
CC   23 or IL-27, e.g., infectious diseases, bacterial, protozoal or virus-
CC   induced inflammation, epithelial airway inflammation such as asthma,
CC   allergic disease, or autoimmune disease such as multiple sclerosis or
CC   inflammatory bowel disease. The present sequence is the coding sequence
CC   of the human interleukin-12 alpha chain used in the exemplification of
CC   the invention.
XX
SQ   Sequence 702 BP; 199 A; 184 C; 147 G; 172 T; 0 U; 0 Other;

  Query Match            11.0%;  Score 65;  DB 12;  Length 702;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 624

Qy        544 ATTCG 548
              |||||
Db        625 ATTCG 629


RESULT 87
AAQ67880
ID   AAQ67880 standard; DNA; 721 BP.
XX
AC   AAQ67880;
XX
DT   25-MAR-2003  (revised)
DT   23-MAR-1995  (first entry)
XX
DE   EPV 42 kD promoter/Human IL-12 p35 subunit expression cassette.
XX
KW   Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant;
KW   murine; interleukin-2; IL-2; pRW825; pmut-1; pBS-SK; pMM151; TK vector;
KW   plasmid; vaccinia; H6 promoter; amplify; primer; antigenic response;
KW   polymerase chain reaction; poxvirus; pSD542; immunological response;
KW   pathogen; human; interferon; IFN; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   promoter        1. .61
FT                   /*tag=  a
FT                   /note= "Vaccinia E3L promoter"
FT   CDS             32. .1018
FT                   /*tag=  b
FT                   /product= "Human IL-12 p35"
XX
PN   WO9416716-A1.
XX
PD   04-AUG-1994.
XX
PF   21-JAN-1994;   94WO-US000888.
XX
PR   21-JAN-1993;   93US-00007115.
PR   19-JAN-1994;   94US-00184009.
XX
PA   (VIRO-) VIROGENETICS CORP.
XX
PI   Paoletti E,  Tartaglia J,  Cox WI;
XX
DR   WPI; 1994-263767/32.
XX
PT   Attenuated recombinant virus used for cancer therapy - comprises DNA
PT   encoding cytokine and/or tumour associated antigen.
XX
PS   Example 27; Fig 34; 232pp; English.
XX
CC   The sequences given in AAQ67879-80 are expression cassettes which contain
CC   the p40 and p35 subunits of human interleukin-12 (IL-12) under the
CC   control of the entomopox virus (EPV) promoter and the vaccinia E3L
CC   promoter, respectively. These sequences were used in the construction of
CC   an ALVAC-based recombinant virus containing the genes for the two
CC   subunits of human IL-12. The p40 subunit was amplified using primers
CC   JP202 and JP189 and placed under the control of the entomopox virus (EPV)
CC   42 kD promoter in plasmid PBSHIL12p40II. The p35 subunit was amplified
CC   using primers JP186 and JP201 and placed under the control of the
CC   vaccinia E3L promoter using primers JP218 and JP220. The expression
CC   cassette was isolated and ligated with pBSSK+ generating plasmid
CC   PBSHIL12p35II. The p35 and p40 expression cassettes were excised and
CC   assembled in pBSSK+ to give PBSHIL12 in which the two expression
CC   cassettes are orientated head-to-head relative to each other. The
CC   combination casette containing the poxvirus promoted genes for both IL-12
CC   subunits was excised from PBSHIL12 and cloned in to ALVAC C6 vector
CC   plasmid pC6L to give pC6HIL12. Recombination between this donor plasmid
CC   and ALVAC rescuing virus produced recombinant virus ALVAC+IL12, which
CC   contains both the human IL-12 genes in the C6 locus. The resulting virus
CC   may be used in a composition for inducing an antigenic or immunological
CC   response, ie. for immunisation against pathogens. (Updated on 25-MAR-2003
CC   to correct PN field.)
XX
SQ   Sequence 721 BP; 209 A; 171 C; 151 G; 190 T; 0 U; 0 Other;

  Query Match            11.0%;  Score 65;  DB 2;  Length 721;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670
```

```
Qy        544 ATTCG 548
              |||||
Db        671 ATTCG 675


RESULT 88
AAZ08515
ID   AAZ08515 standard; DNA; 721 BP.
XX
AC   AAZ08515;
XX
DT   19-OCT-1999  (first entry)
XX
DE   Vaccinia E3L/human IL-12 P35 expression cassette.
XX
KW   Attenuated recombinant virus; cytokine; tumour associated antigen;
KW   NYVAC recombinant virus; ALVAC recombinant virus; gene therapy; rabies;
KW   cancer; tumour necrosis factor; nuclear phosphoprotein; p53; IL-2; GMCSF;
KW   interleukin; interferon; IFN-gamma; IL-4; melanoma associated antigen;
KW   carcinoembryonic antigen; immunisation; antigenic; poxvirus; influenza;
KW   immunological response; immunotherapy; vaccine; Newcastle Disease; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
OS   Vaccinia virus.
XX
PN   US5942235-A.
XX
PD   24-AUG-1999.
XX
PF   02-JUN-1995;   95US-00458356.
XX
PR   24-DEC-1981;   81US-00334456.
PR   08-DEC-1982;   82US-00446824.
PR   19-JUN-1984;   84US-00622135.
PR   27-AUG-1987;   87US-00090209.
PR   28-AUG-1987;   87US-00090711.
PR   20-OCT-1987;   87US-00110335.
PR   25-APR-1988;   88US-00186054.
PR   23-AUG-1988;   88US-00234390.
PR   14-JUN-1990;   90US-00537882.
PR   14-JUN-1990;   90US-00537890.
PR   16-DEC-1991;   91US-00805567.
PR   03-MAR-1992;   92US-00847977.
PR   06-MAR-1992;   92US-00847951.
PR   04-MAY-1992;   92US-00881995.
PR   22-JUL-1992;   92US-00918278.
PR   20-JAN-1993;   93US-00007115.
PR   19-JAN-1994;   94US-00184009.
PR   14-APR-1994;   94US-00228926.
PR   13-SEP-1994;   94US-00306259.
XX
PA   (HEAL-) HEALTH RES INC.
XX
PI   Paoletti E;
XX
DR   WPI; 1999-493494/41.
XX
PT   Recombinant poxviruses comprising exogenous DNA encoding antigenic
PT   determinants useful in immunotherapy to immunize against cancers and
PT   other diseases such as influenza, Newcastle Disease and rabies.
XX
PS   Example 27; Fig 34; 163pp; English.
XX
CC   The present invention describes a recombinant poxvirus (I), comprising
CC   exogenous DNA encoding an antigenic determinant of a pathogen which is
CC   then expressed in vivo in infected host cells after administration to a
CC   patient and therefore induces an immunological response. (I) may be used
CC   to vaccinate patients against a wide range of diseases and disorders
CC   depending on the type of antigen encoded by the exogenous DNA. (I) may be
CC   used to vaccinate against diseases such as rabies, influenza and
CC   Newcastle Disease. It is particularly useful for immunising against
CC   cancers. The poxvirus (I) also provides a means of manipulating
CC   lymphocytes and tumour cells for use in cell-based immunotherapeutic
CC   modalities for cancer. (I) also have enhanced safety compared to
CC   unattenuated viruses (attenuation reduces the virulence of the viruses)
CC   and known recombinant poxvirus vaccines. This increased level of safety
CC   reduces the possibility of a 'runaway' infection in the host and reduces
CC   the chance of transmission from vaccinated to unvaccinated individuals
CC   and contamination of the environment. The present sequence represents a
CC   Vaccinia E3L/human IL-12 P35 expression cassette used in the
CC   exemplification of the present invention
XX
SQ   Sequence 721 BP; 209 A; 171 C; 151 G; 190 T; 0 U; 0 Other;

  Query Match             11.0%;  Score 65;  DB 2;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy        544 ATTCG 548
              |||||
Db        671 ATTCG 675


RESULT 89
ADR21891
ID   ADR21891 standard; DNA; 721 BP.
XX
AC   ADR21891;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Vaccinia E3L/human IL-12 expression cassette.
XX
KW   Cytostatic; Vaccine; recombinant poxvirus; nonessential region;
KW   attenuated avipox Virus; carcinoembryonic antigen; B7 protein;
KW   cancer therapy; ds; human; IL-12; interleukin-12; E3L;
KW   expression cassette.
XX
OS   Vaccinia virus.
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US6780407-B1.
XX
PD   24-AUG-2004.
XX
PF   15-SEP-2000; 2000US-00663667.
XX
PR   08-MAR-1989;   89US-00320471.
PR   14-FEB-1990;   90US-00478179.
PR   07-JAN-1991;   91US-00638080.
PR   07-MAR-1991;   91US-00666056.
PR   11-JUN-1991;   91US-00713967.
PR   16-DEC-1991;   91US-00805567.
PR   03-MAR-1992;   92US-00847977.
PR   06-MAR-1992;   92US-00847951.
PR   21-JAN-1993;   93US-00007115.
PR   19-JAN-1994;   94US-00184009.
PR   30-AUG-1995;   95US-00521016.
XX
PA   (AVET ) AVENTIS PASTEUR.
XX
PI   Paoletti E,  Tartaglia J,  Cox WI;
XX
DR   WPI; 2004-601998/58.
XX
PT   New recombinant poxvirus which is an attenuated avipox Virus that
PT   expresses an exogenous DNA encoding carcinoembryonic antigen and an
PT   exogenous DNA encoding B7 protein, useful for cancer therapy.
XX
```

```
PS   Example 27; SEQ ID NO 199; 181pp; English.
XX
CC   The invention describes a recombinant poxvirus containing exogenous DNA
CC   in a nonessential region of the poxvirus, where the poxvirus is an
CC   attenuated avipox Virus that expresses an exogenous DNA encoding
CC   carcinoembryonic antigen and an exogenous DNA encoding B7 protein. Also
CC   described are: a composition comprising a poxvirus above in admixture
CC   with a carrier; and expressing carcinoembryonic antigen and B7 protein in
CC   vivo comprising administering to a mammal the composition above.
CC   Disclosed are: making recombinant poxvirus defined above; recombinant
CC   poxvirus vaccine having an increased level of safety compared to known
CC   recombinant poxvirus vaccines; and a modified vector for expressing a
CC   gene product in a host. The recombinant poxvirus is useful for providing
CC   a recombinant poxvirus vaccine having an increased level of safety
CC   compared to known recombinant poxvirus vaccines. The recombinant poxvirus
CC   is useful for cancer therapy. This sequence represents a human IL-12
CC   expression cassette used in the creation of NYVAC rescue virus and
CC   canarypox virus vector ALVAC comprising the human IL-12 gene.
XX
SQ   Sequence 721 BP; 209 A; 171 C; 151 G; 190 T; 0 U; 0 Other;

  Query Match             11.0%;  Score 65;  DB 13;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy        544 ATTCG 548
              |||||
Db        671 ATTCG 675


RESULT 90
ADK98708
ID   ADK98708 standard; DNA; 761 BP.
XX
AC   ADK98708;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human interleukin-12 (IL-12) P35 subunit DNA seqid 3.
XX
KW   human; recombinant interleukin-12; IL-12; P35 subunit; P40 subunit; ds.
XX
OS   Homo sapiens.
XX
PN   CN1408727-A.
XX
PD   09-APR-2003.
XX
PF   29-SEP-2001; 2001CN-00126923.
XX
PR   29-SEP-2001; 2001CN-00126923.
XX
PA   (ZHON-) ZHONGXIN GUOJIAN PHARM CO LTD SHANGHAI.
XX
PI   Wan G,  Li C;
XX
DR   WPI; 2003-664076/63.
XX
PT   Method for efficiently expressing recombinant human interleukin 12 in
PT   eukaryotic cell.
XX
PS   Claim 6; SEQ ID NO 3; 14pp; Chinese.
XX
CC   The invention describes the process of producing human recombinant
CC   interleukin-12 (IL-12) includes: providing a nucleotide sequence
CC   corresponding to the P35 subunit with the first signal peptide and a
CC   nucleotide sequence corresponding to the P40 subunit; inserting the
CC   nucleotide sequences into an expression vector; converting the eukaryotic
CC   cell with the expression vector; and culturing the transfected eukaryotic
CC   cell in condition suitable for recombinant human IL-12 expression. The
CC   process balances the expression amount of both P35 and P40 subunits and
CC   thus raises the expression amount of IL-12 with bioactivity via raising
CC   the expression strength of P35 subunit. This sequence represents the
CC   human interleukin-12 (IL-12) P35 subunit polynucleotide.
XX
SQ   Sequence 761 BP; 205 A; 204 C; 164 G; 187 T; 0 U; 1 Other;

  Query Match             11.0%;  Score 65;  DB 10;  Length 761;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        651 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 710

Qy        544 ATTCG 548
              |||||
Db        711 ATTCG 715


RESULT 91
ADK98706
ID   ADK98706 standard; DNA; 761 BP.
XX
AC   ADK98706;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human interleukin-12 (IL-12) P35 subunit DNA seqid 1.
XX
KW   human; recombinant interleukin-12; IL-12; P35 subunit; P40 subunit; ds.
XX
OS   Homo sapiens.
XX
PN   CN1408727-A.
XX
PD   09-APR-2003.
XX
PF   29-SEP-2001; 2001CN-00126923.
XX
PR   29-SEP-2001; 2001CN-00126923.
XX
PA   (ZHON-) ZHONGXIN GUOJIAN PHARM CO LTD SHANGHAI.
XX
PI   Wan G,  Li C;
XX
DR   WPI; 2003-664076/63.
XX
PT   Method for efficiently expressing recombinant human interleukin 12 in
PT   eukaryotic cell.
XX
PS   Claim 4; SEQ ID NO 1; 14pp; Chinese.
XX
CC   The invention describes the process of producing human recombinant
CC   interleukin-12 (IL-12) includes: providing a nucleotide sequence
CC   corresponding to the P35 subunit with the first signal peptide and a
CC   nucleotide sequence corresponding to the P40 subunit; inserting the
CC   nucleotide sequences into an expression vector; converting the eukaryotic
CC   cell with the expression vector; and culturing the transfected eukaryotic
CC   cell in condition suitable for recombinant human IL-12 expression. The
CC   process balances the expression amount of both P35 and P40 subunits and
CC   thus raises the expression amount of IL-12 with bioactivity via raising
CC   the expression strength of P35 subunit. This sequence represents the
CC   human interleukin-12 (IL-12) P35 subunit polynucleotide.
XX
SQ   Sequence 761 BP; 199 A; 209 C; 167 G; 185 T; 0 U; 1 Other;

  Query Match             11.0%;  Score 65;  DB 10;  Length 761;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        651 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 710

Qy        544 ATTCG 548
                |||||
Db        711 ATTCG 715


RESULT 92
AAV83207
ID   AAV83207 standard; cDNA; 762 BP.
XX
AC   AAV83207;
XX
DT   02-MAR-1999  (first entry)
XX
DE   Interleukin (IL)-12A cDNA.
XX
KW   Mouse; immunodeficient; pathogen; tumour; lymphocyte; antigen;
KW   immunomodulator; vector; vaccine; cancer; HIV; Leishmania; Mycobacterium;
KW   Listeria; Plasmodium; retrovirus; evaluation;
KW   human immunodeficiency virus; ds.
XX
OS   Homo sapiens.
XX
PN   WO9844788-A2.
XX
PD   15-OCT-1998.
XX
PF   09-APR-1998;   98WO-US006944.
XX
PR   09-APR-1997;   97US-00838702.
PR   01-MAY-1997;   97US-00848760.
PR   09-DEC-1997;   97US-0069163P.
XX
PA   (CHAN/) CHANG L.
XX
PI   Chang L;
XX
DR   WPI; 1999-024005/02.
XX
PT   Use of immunodeficient mice comprising human cells - particularly
PT   SCTD/beige mice comprising human immune cells for evaluating vaccines
PT   against cancers or human pathogens, e.g. HIV.
XX
PS   Example 10(c)(i); Page 108-109; 154pp; English.
XX
CC   Immunodeficient mice comprising human cells can be used for exposure to
CC   human pathogens and/or their components or human tumour cells and human
CC   peripheral blood lymphocytes. Also claimed is a vaccine comprising a cell
CC   modified to express an antigen and an immune-modulating protein, this is
CC   preferably an expression vector comprising a polynucleotide sequence that
CC   encodes the antigen and immune-modulating protein. Such vectors can be
CC   used to treat a subject having a tumour by transferring the expression
CC   vector into the tumour so that the antigen and the immune-modulator are
CC   expressed by at least the tumour. The methods can be used for producing
CC   and evaluating vaccines including cancer vaccines and vaccines directed
CC   against human pathogens, e.g. HIV, Leishmania, Mycobacterium, Listeria or
CC   Plasmodium. Two primers (AAV83197, AAV83198) were used to amplify the IL-
CC   12B for insertion into expression vectors of the invention
XX
SQ   Sequence 762 BP; 199 A; 211 C; 166 G; 186 T; 0 U; 0 Other;

  Query Match            11.0%;  Score 65;  DB 2;  Length 762;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        544 ATTCG 548
                |||||
Db        712 ATTCG 716


RESULT 93
AAA35201
ID   AAA35201 standard; DNA; 762 BP.
XX
AC   AAA35201;
XX
DT   28-JUL-2000  (first entry)
XX
DE   Human adenosine receptor related polynucleotide 2nd SEQ ID NO:75.
XX
KW   Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW   phosphorothioate; impaired respiration; inflammation; allergy;
KW   allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW   antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW   lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW   respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW   pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW   cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200009525-A2.
XX
PD   24-FEB-2000.
XX
PF   03-AUG-1999;   99WO-US017712.
XX
PR   03-AUG-1998;   98US-0095212P.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-205971/18.
XX
PT   New antisense oligonucleotides useful for treating e.g. pulmonary
PT   vasoconstruction, inflammation, allergies, asthma, hypertension,
PT   bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT   cancers.
XX
PS   Disclosure; Page 1242; 1343pp; English.
XX
CC   The present invention describes a new composition comprising an antisense
CC   oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC   nucleic acids involved in bronchoconstriction, allergies, and/or
CC   inflammation. The ON can have antiinflammatory, antiallergic,
CC   antiasthmatic, cytostatic and analgesic activities. The compositions are
CC   useful for the treatment of diseases associated with inflammation,
CC   impaired airways, including lung disease and diseases whose secondary
CC   effects afflict the lungs of a subject. They can be used for treating
CC   e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC   impeded respiration, respiratory distress syndrome, pain, cystic
CC   fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC   carcinomas, and cancers which may metastasise to the lungs, including
CC   breast and prostate cancer. The reduction of the adenosine content of the
CC   ONs reduces side effects. The A-containing ONs break down with the
CC   release of deoxyadenosine which activates adenosine receptors causing
CC   bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC   nucleotide sequences given in the sequence listing from the present
CC   invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC   sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC   from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC   AAA33992) are specifically claimed ONs from the present invention. N.B.
CC   Sequences given in the disclosure of the present invention do not match
CC   up with their corresponding SEQ ID NO: sequences given in the sequence
CC   listing
XX
SQ   Sequence 762 BP; 199 A; 210 C; 167 G; 186 T; 0 U; 0 Other;
```

```
  Query Match             11.0%;  Score 65;  DB 3;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        544 ATTCG 548
              |||||
Db        712 ATTCG 716


RESULT 94
AAF21323
ID   AAF21323 standard; DNA; 762 BP.
XX
AC   AAF21323;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human low adenosine antisense oligonucleotide related sequence #2890.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW   chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200062736-A2.
XX
PD   26-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US008020.
XX
PR   06-APR-1999;   99US-0127958P.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
PA   (NYCE/) NYCE J W.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-679539/66.
XX
PT   Low adenosine (A) content antisense oligonucleotides which do not trigger
PT   adenosine receptors during metabolism, useful e.g. for treating cancers
PT   and respiratory obstructions.
XX
PS   Disclosure; Page 1326; 1592pp; English.
XX
CC   The present invention describes low adenosine (A) content antisense
CC   oligonucleotides and compositions (I) comprising them. In the antisense
CC   oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC   (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC   immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC   The antisense oligonucleotides and (I) can be used to down-regulate the
CC   expression and or activity of target polypeptides associated with
CC   lung/respiratory disorders and malignancies, such as stimulating and
CC   activating peptide factors and transmitters, transcription factors,
CC   immunoglobulins and antibodies, antibody receptors, cytokines and
CC   chemokines, endogenously produced specific and non-specific enzymes,
CC   binding proteins, adhesion molecules and their receptors, cytokine and
CC   chemokine receptors, adenosine receptors, bradykinin receptors, central
CC   nervous system (CNS) and peripheral nervous and non-nervous system
CC   receptors, CNS and peripheral nervous and non-nervous system peptide
CC   transmitters, defensins, growth factors, vasoactive peptides and
CC   receptors, binding proteins and malignancy associated proteins. The
CC   antisense oligonucleotides may be used in this way to treat disorders
CC   including respiratory obstruction (especially pulmonary obstruction
CC   and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC   surfactant hypoproduction which are associated with a disease or
CC   condition selected from pulmonary vasoconstriction, inflammation,
CC   allergies, asthma, impeded respiration, respiratory distress syndrome
CC   (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC   hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC   pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC   and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC   fragments and antisense oligonucleotides used in the exemplification of
CC   the present invention
XX
SQ   Sequence 762 BP; 199 A; 210 C; 167 G; 186 T; 0 U; 0 Other;

  Query Match             11.0%;  Score 65;  DB 3;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        544 ATTCG 548
              |||||
Db        712 ATTCG 716


RESULT 95
ABZ97017
ID   ABZ97017 standard; DNA; 762 BP.
XX
AC   ABZ97017;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human nucleic acid sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 12259; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
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CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 762 BP; 199 A; 210 C; 167 G; 186 T; 0 U; 0 Other;

  Query Match             11.0%;  Score 65;  DB 10;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        544 ATTCG 548
              |||||
Db        712 ATTCG 716


RESULT 96
ABD20866
ID   ABD20866 standard; DNA; 762 BP.
XX
AC   ABD20866;
XX
DT   29-JUL-2004  (first entry)
XX
DE   Human pulmonary and inflammatory target DNA #477.
XX
KW   Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW   respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW   surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW   analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW   beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW   respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW   emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW   pulmonary transplantation rejection; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285309-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013143.
XX
PR   24-APR-2001; 2001US-0286036P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-093058/08.
XX
PT   Pharmaceutical composition for treating asthma, has antisense
PT   oligonucleotide containing less percentage of adenosine, targeted to
PT   nucleic acids associated with lung airway or lung dysfunction, and
PT   bronchodilating agent.
XX
PS   Claim 15; SEQ ID NO 12259; 763pp; English.
XX
CC   This invention describes a novel composition (a) a first active agent,
CC   comprising oligonucleotides, effective for alleviating
CC   bronchoconstriction, respiratory tract inflammation, allergies and
CC   reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC   surfactant depletion or hyposecretion, when administered to a mammal. The
CC   oligonucleotides are derived from a gene encoding or regulating
CC   expression of a target polypeptide associated with lung airway or lung
CC   dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC   The invention also describes a kit, that comprises: (a) a delivery
CC   device, in separate containers, (b) the oligonucleotides, (c)
CC   instructions for adding a carrier and for use of the kit. The composition
CC   of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC   analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC   beta-adrenergic agonist. The composition is useful for preventing or
CC   treating a respiratory, lung or malignant disease. The administered
CC   composition comprises oligo and is administered to reduce the production
CC   or availability, or to increase the degradation of the target mRNA or to
CC   reduce the amount of target polypeptide present in the lungs. The
CC   pulmonary obstruction, and/or bronchoconstriction and/or lung
CC   inflammation, allergies and/or surfactant hypoproduction are associated
CC   with a disease or condition such as pulmonary vasoconstriction,
CC   inflammation, allergies, asthma, impeded respiration, respiratory
CC   distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC   hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC   transplantation rejection, pulmonary infections, bronchitis or cancer.
CC   The reduced adenosine content of the anti-sense oligos corresponding to
CC   thymidines present in the target RNA serves to prevent the breakdown of
CC   the oligonucleotides into products that free adenosine into the system
CC   e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC   prevent any unwanted effects due to it
XX
SQ   Sequence 762 BP; 199 A; 210 C; 167 G; 186 T; 0 U; 0 Other;

  Query Match             11.0%;  Score 65;  DB 11;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        544 ATTCG 548
              |||||
Db        712 ATTCG 716


RESULT 97
ADO07654
ID   ADO07654 standard; DNA; 762 BP.
XX
AC   ADO07654;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Human interleukin-12 35kDa coding sequence.
XX
KW   cytostatic; virucide; anti-HIV; hepatotropic; neuroprotective;
KW   immunostimulant; expression cassette; viral vector; interleukin-12;
KW   co-stimulatory protein; cancer; infection; ds; gene; human.
XX
OS   Homo sapiens.
XX
PN   WO2004035799-A2.
XX
PD   29-APR-2004.
XX
PF   10-OCT-2003; 2003WO-EP011252.
XX
PR   11-OCT-2002; 2002DE-01048141.
XX
```

PA (UYHA-) UNIV HAMBURG-EPPENDORF KLINIKUM.
XX
PI Waehler R, Schnieders F;
XX
DR WPI; 2004-357221/33.
XX
PT Viral vector that expresses single-chain interleukin-12 and costimulator,
PT useful for treatment of tumors, viral infections, e.g. human
PT immunodeficiency virus, and prion diseases.
XX
PS Claim 4; Fig 20; 129pp; German.
XX
CC The present invention relates to a viral vector that includes a nucleic
CC acid encoding a single-chain interleukin-12 (IL-12) and a co-stimulatory
CC protein. Viral vectors and virus particles derived from them are useful
CC for treatment of tumours, infectious diseases (e.g. HIV, hepatitis A, B
CC or C, cytomegalovirus or human papilloma virus), or prion diseases. The
CC present sequence is a human interleukin-12 coding sequence used in the
CC exemplification of the invention.
XX
SQ Sequence 762 BP; 199 A; 210 C; 167 G; 186 T; 0 U; 0 Other;

Query Match 11.0%; Score 65; DB 12; Length 762;
Best Local Similarity 100.0%; Pred. No. 2.2e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy 544 ATTCG 548
|||||
Db 712 ATTCG 716

RESULT 98
ADS88021
ID ADS88021 standard; DNA; 762 BP.
XX
AC ADS88021;
XX
DT 18-NOV-2004 (first entry)
XX
DE Tumour treatment-related human gene sequence SeqID57.
XX
KW tumour inhibition; tumour treatment; metastasis; infectious lesion;
KW antigen presenting cell; immunostimulatory cytokine; cytostatic;
KW vulnerary; immunomodulator; melanoma; hepatoma; adenocarcinoma;
KW colorectal cancer; basal cell cancer; oral cancer; nasopharyngeal cancer;
KW laryngeal cancer; bladder cancer; head cancer; neck cancer;
KW renal cell cancer; pancreatic cancer; pulmonary cancer; cervical cancer;
KW ovarian cancer; oesophageal cancer; gastric cancer; prostrate cancer;
KW testicular cancer; breast cancer; gene; ds; human.
XX
OS Homo sapiens.
XX
PN WO2004034995-A2.
XX
PD 29-APR-2004.
XX
PF 15-OCT-2003; 2003WO-US032827.
XX
PR 15-OCT-2002; 2002US-0418865P.
XX
PA (UYPI-) UNIV PITTSBURGH.
XX
PI Lotze MT, Tahara H;
XX
DR WPI; 2004-365083/34.
DR P-PSDB; ADS88022.
XX
PT Inhibiting or treating a tumor, metastasis or infectious lesion comprises
PT administering into or near site of a tumor or infectious lesion an
PT antigen presenting cell and an immunostimulatory cytokine or a nucleic
PT acid encoding the cytokine.
XX
PS Disclosure; SEQ ID NO 57; 169pp; English.
XX
CC This invention relates to a novel method of inhibiting or treating a
CC tumour, metastasis or infectious lesion in a subject which comprises
CC administering into or near a site of a tumour or infectious lesion in a
CC subject an antigen presenting cell and an immunostimulatory cytokine or a
CC nucleic acid encoding the cytokine. The invention may be useful for the
CC production of compounds with a cytostatic or vulnerary activity acting as
CC immunomodulators. The method is useful in inhibiting or treating a
CC tumour, metastasis or infectious lesion in a subject, where the size of
CC the tumour, metastasis (where number is also decreased) or infectious
CC lesion is decreased. The tumour is selected from melanoma, hepatoma,
CC adenocarcinoma, colorectal cancer, basal cell cancer, oral cancer,
CC nasopharyngeal cancer, laryngeal cancer, bladder cancer, head and neck
CC cancer, renal cell cancer, pancreatic cancer, pulmonary cancer, cervical
CC cancer, ovarian cancer, oesophageal cancer, gastric cancer, prostrate
CC cancer, testicular cancer and breast cancer. The present sequence is that
CC of a gene which is related to the invention.
XX
SQ Sequence 762 BP; 199 A; 210 C; 167 G; 186 T; 0 U; 0 Other;

Query Match 11.0%; Score 65; DB 13; Length 762;
Best Local Similarity 100.0%; Pred. No. 2.2e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy 544 ATTCG 548
|||||
Db 712 ATTCG 716

RESULT 99
ADV42511
ID ADV42511 standard; cDNA; 762 BP.
XX
AC ADV42511;
XX
DT 10-MAR-2005 (first entry)
XX
DE Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 139.
XX
KW microarray; psychoneuroendocrinimmune; chronic fatigue;
KW non-insulin dependent diabetes; allergy; immune disorder; inflammation;
KW cancer; neoplasm; infection; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO2004108899-A2.
XX
PD 16-DEC-2004.
XX
PF 04-JUN-2004; 2004WO-US017686.
XX
PR 04-JUN-2003; 2003US-0475915P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Nicholson A, Vernon SD;
XX
DR WPI; 2005-031682/03.
XX
PT New microarray comprising probes for genes involved in
PT psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a
PT condition associated with PNI activity, e.g., inflammatory or infectious
PT diseases.
XX
PS Claim 1; SEQ ID NO 139; 254pp; English.

```
XX
CC   The invention relates to a new microarray which comprises probes for
CC   genes involved in psychoneuroendocrinimmune (PNI) activity. The
CC   microarray is useful in diagnosing a condition associated with PNI
CC   activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
CC   cancer and infection. The present sequence represents a
CC   psychoneuroendocrinimmune gene expressed sequence tag. Note the
CC   specificatio mentions SEQ ID NO of up to 3314 but only sequences up to
CC   SEQ ID NO 1829 are provided.
XX
SQ   Sequence 762 BP; 199 A; 210 C; 167 G; 186 T; 0 U; 0 Other;

  Query Match            11.0%;  Score 65;  DB 14;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        544 ATTCG 548
              |||||
Db        712 ATTCG 716


RESULT 100
ACD26420
ID   ACD26420 standard; cDNA; 823 BP.
XX
AC   ACD26420;
XX
DT   15-SEP-2003  (first entry)
XX
DE   cDNA encoding interleukin-12 (IL-12) P35 subunit.
XX
KW   Interleukin-12; IL-12; P35 subunit; tumour; virus infection;
KW   fungal infection; parasite infection; gene; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   CDS             60. .821
FT                   /*tag=  a
FT                   /product= "Interleukin-12 P35 subunit"
XX
PN   CN1373221-A.
XX
PD   09-OCT-2002.
XX
PF   04-FEB-2002; 2002CN-00100866.
XX
PR   04-FEB-2002; 2002CN-00100866.
XX
PA   (VIRO-) INST VIROLOGY CHINESE ACAD PREVENTIVE ME.
XX
PI   Jiao H,  Zhan M;
XX
DR   WPI; 2003-141476/14.
DR   P-PSDB; ABU62768.
XX
PT   Recombinant Chinese interleukin-12 with bio-activity and its preparation
PT   process.
XX
PS   Claim 1; Page 1-2; 20pp; Chinese.
XX
CC   The invention describes a recombinant Chinese interleukin (IL)-12 with
CC   bioactivity for resisting tumour, virus, fungus and parasites. This
CC   sequence encodes the interleukin-12 (IL-12) P35 subunit
XX
SQ   Sequence 823 BP; 222 A; 225 C; 183 G; 193 T; 0 U; 0 Other;

  Query Match            11.0%;  Score 65;  DB 10;  Length 823;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        711 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 770

Qy        544 ATTCG 548
              |||||
Db        771 ATTCG 775


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Job time : 459.52 secs
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 48236798 seqs, 27959665780 residues

Word size : 1

Total number of hits satisfying chosen parameters: 96473154

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 200 summaries

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1: gb_est1:*
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3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	65	9.8	762	14	DQ033872	DQ033872 Homo sapi
	2	65	9.8	863	4	CD013916	CD013916 90138296
	3	65	9.8	935	4	CD013914	CD013914 90138124
	4	65	9.8	1136	4	CD013915	CD013915 90138132
	5	65	9.8	1938	6	BC035571	BC035571 Homo sapi
	6	57	8.6	762	14	DQ033873	DQ033873 Pan trogl
	7	56	8.4	581	3	BP260963	BP260963 BP260963
	8	56	8.4	832	2	BI523569	BI523569 603175938
	9	48	7.2	592	12	CE159257	CE159257 tigr-gss-
	10	47	7.1	812	2	BG702253	BG702253 602683459
	11	41	6.2	342	2	BM257856	BM257856 521721 MA
	12	41	6.2	447	2	BI824638	BI824638 603033580
c	13	40	6.0	1099	2	BI523344	BI523344 603175938
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	15	29	4.4	568	14	CR795312	CR795312 GR0AAA12D
	16	27	4.1	373	7	BF552757	BF552757 UI-R-C0-i
	17	27	4.1	427	10	DT930939	DT930939 S13.1784
	18	27	4.1	456	10	DT913216	DT913216 S13.1426
	19	27	4.1	561	3	BU699383	BU699383 LL2in1157
	20	27	4.1	563	3	BU698113	BU698113 LL2in1206
	21	27	4.1	589	1	AI050362	AI050362 ub30a07.r
	22	27	4.1	692	5	CJ137697	CJ137697 CJ137697
	23	27	4.1	1299	6	AK153729	AK153729 Mus muscu
	24	24	3.6	508	9	DA505380	DA505380 DA505380
	25	24	3.6	571	3	BP261459	BP261459 BP261459
	26	24	3.6	777	14	CT080894	CT080894 Sus scrof
	27	23	3.5	354	4	BY230958	BY230958 BY230958
c	28	23	3.5	528	1	AI332701	AI332701 qq19a07.x
	29	23	3.5	840	11	BZ261813	BZ261813 CH230-420
c	30	22	3.3	588	12	CE841948	CE841948 tigr-gss-
	31	22	3.3	758	14	CT100632	CT100632 Sus scrof
	32	21	3.2	380	11	AQ100596	AQ100596 HS_3064_B
c	33	21	3.2	489	11	AQ393691	AQ393691 CITBI-E1-
c	34	21	3.2	540	8	CV068291	CV068291 Le_mx0_43
	35	21	3.2	679	3	BU002107	BU002107 QGG30D21.
c	36	21	3.2	733	11	AQ631366	AQ631366 RPCI-11-4
c	37	21	3.2	1109	10	W29456	W29456 mc03e02.r1
c	38	20	3.0	229	11	AZ901502	AZ901502 RPCI-24-1
c	39	20	3.0	241	11	AZ891891	AZ891891 RPCI-24-2
	40	20	3.0	344	14	BX537236	BX537236 INRA porc
c	41	20	3.0	377	1	AL731335	AL731335 AL731335
c	42	20	3.0	383	7	BE016666	BE016666 fk67a01.y
	43	20	3.0	389	4	BY394944	BY394944 BY394944
	44	20	3.0	452	4	BW935403	BW935403 BW935403
c	45	20	3.0	467	7	BE557755	BE557755 fl10b12.y
c	46	20	3.0	516	11	AQ478437	AQ478437 RPCI-11-2
c	47	20	3.0	551	3	BQ481093	BQ481093 faa75b02.
c	48	20	3.0	574	11	AZ855572	AZ855572 2M0159K08
	49	20	3.0	598	1	AL731281	AL731281 AL731281
	50	20	3.0	603	14	CNS01PJI	AL154894 Anopheles
c	51	20	3.0	604	10	W63576	W63576 zc55h09.r1
	52	20	3.0	610	7	AW107212	AW107212 um12c12.x
	53	20	3.0	639	13	DU222360	DU222360 109857403
	54	20	3.0	644	1	AL729822	AL729822 AL729822
c	55	20	3.0	647	1	AL729917	AL729917 AL729917
c	56	20	3.0	674	9	DN901552	DN901552 naq21d09.
c	57	20	3.0	691	11	BH373165	BH373165 AG-ND-159
	58	20	3.0	724	4	BW754129	BW754129 BW754129
c	59	20	3.0	734	11	BZ028162	BZ028162 oeg78e09.
c	60	20	3.0	771	10	DT077555	DT077555 AGENCOURT
c	61	20	3.0	822	5	CD357085	CD357085 AGENCOURT
	62	20	3.0	855	11	AQ574005	AQ574005 nbxb0083O
c	63	20	3.0	875	13	CL868149	CL868149 Gma_01_C0
	64	20	3.0	912	5	CF242845	CF242845 AGENCOURT
c	65	20	3.0	920	7	BF530961	BF530961 602072472
	66	20	3.0	959	13	CL465003	CL465003 SAIL_1232
	67	20	3.0	1035	14	CNS01GIY	AL143195 Anopheles
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	69	20	3.0	1321	10	DT990937	DT990937 CNB152-F0
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	71	19	2.9	167	8	CN094503	CN094503 EC2BBA9DE
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	74	19	2.9	219	8	CR583097	CR583097 CR583097
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c	78	19	2.9	247	1	AL640225	AL640225 AL640225
	79	19	2.9	247	4	BX668635	BX668635 BX668635
c	80	19	2.9	247	7	BB425487	BB425487 BB425487
c	81	19	2.9	255	4	BX714043	BX714043 BX714043
	82	19	2.9	261	5	CD190551	CD190551 MS1-0064U
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	84	19	2.9	267	1	AV338007	AV338007 AV338007
c	85	19	2.9	276	1	AL777805	AL777805 AL777805
	86	19	2.9	280	4	BX683343	BX683343 BX683343
	87	19	2.9	283	11	AZ406693	AZ406693 1M0176H05
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	100	19	2.9	354	8	CN106168 CN106168 EC2CAA29A
	101	19	2.9	361	1	AL855295 AL855295 AL855295
c	102	19	2.9	365	10	DR612001 DR612001 EST100212
	103	19	2.9	366	9	DN068916 DN068916 JGI_CABD5
	104	19	2.9	376	5	CF879856 CF879856 tric081xk
c	105	19	2.9	379	8	CR437136 CR437136 CR437136
	106	19	2.9	386	8	CR560333 CR560333 CR560333
c	107	19	2.9	392	5	CD181907 CD181907 MS1-0032T
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c	113	19	2.9	433	1	AL966626 AL966626 AL966626
c	114	19	2.9	433	8	CN106169 CN106169 EC2CAA29A
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c	116	19	2.9	436	11	AQ928052 AQ928052 RPCI-23-2
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c	118	19	2.9	442	8	CR441087 CR441087 CR441087
	119	19	2.9	445	1	AI975050 AI975050 EST269644
c	120	19	2.9	450	11	BH310495 BH310495 CH230-168
	121	19	2.9	456	4	BX691929 BX691929 BX691929
	122	19	2.9	459	11	AQ583994 AQ583994 RPCI-11-4
c	123	19	2.9	465	1	AL677765 AL677765 AL677765
c	124	19	2.9	465	5	CD147810 CD147810 ML1-0007T
	125	19	2.9	466	5	CJ319407 CJ319407 CJ319407
	126	19	2.9	471	3	BQ523107 BQ523107 NISC_nl20
	127	19	2.9	472	2	BG371292 BG371292 dac43b03.
	128	19	2.9	474	8	CV865967 CV865967 PDUts1024
	129	19	2.9	475	1	AA032893 AA032893 mi37e03.r
	130	19	2.9	477	4	BX684618 BX684618 BX684618
c	131	19	2.9	480	1	AL627756 AL627756 AL627756
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	133	19	2.9	481	8	CX333972 CX333972 JGI_XZT69
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	135	19	2.9	485	8	CN092431 CN092431 EC2BBA6CF
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	139	19	2.9	491	3	BQ395792 BQ395792 NISC_ng17
	140	19	2.9	492	4	BX684294 BX684294 BX684294
	141	19	2.9	492	5	CD147721 CD147721 ML1-0007T
c	142	19	2.9	493	5	CD147926 CD147926 ML1-0007T
c	143	19	2.9	497	1	AU304680 AU304680 AU304680
	144	19	2.9	500	8	CR428754 CR428754 CR428754
	145	19	2.9	500	9	CX743226 CX743226 JGI_ANBT1
c	146	19	2.9	500	13	CL872609 CL872609 abe83h09.
c	147	19	2.9	501	11	BH307362 BH307362 CH230-38A
c	148	19	2.9	502	10	DR855771 DR855771 JGI_CABG2
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	151	19	2.9	507	2	BM366900 BM366900 BS3200320
	152	19	2.9	514	11	AQ141318 AQ141318 HS_3150_A
	153	19	2.9	521	9	CX478296 CX478296 JGI_XZG21
c	154	19	2.9	521	11	AZ469984 AZ469984 1M0283M17
	155	19	2.9	523	10	DT917776 DT917776 S13.1419
	156	19	2.9	529	3	BQ525812 BQ525812 NISC_no12
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	158	19	2.9	531	2	BM363212 BM363212 BS320054A
	159	19	2.9	533	2	BM089983 BM089983 503868 MA
c	160	19	2.9	541	8	CR565401 CR565401 CR565401
	161	19	2.9	544	5	CK223678 CK223678 702603448
	162	19	2.9	546	4	BX777982 BX777982 BX777982
	163	19	2.9	548	1	AL634301 AL634301 AL634301
c	164	19	2.9	551	1	AL677668 AL677668 AL677668
c	165	19	2.9	552	9	DN992173 DN992173 TC121105
	166	19	2.9	554	9	CX503960 CX503960 JGI_XZG41
	167	19	2.9	555	8	CR443258 CR443258 CR443258
c	168	19	2.9	555	10	DR595592 DR595592 EST985720
	169	19	2.9	559	1	AL799932 AL799932 AL799932
c	170	19	2.9	559	13	CW068579 CW068579 104_317_1
c	171	19	2.9	561	8	CN092432 CN092432 EC2BBA6CF
	172	19	2.9	562	2	BM364545 BM364545 BS3200020
	173	19	2.9	562	2	BM365948 BM365948 BS3200200
	174	19	2.9	567	3	BQ397507 BQ397507 NISC_ng28
c	175	19	2.9	567	14	AG246693 AG246693 Lotus cor
	176	19	2.9	570	9	CX508565 CX508565 JGI_XZG52
c	177	19	2.9	570	9	DN153146 DN153146 HbGPS11.1
c	178	19	2.9	572	8	CX156315 CX156315 TfEST037E
	179	19	2.9	573	11	AZ797767 AZ797767 2M0054J08
	180	19	2.9	575	3	BQ522020 BQ522020 NISC_nl14
	181	19	2.9	579	3	BQ390468 BQ390468 NISC_mq13
	182	19	2.9	580	4	BX694829 BX694829 BX694829
	183	19	2.9	581	4	BX708856 BX708856 BX708856
	184	19	2.9	582	2	BG817053 BG817053 dad69f11.
	185	19	2.9	584	11	BZ297745 BZ297745 CG3614.r1
	186	19	2.9	585	10	DR904723 DR904723 JGI_XZT68
c	187	19	2.9	586	9	CX418617 CX418617 JGI_XZG65
	188	19	2.9	588	4	BX696697 BX696697 BX696697
	189	19	2.9	588	12	CE412842 CE412842 tigr-gss-
	190	19	2.9	591	9	CX853256 CX853256 JGI_CAAL9
	191	19	2.9	592	8	CR416426 CR416426 CR416426
c	192	19	2.9	594	1	AL682266 AL682266 AL682266
c	193	19	2.9	595	13	CL588251 CL588251 OB__Ba008
	194	19	2.9	596	9	CX741786 CX741786 JGI_ANBT3
c	195	19	2.9	597	1	AL673912 AL673912 AL673912
	196	19	2.9	597	3	BQ521254 BQ521254 NISC_nl10
	197	19	2.9	597	4	BX683918 BX683918 BX683918
	198	19	2.9	597	9	CX746186 CX746186 JGI_ANBT3
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ALIGNMENTS

RESULT 1
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LOCUS DQ033872 762 bp DNA linear GSS 02-JUN-2005
DEFINITION Homo sapiens IL12A gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION DQ033872
VERSION DQ033872.1 GI:66885081
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 762)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 762)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.
FEATURES Location/Qualifiers
source 1. .762

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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
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Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        619 ATTCG 623
              |||||
Db        712 ATTCG 716


RESULT 2
CD013916
LOCUS       CD013916                863 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION  90138296 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD013916
VERSION     CD013916.1  GI:37777446
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 863)
  AUTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
            Au-Young,J. and Stuve,L.L.
  TITLE     PCR isolation and cloning of novel splice variant mRNAs from known
            drug target genes
  JOURNAL   Genomics 83 (4), 566-571 (2004)
   PUBMED   15028279
COMMENT     Contact: Jin, P.
            Incyte Corporation
            3160 Porter Drive, Palo Alto, CA 94304, USA
            Tel: 650 621 8639
            Fax: 650 621 8965
            Email: pjin@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .863
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
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                     /clone_lib="Single gene library"
                     /note="Vector: pDrive Cloning Vector; RT-PCR was performed
                     using gene-specific primers flanking the open-reading
                     frame. PCR products were subcloned into pDrive Cloning
                     Vector and sequenced completely using M13 forward and
                     reverse primers. Sequencing gaps were closed by
                     re-sequencig using primers flanking the gapped areas."
ORIGIN

  Query Match             9.8%;  Score 65;  DB 4;  Length 863;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        641 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 700

Qy        619 ATTCG 623
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Db        701 ATTCG 705


RESULT 3
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LOCUS       CD013914                935 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION  90138124 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD013914
VERSION     CD013914.1  GI:37777444
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 935)
  AUTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
            Au-Young,J. and Stuve,L.L.
  TITLE     PCR isolation and cloning of novel splice variant mRNAs from known
            drug target genes
  JOURNAL   Genomics 83 (4), 566-571 (2004)
   PUBMED   15028279
COMMENT     Contact: Jin, P.
            Incyte Corporation
            3160 Porter Drive, Palo Alto, CA 94304, USA
            Tel: 650 621 8639
            Fax: 650 621 8965
            Email: pjin@incyte.com.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone_lib="Single gene library"
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                     Vector and sequenced completely using M13 forward and
                     reverse primers. Sequencing gaps were closed by
                     re-sequencig using primers flanking the gapped areas."
ORIGIN

  Query Match             9.8%;  Score 65;  DB 4;  Length 935;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        619 ATTCG 623
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Db        773 ATTCG 777


RESULT 4
CD013915
LOCUS       CD013915               1136 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION  90138132 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD013915
VERSION     CD013915.1  GI:37777445
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1136)
  AUTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
            Au-Young,J. and Stuve,L.L.
  TITLE     PCR isolation and cloning of novel splice variant mRNAs from known
            drug target genes
  JOURNAL   Genomics 83 (4), 566-571 (2004)
   PUBMED   15028279
COMMENT     Contact: Jin, P.
```

Incyte Corporation
3160 Porter Drive, Palo Alto, CA 94304, USA
Tel: 650 621 8639
Fax: 650 621 8965
Email: pjin@incyte.com.

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FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
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                     using gene-specific primers flanking the open-reading
                     frame. PCR products were subcloned into pDrive Cloning
                     Vector and sequenced completely using M13 forward and
                     reverse primers. Sequencing gaps were closed by
                     re-sequencig using primers flanking the gapped areas."
ORIGIN

  Query Match             9.8%;  Score 65;  DB 4;  Length 1136;
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Db        914 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 973

Qy        619 ATTCG 623
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Db        974 ATTCG 978


RESULT 5
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LOCUS       BC035571               1938 bp    mRNA    linear   HTC 04-MAR-2003
DEFINITION  Homo sapiens, clone IMAGE:5240216, mRNA.
ACCESSION   BC035571
VERSION     BC035571.1  GI:23958681
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1938)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 69 Row: b Column: 15
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 4504638
            This clone has the following problem: retained intron.
FEATURES             Location/Qualifiers
     source          1. .1938
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240216"
                     /tissue_type="Brain, fetal, whole pooled"
                     /clone_lib="NIH_MGC_121"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 6;  Length 1938;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1335 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1394

Qy        619 ATTCG 623
              |||||
Db       1395 ATTCG 1399


RESULT 6
DQ033873
LOCUS       DQ033873               762 bp    DNA     linear   GSS 02-JUN-2005
DEFINITION  Pan troglodytes IL12A gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   DQ033873
VERSION     DQ033873.1  GI:66885082
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     A Scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
  JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
   PUBMED   15869325
REFERENCE   2  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.  Translation starts at the beginning of
            alignment.
FEATURES             Location/Qualifiers
     source          1. .762
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     gene            <1. .>762
                     /gene="IL12A"
                     /locus_tag="HC3464"
ORIGIN

  Query Match             8.6%;  Score 57;  DB 14;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-19;
  Matches   57;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy        567 GGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 623
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 GGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 716


RESULT 7
BP260963
LOCUS       BP260963                 581 bp    mRNA    linear   EST 16-SEP-2004
DEFINITION  BP260963 Sugano cDNA library, small intestine Homo sapiens cDNA
            clone HSI02082, mRNA sequence.
ACCESSION   BP260963
VERSION     BP260963.1  GI:52176194
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 581)
  AUTHORS   Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
            Mizushima-Sugano,J., Nakai,K. and Sugano,S.
  TITLE     Sequence comparison of human and mouse genes reveals a homologous
            block structure in the promoter regions
  JOURNAL   Genome Res. 14 (9), 1711-1718 (2004)
   PUBMED   15342556
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Tel: 81-3-5449-5343
            Fax: 81-3-5449-5416
            Email: ysuzuki@hgc.jp.
FEATURES             Location/Qualifiers
     source          1. .581
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HSI02082"
                     /tissue_type="small intestine"
                     /clone_lib="Sugano cDNA library, small intestine"
ORIGIN

  Query Match             8.4%;  Score 56;  DB 3;  Length 581;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-18;
  Matches   56;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        208 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 263
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        517 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 572


RESULT 8
BI523569
LOCUS       BI523569                 832 bp    mRNA    linear   EST 29-AUG-2001
DEFINITION  603175938F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 5',
            mRNA sequence.
ACCESSION   BI523569
VERSION     BI523569.1  GI:15348361
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 832)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11605  row: l  column: 09
            High quality sequence start: 23
            High quality sequence stop: 821.
FEATURES             Location/Qualifiers
     source          1. .832
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240216"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_121"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 017. Note:
                     this is a NIH_MGC Library."
ORIGIN

  Query Match             8.4%;  Score 56;  DB 2;  Length 832;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-18;
  Matches   56;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        208 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 263
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        520 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 575


RESULT 9
CE159257
LOCUS       CE159257                 592 bp    DNA     linear   GSS 25-SEP-2003
DEFINITION  tigr-gss-dog-17000371408491 Dog Library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION   CE159257
VERSION     CE159257.1  GI:35287296
KEYWORDS    GSS.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 592)
  AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
            Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
            Venter,J.C.
  TITLE     The dog genome: survey sequencing and comparative analysis
  JOURNAL   Science 301 (5641), 1898-1903 (2003)
   PUBMED   14512627
COMMENT     Contact: Kirkness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirknes@tigr.org
            Class: shotgun.
FEATURES             Location/Qualifiers
     source          1. .592
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /strain="Standard Poodle"
                     /db_xref="taxon:9615"
                     /clone_lib="Dog Library"
                     /note="Site_1: BstXI; Libraries were prepared from
```

peripheral blood"
ORIGIN

Query Match 7.2%; Score 48; DB 12; Length 592;
Best Local Similarity 100.0%; Pred. No. 2.8e-14;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 285
||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 66 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 113

RESULT 10
BG702253
LOCUS BG702253 812 bp mRNA linear EST 07-MAY-2001
DEFINITION 602683459F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4816118 5', mRNA sequence.
ACCESSION BG702253
VERSION BG702253.1 GI:13973409
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 812)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10714 row: e column: 15
High quality sequence stop: 804.
FEATURES Location/Qualifiers
source 1. .812
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4816118"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_95"
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
ORIGIN

Query Match 7.1%; Score 47; DB 2; Length 812;
Best Local Similarity 100.0%; Pred. No. 1.1e-13;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 217 GATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 263
|||||||||||||||||||||||||||||||||||||||||||||||
Db 624 GATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 670

RESULT 11
BM257856
LOCUS BM257856 342 bp mRNA linear EST 17-DEC-2001
DEFINITION 521721 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BM257856
VERSION BM257856.1 GI:17893455
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 342)
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.
TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
JOURNAL Genome Res. 11 (4), 626-630 (2001)
PUBMED 11282978
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
PCR PRimers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 125 row: E column: 18
Seq primer: ATTTAGGTGACACTATAG.
FEATURES Location/Qualifiers
source 1. .342
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 3BOV"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."
ORIGIN

Query Match 6.2%; Score 41; DB 2; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 166 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTC 206
|||||||||||||||||||||||||||||||||||||||
Db 294 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTC 334

RESULT 12
BI824638
LOCUS BI824638 447 bp mRNA linear EST 04-OCT-2001
DEFINITION 603033580F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175018 5', mRNA sequence.
ACCESSION BI824638
VERSION BI824638.1 GI:15936188
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 447)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

```
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11435  row: o  column: 19
            High quality sequence start: 3
            High quality sequence stop: 445.
FEATURES             Location/Qualifiers
     source          1. .447
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5175018"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_115"
                     /note="Organ: pooled brain, lung, testis; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of 6 male brains, age range 23-27; 1
                     male lung, age 27; and 1 male testis, age 69.  Library is
                     oligo-dT primed and directionally cloned (EcoRV site is
                     destroyed upon  cloning).  Average insert size 1.8 kb,
                     insert size range 1-3 kb. Library is normalized and
                     enriched for full-length clones and was  constructed by C.
                     Gruber (Invitrogen).  Research Genetics tracking  code
                     021. Note: this is a NIH_MGC Library."
ORIGIN

  Query Match              6.2%;  Score 41;  DB 2;  Length 447;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-10;
  Matches   41;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        583 AAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 623
              |||||||||||||||||||||||||||||||||||||||||
Db          1 AAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 41


RESULT 13
BI523344/c
LOCUS       BI523344                1099 bp    mRNA    linear   EST 29-AUG-2001
DEFINITION  603175938T1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 3',
            mRNA sequence.
ACCESSION   BI523344
VERSION     BI523344.1  GI:15348136
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1099)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11605  row: l  column: 09
            High quality sequence start: 40
            High quality sequence stop: 727.
FEATURES             Location/Qualifiers
     source          1. .1099
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240216"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_121"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 017. Note:
                     this is a NIH_MGC Library."
ORIGIN

  Query Match              6.0%;  Score 40;  DB 2;  Length 1099;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-10;
  Matches   40;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        584 AAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 623
              ||||||||||||||||||||||||||||||||||||||||
Db        524 AAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 485


RESULT 14
CR813130
LOCUS       CR813130                539 bp    DNA     linear   GSS 27-SEP-2004
DEFINITION  GR0AAA37CD06RM1 INRA BAC Bos taurus genomic clone INRAb_622G01, DNA
            sequence, genomic survey sequence.
ACCESSION   CR813130
VERSION     CR813130.1  GI:52749218
KEYWORDS    GSS.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 539)
  AUTHORS   Eggen,A., Schibler,L. and Roy,A.
  TITLE     Bovine BAC End Sequences from the INRA bovine BAC library
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 539)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-SEP-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Contact: Andre Eggen
            Department of Animal Genetics - LGbC
            INRA
            78350 Jouy-en-Josas, France
            Tel: 33 1 34 65 24 24
            Fax: 33 1 34 65 24 78
            Email: eggen@jouy.inra.fr
            Clones are derived from the INRA bovine BAC library
            (http://locus.jouy.inra.fr/fpc/cattle_bac_map.htm). For BAC library
            availability, please contact Andre Eggen (eggen@jouy.inra.fr). This
            work  was undertaken as part of the International Bovine BAC
            Mapping Consortium (IBBMC) by INRA (Jouy-en-Josas) and Genoscope
            (Evry) Plate: 622 row: G column: 01
            Seq primer: M13 Reverse
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .539
                     /organism="Bos taurus"
                     /mol_type="genomic DNA"
                     /strain="breed: Holstein"
                     /db_xref="taxon:9913"
                     /clone="INRAb_622G01"
                     /sex="Male"
```

```
                     /cell_type="fibroblast"
                     /clone_lib="INRA bovine BAC"
                     /note="Vector: pBeloBAC11; Site_1: HindIII; Holstein bull;
                     INRA Bovine BAC library (Male) produced by Andre Eggen
                     Genoscope sequence ID : GR0AAA37CD06RM1"
ORIGIN

  Query Match             4.4%;  Score 29;  DB 14;  Length 539;
  Best Local Similarity   100.0%;  Pred. No. 0.00081;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        285 GAATGAGAGTTGCCTGGCTTCCAGAGAGA 313
              |||||||||||||||||||||||||||||
Db        330 GAATGAGAGTTGCCTGGCTTCCAGAGAGA 358


RESULT 15
CR795312
LOCUS       CR795312                568 bp    DNA     linear   GSS 24-SEP-2004
DEFINITION  GR0AAA12DG09RM1 INRA BAC Bos taurus genomic clone INRAb_238E06, DNA
            sequence, genomic survey sequence.
ACCESSION   CR795312
VERSION     CR795312.1  GI:52676311
KEYWORDS    GSS.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 568)
  AUTHORS   Eggen,A., Schibler,L. and Roy,A.
  TITLE     Bovine BAC End Sequences from the INRA bovine BAC library
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 568)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-SEP-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Contact: Andre Eggen
            Department of Animal Genetics - LGbC
            INRA
            78350 Jouy-en-Josas, France
            Tel: 33 1 34 65 24 24
            Fax: 33 1 34 65 24 78
            Email: eggen@jouy.inra.fr
            Clones are derived from the INRA bovine BAC library
            (http://locus.jouy.inra.fr/fpc/cattle_bac_map.htm). For BAC library
            availability, please contact Andre Eggen (eggen@jouy.inra.fr). This
            work  was undertaken as part of the International Bovine BAC
            Mapping Consortium (IBBMC) by INRA (Jouy-en-Josas) and Genoscope
            (Evry) Plate: 238 row: E column: 06
            Seq primer: M13 Reverse
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .568
                     /organism="Bos taurus"
                     /mol_type="genomic DNA"
                     /strain="breed: Holstein"
                     /db_xref="taxon:9913"
                     /clone="INRAb_238E06"
                     /sex="Male"
                     /cell_type="fibroblast"
                     /clone_lib="INRA bovine BAC"
                     /note="Vector: pBeloBAC11; Site_1: HindIII; Holstein bull;
                     INRA Bovine BAC library (Male) produced by Andre Eggen
                     Genoscope sequence ID : GR0AAA12DG09RM1"
ORIGIN

  Query Match             4.4%;  Score 29;  DB 14;  Length 568;
  Best Local Similarity   100.0%;  Pred. No. 0.00082;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        285 GAATGAGAGTTGCCTGGCTTCCAGAGAGA 313
              |||||||||||||||||||||||||||||
Db        329 GAATGAGAGTTGCCTGGCTTCCAGAGAGA 357


RESULT 16
BF552757
LOCUS       BF552757                373 bp    mRNA    linear   EST 12-DEC-2000
DEFINITION  UI-R-C0-iz-d-02-0-UI.r1 UI-R-C0 Rattus norvegicus cDNA clone
            UI-R-C0-iz-d-02-0-UI 5', mRNA sequence.
ACCESSION   BF552757
VERSION     BF552757.1  GI:11662487
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 373)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
   PUBMED   8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156  MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            cDNA Library Preparation: M.B. Soares Lab Clone distribution:
            clones will be available through Research Genetics (www.resgen.com)
            This clone is also available through the I.M.A.G.E. Consortium at
            LLNL (info@image.llnl.gov). IMAGE ID= 1782759
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .373
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="UI-R-C0-iz-d-02-0-UI"
                     /dev_stage="adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="UI-R-C0"
                     /note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI;
                     The UI-R-C0 library is a subtracted library derived from
                     the UI-R-A1 and UI-R-E1 libraries. The UI-R-A1 library
                     consisted of a mixture of individually tagged normalized
                     libraries constructed from rat  placenta, adult lung,
                     brain, liver, kidney, heart, spleen, ovary,  and muscle.
                     The UI-R-E1 library  consisted of a mixture of
                     individually tagged normalized libraries constructed from
                     8, 12 and 18-day embryo. The tag is a string of 3-5
                     nucleotides present between the Not I  site and the
                     oligo-dT track which allows identification of the library
                     of origin of a clone within the mixture. The subtracted
                     library (UI-R-C0) was constructed as follows: PCR
                     amplified cDNA inserts from a pool of UI-R-A1 and UI-R-E1
                     clones from which 3' ESTs had been derived was used as a
                     driver in a hybridization with the pooled UI-R-A1 and
                     UI-R-E1 library in the form of single-stranded circles.
                     The remaining single-stranded circles (subtracted library)
                     was purified by hydroxyapatite column chromatography,
                     converted to double-stranded circles and electroporated
                     into DH10B bacteria (Life Technologies) to generate the
                     UI-R-C0 library. This procedure has been previously
                     described (Bonaldo, Lennon and Soares, Genome Research 6:
                     791-806, 1996)"
ORIGIN

  Query Match             4.1%;  Score 27;  DB 7;  Length 373;
```

```
  Best Local Similarity   100.0%;  Pred. No. 0.0096;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        388 ATCTATGAGGACTTGAAGATGTACCAG 414
              ||||||||||||||||||||||||||||
Db        101 ATCTATGAGGACTTGAAGATGTACCAG 127


RESULT 17
DT930939
LOCUS       DT930939                427 bp    mRNA    linear   EST 20-SEP-2005
DEFINITION  S13.1784 Hematopoietic stem cells Mus musculus cDNA, mRNA sequence.
ACCESSION   DT930939
VERSION     DT930939.1  GI:75963455
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 427)
  AUTHORS   Pritsker,M., Doniger,T.T., Kramer,L.C., Westcot,S.E. and
            Lemischka,I.R.
  TITLE     Diversification of Stem Cell Molecular Repertoire by Alternative
            Splicing
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. (2005) In press
COMMENT     Contact: Pritsker M
            Lab of Ihor Lemischka, Department of Molecular Biology
            Princeton University
            Princeton, NJ 08544, USA
            Tel: 609 258 5657
            Fax: 609 258 1704
            Email: pritsker@molbio.princeton.edu.
FEATURES             Location/Qualifiers
     source          1. .427
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /tissue_type="Hematopoietic stem cells"
                     /cell_type="Hematopoietic stem cells"
                     /clone_lib="Hematopoietic stem cells"
                     /note="cDNA library was made from FACS-purified
                     hematopoietic stem cells"
ORIGIN

  Query Match             4.1%;  Score 27;  DB 10;  Length 427;
  Best Local Similarity   100.0%;  Pred. No. 0.0098;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        388 ATCTATGAGGACTTGAAGATGTACCAG 414
              ||||||||||||||||||||||||||||
Db        385 ATCTATGAGGACTTGAAGATGTACCAG 411


RESULT 18
DT913216
LOCUS       DT913216                456 bp    mRNA    linear   EST 19-SEP-2005
DEFINITION  S13.1426 Hematopoietic stem cells Mus musculus cDNA, mRNA sequence.
ACCESSION   DT913216
VERSION     DT913216.1  GI:75893697
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   Pritsker,M., Doniger,T.T., Kramer,L.C., Westcot,S.E. and
            Lemischka,I.R.
  TITLE     Diversification of Stem Cell Molecular Repertoire by Alternative
            Splicing
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. (2005) In press
COMMENT     Contact: Pritsker M
            Lab of Ihor Lemischka, Department of Molecular Biology
            Princeton University
            Princeton, NJ 08544, USA
            Tel: 609 258 5657
            Fax: 609 258 1704
            Email: pritsker@molbio.princeton.edu.
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /tissue_type="Hematopoietic stem cells"
                     /cell_type="Hematopoietic stem cells"
                     /clone_lib="Hematopoietic stem cells"
                     /note="cDNA library was made from FACS-purified
                     hematopoietic stem cells"
ORIGIN

  Query Match             4.1%;  Score 27;  DB 10;  Length 456;
  Best Local Similarity   100.0%;  Pred. No. 0.01;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        388 ATCTATGAGGACTTGAAGATGTACCAG 414
              ||||||||||||||||||||||||||||
Db        385 ATCTATGAGGACTTGAAGATGTACCAG 411


RESULT 19
BU699383
LOCUS       BU699383                561 bp    mRNA    linear   EST 09-OCT-2002
DEFINITION  LL2in11573T7 Hematopoietic Stem Cell Subtracted Library Mus
            musculus cDNA 5' similar to interleukin 12 p35 subunit, mRNA
            sequence.
ACCESSION   BU699383
VERSION     BU699383.1  GI:23615967
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 561)
  AUTHORS   Phillips,R.L., Ernst,R.E., Brunk,B.P., Ivanova,N., Mahan,M.A.,
            Deanehan,J.K., Moore,K.A., Overton,G.C. and Lemischka,I.R.
  TITLE     The genetic program of hematopoietic stem cells
  JOURNAL   Science 288 (5471), 1635-1640 (2000)
   PUBMED   10834841
COMMENT     Contact: Lemischka, Ihor R.
            Department of Molecular Biology
            Princeton University
            Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544, USA
            Tel: 609 258 2838
            Fax: 609 258 2759
            Email: ilemischka@molbio.princeton.edu
            These ESTs are derived from a subtracted cDNA library enriched for
            gene products expressed in day 14-14.5 fetal liver hematopoietic
            stem cells defined as Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E
            (Sca-1)pos
            Seq primer: M13Reverse or T7.
FEATURES             Location/Qualifiers
     source          1. .561
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /tissue_type="Hematopoietic"
                     /cell_type="Stem Cells; Lineageneg/lo, AA4.1pos, cKitpos,
                     Ly6A/E (Sca-1)pos"
                     /dev_stage="Embryonic day 14-14.5"
                     /lab_host="DH10B"
                     /clone_lib="Hematopoietic Stem Cell Subtracted Library"
                     /note="Organ: Fetal Liver; Vector: Sport 1; Site_1: Sal I;
                     Site_2: Not I; Two directionally cloned cDNA libraries
```

were made from fetal liver hematopoietic stem cells enriched to be Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E (Sca-1)pos called Scapos and from AA4.1neg fetal liver cells. Subtractive hybridization was performed by hybridization of the target, Scapos, single stranded cDNA library in pSport1 to biotinylated RNA transcribed from the driver, AA4.1neg cDNA library in pSport2 with inserts cloned in the complementary orientation. For detailed protocols and additional information please see our website at http://stemcell.princeton.edu."

ORIGIN

Query Match 4.1%; Score 27; DB 3; Length 561;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        388 ATCTATGAGGACTTGAAGATGTACCAG 414
              ||||||||||||||||||||||||||
Db        302 ATCTATGAGGACTTGAAGATGTACCAG 328
```

RESULT 20
BU698113
LOCUS BU698113 563 bp mRNA linear EST 09-OCT-2002
DEFINITION LL2in12067T7 Hematopoietic Stem Cell Subtracted Library Mus musculus cDNA 5' similar to interleukin 12 p35 subunit, mRNA sequence.
ACCESSION BU698113
VERSION BU698113.1 GI:23610620
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 563)
AUTHORS Phillips,R.L., Ernst,R.E., Brunk,B.P., Ivanova,N., Mahan,M.A., Deanehan,J.K., Moore,K.A., Overton,G.C. and Lemischka,I.R.
TITLE The genetic program of hematopoietic stem cells
JOURNAL Science 288 (5471), 1635-1640 (2000)
PUBMED 10834841
COMMENT Contact: Lemischka, Ihor R.
Department of Molecular Biology
Princeton University
Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544, USA
Tel: 609 258 2838
Fax: 609 258 2759
Email: ilemischka@molbio.princeton.edu
These ESTs are derived from a subtracted cDNA library enriched for gene products expressed in day 14-14.5 fetal liver hematopoietic stem cells defined as Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E (Sca-1)pos
Seq primer: M13Reverse or T7.
FEATURES Location/Qualifiers
source 1. .563
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/tissue_type="Hematopoietic"
/cell_type="Stem Cells; Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E (Sca-1)pos"
/dev_stage="Embryonic day 14-14.5"
/lab_host="DH10B"
/clone_lib="Hematopoietic Stem Cell Subtracted Library"
/note="Organ: Fetal Liver; Vector: Sport 1; Site_1: Sal I; Site_2: Not I; Two directionally cloned cDNA libraries were made from fetal liver hematopoietic stem cells enriched to be Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E (Sca-1)pos called Scapos and from AA4.1neg fetal liver cells. Subtractive hybridization was performed by hybridization of the target, Scapos, single stranded cDNA library in pSport1 to biotinylated RNA transcribed from the driver, AA4.1neg cDNA library in pSport2 with inserts cloned in the complementary orientation. For detailed protocols and additional information please see our website at http://stemcell.princeton.edu."

ORIGIN

Query Match 4.1%; Score 27; DB 3; Length 563;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        388 ATCTATGAGGACTTGAAGATGTACCAG 414
              ||||||||||||||||||||||||||
Db        318 ATCTATGAGGACTTGAAGATGTACCAG 344
```

RESULT 21
AI050362
LOCUS AI050362 589 bp mRNA linear EST 09-JUL-1998
DEFINITION ub30a07.r1 Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:1379220 5' similar to gb:M65291 INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (HUMAN); gb:M86672 Mus musculus interleukin 12 p35 subunit, complete cds (MOUSE);, mRNA sequence.
ACCESSION AI050362
VERSION AI050362.1 GI:3299479
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 589)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:901688
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 60.
FEATURES Location/Qualifiers
source 1. .589
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1379220"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares_thymus_2NbMT"
/note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGGAGCGGCCGCGTTTTTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

```
  Query Match             4.1%;  Score 27;  DB 1;  Length 589;
  Best Local Similarity   100.0%;  Pred. No. 0.01;
  Matches  27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        388 ATCTATGAGGACTTGAAGATGTACCAG 414
              |||||||||||||||||||||||||||
Db        327 ATCTATGAGGACTTGAAGATGTACCAG 353


RESULT 22
CJ137697
LOCUS       CJ137697                692 bp    mRNA    linear   EST 23-SEP-2005
DEFINITION  CJ137697 RIKEN full-length enriched mouse cDNA library, C57BL/6J
            thymus 3 days neonate Mus musculus cDNA clone A630064E02 5', mRNA
            sequence.
ACCESSION   CJ137697
VERSION     CJ137697.1  GI:76238025
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 692)
  AUTHORS   The FANTOM Consortium and RIKEN Genome Exploration Research Group
            and Genome Science Group (Genome Network Project Core Group).
  TITLE     The transcriptional landscape of the mammalian genome
  JOURNAL   Science 309 (5740), 1559-1563 (2005)
   PUBMED   16141072
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. Tissues were provided by Dr. John Todd (
            Dept. of Medical Genetics Wellcome Trust Centre for Molecular
            Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes
            Hospital Cambridge ) whose assistance we gratefully acknowledge.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/.
FEATURES             Location/Qualifiers
     source          1. .692
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="A630064E02"
                     /tissue_type="thymus"
                     /dev_stage="3 days neonate"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library,
                     C57BL/6J thymus 3 days neonate"
ORIGIN

  Query Match             4.1%;  Score 27;  DB 5;  Length 692;
  Best Local Similarity   100.0%;  Pred. No. 0.011;
  Matches  27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        388 ATCTATGAGGACTTGAAGATGTACCAG 414
              |||||||||||||||||||||||||||
Db        521 ATCTATGAGGACTTGAAGATGTACCAG 547


RESULT 23
AK153729
LOCUS       AK153729                1299 bp    mRNA    linear   HTC 21-SEP-2005
DEFINITION  Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
            library, clone:A630064E02 product:interleukin 12a, full insert
            sequence.
ACCESSION   AK153729
VERSION     AK153729.1  GI:74148962
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
            Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
            Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
            Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
            Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
            Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
            Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
            Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
            Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  CONSRTM   RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
   PUBMED   11217851
REFERENCE   5
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
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Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420 (6915), 563-573 (2002)

PUBMED 12466851

REFERENCE 6

AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE The transcriptional landscape of the mammalian genome

JOURNAL Science 309 (5740), 1559-1563 (2005)

PUBMED 16141072

REFERENCE 7

AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.

CONSRTM RIKEN Genome Exploration Research Group

TITLE Antisense transcription in the mammalian transcriptome

JOURNAL Science 309 (5740), 1564-1566 (2005)

PUBMED 16141073

REFERENCE 8 (bases 1 to 1299)

AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

source 1. .1299
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:A630064E02"
/db_xref="taxon:10090"
/clone="A630064E02"
/tissue_type="thymus"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="3 days neonate"

misc_feature 1. .1299
/note="interleukin 12a (MGD|MGI:96539 GB|NM_008351, evidence: BLASTN, 100%, match=776)
putative"

ORIGIN

Query Match 4.1%; Score 27; DB 6; Length 1299;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        388 ATCTATGAGGACTTGAAGATGTACCAG 414
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Db        521 ATCTATGAGGACTTGAAGATGTACCAG 547
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RESULT 24
DA505380
LOCUS DA505380 508 bp mRNA linear EST 05-NOV-2005
DEFINITION DA505380 FCBBF3 Homo sapiens cDNA clone FCBBF3020869 5', mRNA sequence.
ACCESSION DA505380
VERSION DA505380.1 GI:80794577
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 508)

AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H., Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N., Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M., Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.

TITLE Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes

```
  JOURNAL   Genome Res. 16 (1), 55-65 (2006)
   PUBMED   16344560
COMMENT     Contact: Takao Isogai
            FLJ Project (HRI Team)
            Helix Research Institute
            2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: flj-cdna@nifty.com
            NEDO human cDNA project (New Energy and Industrial Technology
            Developmental Organization, Japan); cDNA library construction:
            Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
            Research Association for Biotechnology (RAB) and Biotechnology
            Center, National Institute of Technology and Evaluation; 3'-end one
            pass sequencing: RAB.
FEATURES             Location/Qualifiers
     source          1. .508
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="FCBBF3020869"
                     /tissue_type="brain"
                     /dev_stage="fetal"
                     /clone_lib="FCBBF3"
                     /note="Vector: pME18SFL3"
ORIGIN

  Query Match             3.6%;  Score 24;  DB 9;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 0.46;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         54 CCTGGACCACCTCAGTTTGGCCAG 77
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Db        371 CCTGGACCACCTCAGTTTGGCCAG 394


RESULT 25
BP261459
LOCUS       BP261459                 571 bp    mRNA    linear   EST 16-SEP-2004
DEFINITION  BP261459 Sugano cDNA library, small intestine Homo sapiens cDNA
            clone HSI03652, mRNA sequence.
ACCESSION   BP261459
VERSION     BP261459.1  GI:52176690
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 571)
  AUTHORS   Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
            Mizushima-Sugano,J., Nakai,K. and Sugano,S.
  TITLE     Sequence comparison of human and mouse genes reveals a homologous
            block structure in the promoter regions
  JOURNAL   Genome Res. 14 (9), 1711-1718 (2004)
   PUBMED   15342556
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Tel: 81-3-5449-5343
            Fax: 81-3-5449-5416
            Email: ysuzuki@hgc.jp.
FEATURES             Location/Qualifiers
     source          1. .571
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HSI03652"
                     /tissue_type="small intestine"
                     /clone_lib="Sugano cDNA library, small intestine"
ORIGIN

  Query Match             3.6%;  Score 24;  DB 3;  Length 571;
  Best Local Similarity   100.0%;  Pred. No. 0.47;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         54 CCTGGACCACCTCAGTTTGGCCAG 77
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Db        363 CCTGGACCACCTCAGTTTGGCCAG 386


RESULT 26
CT080894
LOCUS       CT080894                 777 bp    DNA     linear   GSS 01-NOV-2005
DEFINITION  Sus scrofa genomic clone PigE-253A7, genomic survey sequence.
ACCESSION   CT080894
VERSION     CT080894.1  GI:78647963
KEYWORDS    GSS.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 777)
  AUTHORS   Humphray,S.J., Plumb,R.W. and Durham,J.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Unpublished
COMMENT     This sequence was generated from the SP6 end of BAC 253A7. 253A7 is
            part of the PigEBAC BAC Library created by Roslin Institute/RFCGR.
            Further details: http://www.sanger.ac.uk/Projects/S_scrofa/.
FEATURES             Location/Qualifiers
     source          1. .777
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                     /db_xref="taxon:9823"
                     /clone="PigE-253A7"
                     /tissue_type="Blood cells"
                     /note="vector pBeloBAC11
                     sex male"
ORIGIN

  Query Match             3.6%;  Score 24;  DB 14;  Length 777;
  Best Local Similarity   100.0%;  Pred. No. 0.49;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         369 GACCCTGTGCCTTAGCAGTATCTA 392
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Db         551 GACCCTGTGCCTTAGCAGTATCTA 574


RESULT 27
BY230958
LOCUS       BY230958                 354 bp    mRNA    linear   EST 10-DEC-2002
DEFINITION  BY230958 RIKEN full-length enriched, adult inner ear Mus musculus
            cDNA clone F930017D02 5', mRNA sequence.
ACCESSION   BY230958
VERSION     BY230958.1  GI:26412068
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 354)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
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Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

PUBMED 12466851

COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Kirk W. Beisel (Boys Town National Research Hospital 555 North 30th Street Omaha,NE 68131 USA) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES Location/Qualifiers
source 1. .354
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="F930017D02"
/tissue_type="inner ear"
/dev_stage="adult"
/clone_lib="RIKEN full-length enriched, adult inner ear"

ORIGIN

Query Match 3.5%; Score 23; DB 4; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        388 ATCTATGAGGACTTGAAGATGTA 410
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Db        332 ATCTATGAGGACTTGAAGATGTA 354
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RESULT 28
AI332701/c
LOCUS AI332701 528 bp mRNA linear EST 13-FEB-1999
DEFINITION qq19a07.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1932948 3' similar to gb:M65291 INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION AI332701
VERSION AI332701.1 GI:4069260
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 528)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1469 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 451.

FEATURES Location/Qualifiers
source 1. .528
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1932948"
/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab_host="DH10B"
/clone_lib="Soares_NhHMPu_S1"
/note="Organ: mixed (see below); Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

ORIGIN

Query Match 3.5%; Score 23; DB 1; Length 528;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        644 TGATGAGCTATCTGAATGCTTCC 666
              ||||||||||||||||||||||||
Db        482 TGATGAGCTATCTGAATGCTTCC 460
```

RESULT 29
BZ261813
LOCUS BZ261813 840 bp DNA linear GSS 15-OCT-2002
DEFINITION CH230-420O11.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone CH230-420O11, genomic survey sequence.
ACCESSION BZ261813
VERSION BZ261813.1 GI:23972184
KEYWORDS GSS.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

```
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 840)
  AUTHORS   Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
            Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D.,
            Riggs,F., de Jong,P. and Fraser,C.M.
  TITLE     Rat BAC End Sequences from Library CHORI-230 MboI segment
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the rat BAC library CHORI-230
            (http://www.chori.org/bacpac/rat230.htm). For BAC library
            availability, please contact Pieter de Jong (pdejong@mail.cho.org).
            Clones may be purchased from BACPAC Resources
            (http://www.chori.org/bacpac/or ering_information.htm). BAC end
            page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
            Plate: 420  row: O  column: 11
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .840
                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /strain="BN/SsNHsd/MCW"
                     /db_xref="taxon:10116"
                     /clone="CH230-420O11"
                     /sex="Female"
                     /cell_type="Brain"
                     /clone_lib="CHORI-230 Segment 2"
                     /note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
                     CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
                     Pieter de Jong"
ORIGIN

  Query Match             3.5%;  Score 23;  DB 11;  Length 840;
  Best Local Similarity   100.0%;  Pred. No. 1.8;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        254 TGGAGGCCTGCTTACCACTGGAA 276
              |||||||||||||||||||||||
Db        377 TGGAGGCCTGCTTACCACTGGAA 399


RESULT 30
CE841948/c
LOCUS       CE841948                588 bp    DNA     linear   GSS 01-OCT-2003
DEFINITION  tigr-gss-dog-17000332674172 Dog Library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION   CE841948
VERSION     CE841948.1  GI:37204217
KEYWORDS    GSS.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 588)
  AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
            Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
            Venter,J.C.
  TITLE     The dog genome: survey sequencing and comparative analysis
  JOURNAL   Science 301 (5641), 1898-1903 (2003)
   PUBMED   14512627
COMMENT     Contact: Kirkness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirknes@tigr.org
            Class: shotgun.
FEATURES             Location/Qualifiers
     source          1. .588
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /strain="Standard Poodle"
                     /db_xref="taxon:9615"
                     /clone_lib="Dog Library"
                     /note="Site_1: BstXI; Libraries were prepared from
                     peripheral blood"
ORIGIN

  Query Match             3.3%;  Score 22;  DB 12;  Length 588;
  Best Local Similarity   100.0%;  Pred. No. 5.9;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        569 ATTTTTATAAAACTAAAATCAA 590
              ||||||||||||||||||||||
Db        166 ATTTTTATAAAACTAAAATCAA 145


RESULT 31
CT100632
LOCUS       CT100632                758 bp    DNA     linear   GSS 01-NOV-2005
DEFINITION  Sus scrofa genomic clone CH242-93N13, genomic survey sequence.
ACCESSION   CT100632
VERSION     CT100632.1  GI:78654237
KEYWORDS    GSS.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 758)
  AUTHORS   Humphray,S.J., Plumb,R.W. and Durham,J.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Unpublished
COMMENT     This sequence was generated from the SP6 end of BAC 93N13. 93N13 is
            part of the CHORI-242 BAC Library created by P. de Jong. Further
            details: http://www.sanger.ac.uk/Projects/S_scrofa/.
FEATURES             Location/Qualifiers
     source          1. .758
                     /organism="Sus scrofa"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9823"
                     /clone="CH242-93N13"
                     /tissue_type="White blood cells"
                     /note="vector pTARBAC1.3_BamHI
                     sex female"
ORIGIN

  Query Match             3.3%;  Score 22;  DB 14;  Length 758;
  Best Local Similarity   100.0%;  Pred. No. 6.2;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        491 CAGCTATTGATGAGCTGTTACA 512
              ||||||||||||||||||||||
Db        351 CAGCTATTGATGAGCTGTTACA 372


RESULT 32
AQ100596
LOCUS       AQ100596                380 bp    DNA     linear   GSS 27-AUG-1998
DEFINITION  HS_3064_B1_F08_MR CIT Approved Human Genomic Sperm Library D Homo
            sapiens genomic clone Plate=3064 Col=15 Row=L, genomic survey
            sequence.
ACCESSION   AQ100596
VERSION     AQ100596.1  GI:3471625
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
```

```
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 380)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
   PUBMED   10449764
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Sequence Tagged Connector
            Plate: 3064  row: L  column: 15
            Class: BAC ends
            High quality sequence stop: 380.
FEATURES             Location/Qualifiers
     source          1. .380
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="Plate=3064 Col=15 Row=L"
                     /sex="male"
                     /clone_lib="CIT Approved Human Genomic Sperm Library D"
                     /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                     E-Coli DH10B"
ORIGIN

  Query Match             3.2%;  Score 21;  DB 11;  Length 380;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        325 ACTAATGGGAGTTGCCTGGCC 345
              |||||||||||||||||||||
Db         42 ACTAATGGGAGTTGCCTGGCC 62


RESULT 33
AQ393691/c
LOCUS       AQ393691                489 bp    DNA     linear   GSS 06-MAR-1999
DEFINITION  CITBI-E1-2544N3.TF CITBI-E1 Homo sapiens genomic clone 2544N3,
            genomic survey sequence.
ACCESSION   AQ393691
VERSION     AQ393691.1  GI:4364714
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 489)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
            Venter,J.C.
  TITLE     Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Other_GSSs: CITBI-E1-2544N3.TR
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are available from Research Genetics (info@resgen.com). BAC
            end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: M13-21
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .489
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="2544N3"
                     /sex="male"
                     /cell_type="sperm"
                     /clone_lib="CITBI-E1"
                     /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
                     CalTech Human BAC Library D"
ORIGIN

  Query Match             3.2%;  Score 21;  DB 11;  Length 489;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        287 ATGAGAGTTGCCTGGCTTCCA 307
              |||||||||||||||||||||
Db        441 ATGAGAGTTGCCTGGCTTCCA 421


RESULT 34
CV068291/c
LOCUS       CV068291                540 bp    mRNA    linear   EST 24-AUG-2004
DEFINITION  Le_mx0_43b06_SP6 Little Skate Multiple Tissues, Normalized
            Leucoraja erinacea cDNA clone Le_mx0_43b06 5' similar to
            emb|CAG02559.1| unnamed protein product - Tetraodon nigroviridis.
            Score = 248 bits (632), Expect = 6e-65, mRNA sequence.
ACCESSION   CV068291
VERSION     CV068291.1  GI:51531455
KEYWORDS    EST.
SOURCE      Leucoraja erinacea (little skate)
  ORGANISM  Leucoraja erinacea
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
            Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
            Rajiformes; Rajidae; Leucoraja.
REFERENCE   1  (bases 1 to 540)
  AUTHORS   Towle,D.W. and Smith,C.M.
  TITLE     Expressed sequence tags in a normalized cDNA library prepared from
            multiple tissues of adult little skate, Leucoraja erinacea
  JOURNAL   Unpublished (2004)
COMMENT     Contact: David W. Towle
            Marine DNA Sequencing and Analysis Center
            Mount Desert Island Biological Laboratory
            Old Bar Harbor Road, Salsbury Cove, ME 04672 USA
            Tel: 207-288-9880 x474
            Fax: 207-288-2130
            Email: dtowle@mdibl.org
            Plate: 43  row: b  column: 06
            Seq primer: SP6
            High quality sequence stop: 501.
FEATURES             Location/Qualifiers
     source          1. .540
                     /organism="Leucoraja erinacea"
                     /mol_type="mRNA"
                     /db_xref="taxon:7782"
                     /clone="Le_mx0_43b06"
                     /tissue_type="Liver, kidney, brain, testis, ovary, gill,
                     heart, spleen, rectal gland"
                     /dev_stage="Adult"
                     /clone_lib="Little Skate Multiple Tissues, Normalized"
                     /note="Vector: pCMV Sport 6.1; Total RNA samples were
                     prepared individually from each tissue, checked for
                     quality, then pooled for construction and normalization of
                     cDNA library by Invitrogen. Plasmids were isolated and
                     inserts end-sequenced by the Marine DNA Sequencing and
                     Analysis Facility at Mount Desert Island Biological
                     Laboratory. Traces were processed for submission to dbEST
                     by trace2dbest software (Parkinson, Anthony and Blaxter,
```

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                    unpublished software)."
ORIGIN

  Query Match             3.2%;  Score 21;  DB 8;  Length 540;
  Best Local Similarity   100.0%;  Pred. No. 21;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         85 CCCACACCCACACCAAGCCCA 105
              |||||||||||||||||||||
Db        528 CCCACACCCACACCAAGCCCA 508


RESULT 35
BU002107
LOCUS       BU002107                679 bp    mRNA    linear   EST 03-OCT-2005
DEFINITION  QGG30D21.yg.ab1 QG_EFGHJ lettuce serriola Lactuca serriola cDNA
            clone QGG30D21, mRNA sequence.
ACCESSION   BU002107
VERSION     BU002107.1  GI:22436502
KEYWORDS    EST.
SOURCE      Lactuca serriola
  ORGANISM  Lactuca serriola
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
            Cichorieae; Lactuca.
REFERENCE   1  (bases 1 to 679)
  AUTHORS   Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
            Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J.,
            Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,
            Lai,Z., Church,S., Jackson,L. and Bradford,K.
  TITLE     Lettuce and Sunflower ESTs from the Compositae Genome Project
            http://compgenomics.ucdavis.edu/
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Alexander Kozik [R.W.Michelmore]
            Department of Vegetable Crops, R.W.Michelmore Lab
            University of California at Davis (UCD)
            Asmundson Hall, UCD, Davis, CA 95616, USA
            Tel: 1-(530)-742-1742
            Fax: 1-(530)-752-9659
            Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
            singleton, see http://cgpdb.ucdavis.edu/ for details.
            Plate: QGG30  row: D  column: 21.
FEATURES             Location/Qualifiers
     source          1. .679
                     /organism="Lactuca serriola"
                     /mol_type="mRNA"
                     /db_xref="taxon:75943"
                     /clone="QGG30D21"
                     /lab_host="E.coli"
                     /clone_lib="QG_EFGHJ lettuce serriola"
                     /note="Vector: pBRcDNASfiAB; The library was constructed
                     from 10 different sources of RNA from a single genotype.
                     Separate cDNAs were generated using primers that
                     incorporated unique 5' and 3' tags to distinguish each
                     source of RNA. cDNAs were then pooled, size-fractionated,
                     directionally cloned into a custom medium-copy vector and
                     transformations made with four size classes to minimize
                     size bias. Details of each source of RNA and library
                     construction can be obtained at http://cgpdb.ucdavis.edu/
                     TAG_TISSUE=flowers pre-fertilized
                     TAG_LIB=QG_EFGHJ lettuce serriola
                     TAG_SEQ=GCTTGACGGG"
ORIGIN

  Query Match             3.2%;  Score 21;  DB 3;  Length 679;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        273 GGAATTAACCATGAATGAGAG 293
              |||||||||||||||||||||
Db          8 GGAATTAACCATGAATGAGAG 28


RESULT 36
AQ631366/c
LOCUS       AQ631366                733 bp    DNA     linear   GSS 17-JUN-1999
DEFINITION  RPCI-11-482B16.TV RPCI-11 Homo sapiens genomic clone
            RPCI-11-482B16, genomic survey sequence.
ACCESSION   AQ631366
VERSION     AQ631366.1  GI:5094001
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 733)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
            Venter,J.C.
  TITLE     Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genet cs (info@resgen.com). BAC end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .733
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="GDB:7684743"
                     /db_xref="taxon:9606"
                     /clone="RPCI-11-482B16"
                     /sex="Male"
                     /cell_type="Lymphocytes"
                     /clone_lib="RPCI-11"
                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     RPCI11 Human Male BAC Library"
ORIGIN

  Query Match             3.2%;  Score 21;  DB 11;  Length 733;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        569 ATTTTTATAAAACTAAAATCA 589
              |||||||||||||||||||||
Db        145 ATTTTTATAAAACTAAAATCA 125


RESULT 37
W29456/c
LOCUS       W29456                  1109 bp    mRNA    linear   EST 11-SEP-1996
DEFINITION  mc03e02.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone
            IMAGE:337850 5' similar to SW:IF4G_RABIT P41110 EUKARYOTIC
            INITIATION FACTOR 4 GAMMA ;, mRNA sequence.
ACCESSION   W29456
VERSION     W29456.1  GI:1309666
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1109)
```

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  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:219250
            Seq primer: ETPrimer
            High quality sequence stop: 285.
FEATURES             Location/Qualifiers
     source          1. .1109
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:337850"
                     /dev_stage="19.5 dpc total fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares mouse p3NMF19.5"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo. RNA was kindly provided by
                     Dr. Minoru Ko (Wayne State University)."
ORIGIN

  Query Match             3.2%;  Score 21;  DB 10;  Length 1109;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         84 CCCCACACCCACACCAAGCCC 104
              |||||||||||||||||||||
Db       1078 CCCCACACCCACACCAAGCCC 1058


RESULT 38
AZ901502/c
LOCUS       AZ901502                229 bp    DNA     linear   GSS 05-MAR-2001
DEFINITION  RPCI-24-154C7.TJ RPCI-24 Mus musculus genomic clone RPCI-24-154C7,
            genomic survey sequence.
ACCESSION   AZ901502
VERSION     AZ901502.1  GI:13220447
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 229)
  AUTHORS   Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
            Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
            Russell,D., de Jong,P. and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-24
  JOURNAL   Unpublished (1999)
COMMENT     Other_GSSs: RPCI-24-154C7.TV
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-24. For BAC
            library availability, please contact Pieter de Jong
            (pdejong@mail.cho.org). Clones may be purchased from BACPAC
            Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
            page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 154  row: C  column: 7
            Seq primer: SP6
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .229
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="RPCI-24-154C7"
                     /sex="Male"
                     /cell_type="Spleen/Brain"
                     /clone_lib="RPCI-24"
                     /note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
                     RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
                     library was  cloned in the pTARBAC1 cloning vector at the
                     BamH1 sites using MboI  partially digested male C57BL/6J
                     DNA."
ORIGIN

  Query Match             3.0%;  Score 20;  DB 11;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         83 TCCCCACACCCACACCAAGC 102
              ||||||||||||||||||||
Db        229 TCCCCACACCCACACCAAGC 210


RESULT 39
AZ891891/c
LOCUS       AZ891891                241 bp    DNA     linear   GSS 05-MAR-2001
DEFINITION  RPCI-24-201J11.TV RPCI-24 Mus musculus genomic clone
            RPCI-24-201J11, genomic survey sequence.
ACCESSION   AZ891891
VERSION     AZ891891.1  GI:13210836
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 241)
  AUTHORS   Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
            Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
            Russell,D., de Jong,P. and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-24
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-24. For BAC
            library availability, please contact Pieter de Jong
            (pdejong@mail.cho.org). Clones may be purchased from BACPAC
            Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
            page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 201  row: J  column: 11
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
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     source          1. .241
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="RPCI-24-201J11"
                     /sex="Male"
                     /cell_type="Spleen/Brain"
                     /clone_lib="RPCI-24"
                     /note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
                     RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
                     library was  cloned in the pTARBAC1 cloning vector at the
                     BamH1 sites using MboI  partially digested male C57BL/6J
                     DNA."
ORIGIN

  Query Match             3.0%;  Score 20;  DB 11;  Length 241;
  Best Local Similarity   100.0%;  Pred. No. 64;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        569 ATTTTTATAAAACTAAAATC 588
              ||||||||||||||||||||
Db         20 ATTTTTATAAAACTAAAATC 1


RESULT 40
BX537236
LOCUS       BX537236                344 bp    DNA     linear   GSS 05-JUN-2003
DEFINITION  INRA porcine BAC library, clone 0849A01 BAC end sequence (Uni M13),
            genomic survey sequence.
ACCESSION   BX537236
VERSION     BX537236.1  GI:31455351
KEYWORDS    GSS; genome survey sequence.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1
  AUTHORS   Rogel-Gaillard,C., Bourgeaux,N., Billault,A., Vaiman,M. and
            Chardon,P.
  TITLE     Construction of a swine BAC library: application to the
            characterization and mapping of porcine type C endoviral elements
  JOURNAL   Cytogenet. Cell Genet. 85 (3-4), 205-211 (1999)
   PUBMED   10449899
REFERENCE   2  (bases 1 to 344)
  AUTHORS   Robic,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JUN-2003) Robic A., INRA, Laboratoire de Genetique
            Cellulaire, chemin de Borde rouge, BP27, Auzeville, 31626, FRANCE
            Phone : 05 61 28 51 15 Fax : 05 61 28 53 08 Email :
            arobic@toulouse.inra.fr
FEATURES             Location/Qualifiers
     source          1. .344
                     /organism="Sus scrofa"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9823"
                     /clone="0849A01"
                     /note="library Rogel gaillard et al 1999, clone 0849A01
                     Clone distribution : AGENAE Resource center. Francois
                     PIUMI, Francois.Piumi@jouy.inra.fr, INRA, CEA
                     Radiobiologie et Etude du genome (LREG), Domaine de
                     Vilvert, 78352, Jouy-en-Josas cedex, FRANCE"
ORIGIN

  Query Match             3.0%;  Score 20;  DB 14;  Length 344;
  Best Local Similarity   100.0%;  Pred. No. 68;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        460 AGGCAGATCTTTCTGGATCA 479
              ||||||||||||||||||||
Db         22 AGGCAGATCTTTCTGGATCA 41


RESULT 41
AL731335/c
LOCUS       AL731335                377 bp    mRNA    linear   EST 18-APR-2002
DEFINITION  AL731335 Danio rerio embryonic inner ear subtracted cDNA Danio
            rerio cDNA clone BN0AA121ZC10 3', mRNA sequence.
ACCESSION   AL731335
VERSION     AL731335.1  GI:20195939
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 377)
  AUTHORS   Coimbra,R., Weil,D., Brottier,P., Blanchard,S., Levi,M.,
            Hardelin,J.P., Weissenbach,J. and Petit,C.
  TITLE     A subtracted cDNA library from the zebrafish (Danio rerio)
            embryonic inner ear
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .377
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="BN0AA121ZC10"
                     /tissue_type="inner ear"
                     /dev_stage="embryonic"
                     /clone_lib="Danio rerio embryonic inner ear subtracted
                     cDNA"
                     /note="subtracted cDNA library"
ORIGIN

  Query Match             3.0%;  Score 20;  DB 1;  Length 377;
  Best Local Similarity   100.0%;  Pred. No. 69;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         31 ACCATCCTGGTCCTGTTAAA 50
              ||||||||||||||||||||
Db        121 ACCATCCTGGTCCTGTTAAA 102


RESULT 42
BE016666/c
LOCUS       BE016666                383 bp    mRNA    linear   EST 30-AUG-2000
DEFINITION  fk67a01.y1 Zebrafish Research Genetics C32 fin Danio rerio cDNA 5',
            mRNA sequence.
ACCESSION   BE016666
VERSION     BE016666.1  GI:8281118
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 383)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
            Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
```

```
            Email: zbrafish@watson.wustl.edu
            cDNA Library Preparation: Ning Wu. cDNA Library Arrayed by:
            Research Genetics. DNA Sequencing by: Washington University Genome
            Sequencing Center Clone distribution: Research Genetics web
            address: http://www.researchgenetics.com/
            Seq primer: T3 ET from Amersham
            High quality sequence stop: 339.
FEATURES              Location/Qualifiers
     source           1. .383
                      /organism="Danio rerio"
                      /mol_type="mRNA"
                      /db_xref="taxon:7955"
                      /tissue_type="Fin"
                      /lab_host="GeneHogs (HS996, a phage-resistant isolate of
                      DH10B)"
                      /clone_lib="Zebrafish Research Genetics C32 fin"
                      /note="Vector: pT7T3D-PacI; Site_1: EcoRI; Site_2: NotI;
                      1st strand cDNA was prepared from zebrafish(C32) fin, and
                      was then primed with a Not I - oligo(dT) primer.
                      Double-stranded cDNA was ligated to Eco RI adaptors
                      (Pharmacia), digested with Not I and cloned into the Not I
                      and Eco RI sites of the modified pT7T3 vector.  Library is
                      non-normalized. Library was constructed by Ning Wu. NOTE:
                      This clone is available royalty-free through LLNL; contact
                      the IMAGE Consortium (info.llnl.gov)for further
                      information"
ORIGIN

  Query Match              3.0%;  Score 20;  DB 7;  Length 383;
  Best Local Similarity   100.0%;  Pred. No. 69;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         31 ACCATCCTGGTCCTGTTAAA 50
              ||||||||||||||||||||
Db        218 ACCATCCTGGTCCTGTTAAA 199


RESULT 43
BY394944
LOCUS       BY394944                389 bp    mRNA    linear   EST 12-DEC-2002
DEFINITION  BY394944 RIKEN full-length enriched, CRL-1722 L5178Y-R Mus musculus
            cDNA clone I730003H17 3', mRNA sequence.
ACCESSION   BY394944
VERSION     BY394944.1  GI:26624432
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 389)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
            Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
            Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
            Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
            Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
            Hayashizaki,Y. Direct Submission
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
             cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES              Location/Qualifiers
     source           1. .389
                      /organism="Mus musculus"
                      /mol_type="mRNA"
                      /strain="DBA/2"
                      /db_xref="taxon:10090"
                      /clone="I730003H17"
                      /cell_line="CRL-1722 L5178Y-R"
                      /clone_lib="RIKEN full-length enriched, CRL-1722 L5178Y-R"
ORIGIN

  Query Match              3.0%;  Score 20;  DB 4;  Length 389;
  Best Local Similarity   100.0%;  Pred. No. 69;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         84 CCCCACACCCACACCAAGCC 103
              ||||||||||||||||||||
Db        179 CCCCACACCCACACCAAGCC 198


RESULT 44
BW935403
LOCUS       BW935403                452 bp    mRNA    linear   EST 24-DEC-2005
DEFINITION  BW935403 Amphioxus Branchiostoma floridae unpublished cDNA library,
            neurula whole animal Branchiostoma floridae cDNA clone bfne121g22
            3', mRNA sequence.
ACCESSION   BW935403
VERSION     BW935403.1  GI:66569299
KEYWORDS    EST.
SOURCE      Branchiostoma floridae (Florida lancelet)
  ORGANISM  Branchiostoma floridae
            Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
```

```
            Branchiostoma.
REFERENCE   1  (bases 1 to 452)
  AUTHORS   Yu,J., Holland,L.Z., Shin-i,T., Kohara,Y., Satou,Y. and Satoh,N.
  TITLE     Expressed genes in Branchiostoma floridae
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp
            If you want to have a cDNA clone for this EST or if you have any
            questions, please send an e-mail to Nori Satoh
            (satoh@ascidian.zool.kyoto-u.ac.jp) and its cc to Yutaka Satou
            (yutaka@ascidian.zool.kyoto-u.ac.jp).
FEATURES             Location/Qualifiers
     source          1. .452
                     /organism="Branchiostoma floridae"
                     /mol_type="mRNA"
                     /db_xref="taxon:7739"
                     /clone="bfne121g22"
                     /tissue_type="whole animal"
                     /dev_stage="neurula"
                     /clone_lib="Amphioxus Branchiostoma floridae unpublished
                     cDNA library, neurula whole animal"
ORIGIN

  Query Match             3.0%;  Score 20;  DB 4;  Length 452;
  Best Local Similarity   100.0%;  Pred. No. 71;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        218 ATCATGAAGATATCACAAAA 237
              ||||||||||||||||||||
Db        375 ATCATGAAGATATCACAAAA 394


RESULT 45
BE557755/c
LOCUS       BE557755                467 bp    mRNA    linear   EST 30-AUG-2000
DEFINITION  fl10b12.y1 Zebrafish Research Genetics C32 fin Danio rerio cDNA 5',
            mRNA sequence.
ACCESSION   BE557755
VERSION     BE557755.1  GI:9822245
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 467)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
            Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library Preparation: Ning Wu. cDNA Library Arrayed by:
            Research Genetics. DNA Sequencing by: Washington University Genome
            Sequencing Center Clone distribution: Research Genetics web
            address: http://www.researchgenetics.com/
            Seq primer: T3 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .467
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /tissue_type="Fin"
                     /lab_host="GeneHogs (HS996, a phage-resistant isolate of
                     DH10B)"
                     /clone_lib="Zebrafish Research Genetics C32 fin"
                     /note="Vector: pT7T3D-PacI; Site_1: EcoRI; Site_2: NotI;
                     1st strand cDNA was prepared from zebrafish(C32) fin, and
                     was then primed with a Not I - oligo(dT) primer.
                     Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector.  Library is
                     non-normalized. Library was constructed by Ning Wu. NOTE:
                     This clone is available royalty-free through LLNL; contact
                     the IMAGE Consortium (info.llnl.gov)for further
                     information"
ORIGIN

  Query Match             3.0%;  Score 20;  DB 7;  Length 467;
  Best Local Similarity   100.0%;  Pred. No. 72;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         31 ACCATCCTGGTCCTGTTAAA 50
              ||||||||||||||||||||
Db        208 ACCATCCTGGTCCTGTTAAA 189


RESULT 46
AQ478437/c
LOCUS       AQ478437                516 bp    DNA     linear   GSS 23-APR-1999
DEFINITION  RPCI-11-248M18.TJ RPCI-11 Homo sapiens genomic clone
            RPCI-11-248M18, genomic survey sequence.
ACCESSION   AQ478437
VERSION     AQ478437.1  GI:4660556
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 516)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
            Venter,J.C.
  TITLE     Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genet cs (info@resgen.com). BAC end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: SP6
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .516
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="GDB:7595153"
                     /db_xref="taxon:9606"
                     /clone="RPCI-11-248M18"
                     /sex="Male"
                     /cell_type="Lymphocytes"
                     /clone_lib="RPCI-11"
                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     RPCI11 Human Male BAC Library"
```

```
ORIGIN

  Query Match             3.0%;  Score 20;  DB 11;  Length 516;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        160 ACGCTTCAGAAGGCCAGACA 179
              ||||||||||||||||||||
Db         57 ACGCTTCAGAAGGCCAGACA 38


RESULT 47
BQ481093/c
LOCUS       BQ481093                551 bp    mRNA    linear   EST 03-JUN-2002
DEFINITION  faa75b02.x1 Gong zebrafish testis Danio rerio cDNA clone
            IMAGE:5899347 3', mRNA sequence.
ACCESSION   BQ481093
VERSION     BQ481093.1  GI:21317060
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 551)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
            Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            The library was constructed by Dr. Z. Gong. DNA Sequencing by:
            Washington University Genome Sequencing Center St. Louis. Please
            contact Zhiyuan Gong for further information on this library
            (National University of Singapore, Department of Biological
            Sciences, Lower Kent Ridge Road, Singapore 119260).
            Seq primer: T7 from Gibco
            High quality sequence stop: 471.
FEATURES             Location/Qualifiers
     source          1. .551
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:5899347"
                     /sex="male"
                     /dev_stage="4-5 month"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="Gong zebrafish testis"
                     /note="Organ: testis (pooled); Vector: pBluescript SK-;
                     Site_1: XhoI; Site_2: EcoRI; Poly A+ RNA was isolatd from
                     the testes of 31 male adult zebrafish (4-5 month  old).
                     cDNAs were made using oligo-dT primers and inserted into
                     lambda ZAP II vector  (Stratagene) by Dr. Z. Gong, in vivo
                     mass-excised to pBluescript SK- following the  Washington
                     University protocol
                     (http://genome.wustl.edu/est/lambda_protocol.shtml).
                     Please contact Zhiyuan Gong for further information on
                     this library (National University  of Singapore,
                     Department of Biological Sciences, Lower Kent Ridge Road,
                     Singapore 119260)."
ORIGIN

  Query Match             3.0%;  Score 20;  DB 3;  Length 551;
  Best Local Similarity   100.0%;  Pred. No. 74;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         31 ACCATCCTGGTCCTGTTAAA 50
              ||||||||||||||||||||
Db        316 ACCATCCTGGTCCTGTTAAA 297


RESULT 48
AZ855572/c
LOCUS       AZ855572                574 bp    DNA     linear   GSS 21-FEB-2001
DEFINITION  2M0159K08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0159K08 R, genomic survey sequence.
ACCESSION   AZ855572
VERSION     AZ855572.1  GI:13045870
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 574)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0159  row: K  column: 08
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 574.
FEATURES             Location/Qualifiers
     source          1. .574
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0159K08"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             3.0%;  Score 20;  DB 11;  Length 574;
  Best Local Similarity   100.0%;  Pred. No. 74;
```

```
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        428 CCATGAATGCAAAGCTGTTA 447
              ||||||||||||||||||||
Db        232 CCATGAATGCAAAGCTGTTA 213


RESULT 49
AL731281
LOCUS       AL731281                598 bp    mRNA    linear   EST 18-APR-2002
DEFINITION  AL731281 Danio rerio embryonic inner ear subtracted cDNA Danio
            rerio cDNA clone BN0AA121ZC10 5', mRNA sequence.
ACCESSION   AL731281
VERSION     AL731281.1  GI:20195885
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 598)
  AUTHORS   Coimbra,R., Weil,D., Brottier,P., Blanchard,S., Levi,M.,
            Hardelin,J.P., Weissenbach,J. and Petit,C.
  TITLE     A subtracted cDNA library from the zebrafish (Danio rerio)
            embryonic inner ear
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .598
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="BN0AA121ZC10"
                     /tissue_type="inner ear"
                     /dev_stage="embryonic"
                     /clone_lib="Danio rerio embryonic inner ear subtracted
                     cDNA"
                     /note="subtracted cDNA library"
ORIGIN

  Query Match             3.0%;  Score 20;  DB 1;  Length 598;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         31 ACCATCCTGGTCCTGTTAAA 50
              ||||||||||||||||||||
Db        479 ACCATCCTGGTCCTGTTAAA 498


RESULT 50
CNS01PJI
LOCUS       CNS01PJI                603 bp    DNA     linear   GSS 14-JUN-2001
DEFINITION  Anopheles gambiae GSS SP6 end of clone 28L22 of NotreDame1 library
            from strain PEST of Anopheles gambiae (African malaria mosquito),
            genomic survey sequence.
ACCESSION   AL154894
VERSION     AL154894.1  GI:7015813
KEYWORDS    GSS.
SOURCE      Anopheles gambiae (African malaria mosquito)
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Culicidae; Anophelinae; Anopheles.
REFERENCE   1  (bases 1 to 603)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
REFERENCE   2  (bases 1 to 603)
  AUTHORS   Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.
            Roux, Paris 75015, France
COMMENT     This clone is from an A. gambiae BAC library provided by F.H.
            Collins and sequenced by Genoscope in collaboration with the
            Laboratory of Biochem. and Biol. Molec. of Insects, Institut
            Pasteur.
FEATURES             Location/Qualifiers
     source          1. .603
                     /organism="Anopheles gambiae"
                     /mol_type="genomic DNA"
                     /strain="PEST"
                     /db_xref="taxon:7165"
                     /clone="28L22"
                     /clone_lib="NotreDame1"
                     /note="end : SP6"
ORIGIN

  Query Match             3.0%;  Score 20;  DB 14;  Length 603;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        301 GCTTCCAGAGAGATCTCTCT 320
              ||||||||||||||||||||
Db        496 GCTTCCAGAGAGATCTCTCT 515


RESULT 51
W63576/c
LOCUS       W63576                  604 bp    mRNA    linear   EST 11-OCT-1996
DEFINITION  zc55h09.r1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA
            clone IMAGE:326273 5', mRNA sequence.
ACCESSION   W63576
VERSION     W63576.1  GI:1371149
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 604)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 566   Std Error: 0.00
            Seq primer: ETPrimer
            High quality sequence stop: 400.
FEATURES             Location/Qualifiers
     source          1. .604
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:1257786"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:326273"
                     /tissue_type="senescent fibroblast"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares_senescent_fibroblasts_NbHSF"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco
                     RI; 1st strand cDNA was primed with a Not I - oligo(dT)
```

primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCATTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 3.0%; Score 20; DB 10; Length 604;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        476 ATCAAAACATGCTGACAGCT 495
              ||||||||||||||||||||
Db        357 ATCAAAACATGCTGACAGCT 338
```

RESULT 52
AW107212
LOCUS AW107212 610 bp mRNA linear EST 20-OCT-1999
DEFINITION um12c12.x1 Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:2182870 3', mRNA sequence.
ACCESSION AW107212
VERSION AW107212.1 GI:6078012
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 610)
AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
TITLE The WashU-NCI Mouse EST Project 1999
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: um12c12.y1
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1004538
Seq primer: custom primer used
High quality sequence stop: 516.
FEATURES Location/Qualifiers
source 1. .610
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:2182870"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Sugano mouse kidney mkia"
/note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."

ORIGIN

Query Match 3.0%; Score 20; DB 7; Length 610;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         83 TCCCCACACCCACACCAAGC 102
              ||||||||||||||||||||
Db        488 TCCCCACACCCACACCAAGC 507
```

RESULT 53
DU222360
LOCUS DU222360 639 bp DNA linear GSS 04-OCT-2005
DEFINITION 1098574031072 CHORI-243 Ovis aries genomic clone CH243-470K10, genomic survey sequence.
ACCESSION DU222360
VERSION DU222360.1 GI:76938462
KEYWORDS GSS.
SOURCE Ovis aries (sheep)
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.
REFERENCE 1 (bases 1 to 639)
AUTHORS Kirkness,E., Shetty,J., de Jong,P., McEwan,J.C., Oddy,H. and Cockett,N.
TITLE Ovine BAC End Sequences from Library CHORI-243
JOURNAL Unpublished (2004)
COMMENT Other_GSSs: 1098583010336
Contact: Ewen Kirkness
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-795-7536
Email: ekirknes@tigr.org
Sequences generated at the J. Craig Venter Institute Joint Technology Center (JCVIJTC; http://www.venterinstitute.org/).
Original Trace: 1098574031072 Trace TI: gnl|ti|918749212
Insert Length: 184000 Std Error: 0.00 row: K column: 10
Seq primer: T7
Class: BAC ends.
FEATURES Location/Qualifiers
source 1. .639
/organism="Ovis aries"
/mol_type="genomic DNA"
/strain="Texel breed"
/db_xref="taxon:9940"
/clone="CH243-470K10"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-243"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI; The CHORI-243 sheep (M) (Ovis aries) BAC library produced by Pieter de Jong's lab at CHORI http://bacpac.chori.org/library.php?id=162"

ORIGIN

Query Match 3.0%; Score 20; DB 13; Length 639;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         10 CCGCGTGGCCTCCTCCTTGT 29
              ||||||||||||||||||||
Db        105 CCGCGTGGCCTCCTCCTTGT 124
```

RESULT 54
AL729822
LOCUS AL729822 644 bp mRNA linear EST 18-APR-2002
DEFINITION AL729822 Danio rerio embryonic inner ear subtracted cDNA Danio

```
            rerio cDNA clone BN0AA110ZD11 3', mRNA sequence.
ACCESSION   AL729822
VERSION     AL729822.1  GI:20194426
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 644)
  AUTHORS   Coimbra,R., Weil,D., Brottier,P., Blanchard,S., Levi,M.,
            Hardelin,J.P., Weissenbach,J. and Petit,C.
  TITLE     A subtracted cDNA library from the zebrafish (Danio rerio)
            embryonic inner ear
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .644
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="BN0AA110ZD11"
                     /tissue_type="inner ear"
                     /dev_stage="embryonic"
                     /clone_lib="Danio rerio embryonic inner ear subtracted
                     cDNA"
                     /note="subtracted cDNA library"
ORIGIN

  Query Match             3.0%;  Score 20;  DB 1;  Length 644;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         31 ACCATCCTGGTCCTGTTAAA 50
              ||||||||||||||||||||
Db        476 ACCATCCTGGTCCTGTTAAA 495


RESULT 55
AL729917/c
LOCUS       AL729917                647 bp    mRNA    linear   EST 18-APR-2002
DEFINITION  AL729917 Danio rerio embryonic inner ear subtracted cDNA Danio
            rerio cDNA clone BN0AA110ZD11 5', mRNA sequence.
ACCESSION   AL729917
VERSION     AL729917.1  GI:20194521
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 647)
  AUTHORS   Coimbra,R., Weil,D., Brottier,P., Blanchard,S., Levi,M.,
            Hardelin,J.P., Weissenbach,J. and Petit,C.
  TITLE     A subtracted cDNA library from the zebrafish (Danio rerio)
            embryonic inner ear
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .647
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="BN0AA110ZD11"
                     /tissue_type="inner ear"
                     /dev_stage="embryonic"
                     /clone_lib="Danio rerio embryonic inner ear subtracted
                     cDNA"
                     /note="subtracted cDNA library"
ORIGIN

  Query Match             3.0%;  Score 20;  DB 1;  Length 647;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         31 ACCATCCTGGTCCTGTTAAA 50
              ||||||||||||||||||||
Db        521 ACCATCCTGGTCCTGTTAAA 502


RESULT 56
DN901552/c
LOCUS       DN901552                674 bp    mRNA    linear   EST 25-APR-2005
DEFINITION  naq21d09.y1 Zebrafish retina. Unnormalized (naq) Danio rerio cDNA
            clone naq21d09 5', mRNA sequence.
ACCESSION   DN901552
VERSION     DN901552.1  GI:62886315
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 674)
  AUTHORS   Wistow,G.
  TITLE     NEIBank analysis of Zebrafish retina
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Wistow G
            Section on Molecular Structure and Function
            National Eye Institute
            6/331, NIH, Bethesda, MD 20892-2740, USA
            Tel: 301 402 3452
            Fax: 301 496 0078
            Email: graeme@helix.nih.gov
            Plate: 21  row: d  column: 09
            Seq primer: Universal M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .674
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="naq21d09"
                     /tissue_type="Retina"
                     /dev_stage="Adult"
                     /lab_host="EMDH10B"
                     /clone_lib="Zebrafish retina. Unnormalized (naq)"
                     /note="Organ: Eye; Vector: pCMVSport6; RNA was extracted
                     from Zebrafish retina tissue. A directionally cloned cDNA
                     library in the pCMVSPORT6 vector (Invitrogen) was
                     constructed at Bioserve Biotechnology (Laurel MD)
                     essentially following the protocols of the SuperScript
                     Plasmid System, full details of which are contained in the
                     manufacturer's Instruction manual
                     (http://www.lifetech.com/). First strand synthesis was
                     carried out using a Not I primer-adapter
                     [5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)15-3']. cDNA was
                     cloned in Not I/Sal I sites. EST analysis was performed at
                     the NIH Intramural Sequencing Center (NISC). Analyzed data
                     available through http://neibank.nei.nih.gov."
ORIGIN

  Query Match             3.0%;  Score 20;  DB 9;  Length 674;
  Best Local Similarity   100.0%;  Pred. No. 77;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         31 ACCATCCTGGTCCTGTTAAA 50
              ||||||||||||||||||||
Db        337 ACCATCCTGGTCCTGTTAAA 318
```

```
RESULT 57
BH373165/c
LOCUS       BH373165                691 bp    DNA     linear   GSS 10-DEC-2001
DEFINITION  AG-ND-159L10.TR ND-TAM Anopheles gambiae genomic clone
            AG-ND-159L10, genomic survey sequence.
ACCESSION   BH373165
VERSION     BH373165.1  GI:17319307
KEYWORDS    GSS.
SOURCE      Anopheles gambiae (African malaria mosquito)
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Culicidae; Anophelinae; Anopheles.
REFERENCE   1  (bases 1 to 691)
  AUTHORS   Hong,Y.S., Hogan,J.R., Wang,X., Sarkar,A., Sim,C., Loftus,B.J.,
            Ren,C., Huff,E.R., Carlile,J.L., Black,K., Zhang,H.-B.,
            Gardner,M.J. and Collins,F.H.
  TITLE     Construction of a BAC library and generation of BAC end
            sequence-tagged connectors for genome sequencing of the African
            malaria mosquito Anopheles gambiae
  JOURNAL   Mol. Genet. Genomics 268 (6), 720-728 (2003)
   PUBMED   12655398
COMMENT     Other_GSSs: AG-ND-159L10.TF
            Contact: Brendan J Loftus
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0208
            Fax: 301 838 3543
            Email: bjloftus@tigr.org
            This clone is from an A. gambiae BAC library (ND-TAM) provided by
            F.H. Collins and sequenced by The Institute for Genomic Research
            (TIGR). The BAC library was generated from A. gambiae PEST strain
            DNA. All DNA was extracted from newly hatched first instar larvae
            to minimize the inclusion of DNA from microorganisms that inhabit
            the gut. The DNA is derived from mixed sexes of larvae. The BAC
            library was constructed at Texas A&M Universty BAC Center
            University, College Station, Texas 77843-2123, USA using a HindIII
            partial digest.
            Seq primer: M13 Rev
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .691
                     /organism="Anopheles gambiae"
                     /mol_type="genomic DNA"
                     /strain="PEST"
                     /db_xref="taxon:7165"
                     /clone="AG-ND-159L10"
                     /clone_lib="ND-TAM"
                     /note="Vector: pECBAC1; Site_1: HindIII"
ORIGIN

  Query Match             3.0%;  Score 20;  DB 11;  Length 691;
  Best Local Similarity   100.0%;  Pred. No. 77;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        435 TGCAAAGCTGTTAATGGATC 454
              ||||||||||||||||||||
Db        384 TGCAAAGCTGTTAATGGATC 365


RESULT 58
BW754129
LOCUS       BW754129                724 bp    mRNA    linear   EST 22-OCT-2005
DEFINITION  BW754129 Amphioxus Branchiostoma floridae unpublished cDNA library,
            egg whole animal Branchiostoma floridae cDNA clone bfeg020c16 3',
            mRNA sequence.
ACCESSION   BW754129
VERSION     BW754129.1  GI:66340777
KEYWORDS    EST.
SOURCE      Branchiostoma floridae (Florida lancelet)
  ORGANISM  Branchiostoma floridae
            Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
            Branchiostoma.
REFERENCE   1  (bases 1 to 724)
  AUTHORS   Yu,J., Holland,L.Z., Shin-i,T., Kohara,Y., Satou,Y. and Satoh,N.
  TITLE     Expressed genes in Branchiostoma floridae
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp
            If you want to have a cDNA clone for this EST or if you have any
            questions, please send an e-mail to Nori Satoh
            (satoh@ascidian.zool.kyoto-u.ac.jp) and its cc to Yutaka Satou
            (yutaka@ascidian.zool.kyoto-u.ac.jp).
FEATURES             Location/Qualifiers
     source          1. .724
                     /organism="Branchiostoma floridae"
                     /mol_type="mRNA"
                     /db_xref="taxon:7739"
                     /clone="bfeg020c16"
                     /tissue_type="whole animal"
                     /dev_stage="egg"
                     /clone_lib="Amphioxus Branchiostoma floridae unpublished
                     cDNA library, egg whole animal"
ORIGIN

  Query Match             3.0%;  Score 20;  DB 4;  Length 724;
  Best Local Similarity   100.0%;  Pred. No. 78;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        218 ATCATGAAGATATCACAAAA 237
              ||||||||||||||||||||
Db        366 ATCATGAAGATATCACAAAA 385


RESULT 59
BZ028162/c
LOCUS       BZ028162                734 bp    DNA     linear   GSS 08-OCT-2002
DEFINITION  oeg78e09.g1 B.oleracea002 Brassica oleracea genomic, genomic survey
            sequence.
ACCESSION   BZ028162
VERSION     BZ028162.1  GI:23591436
KEYWORDS    GSS.
SOURCE      Brassica oleracea
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 734)
  AUTHORS   Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
            Nash,W., Rabinowicz,P.D. and Wilson,R.K.
  TITLE     Whole genome shotgun reads from Brassica oleracea
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Richard K. Wilson
            Genome Sequencing Center
            Washington University School of Medicine
            Email: submissions@watson.wustl.edu
            Plate: oeg78  row: e  column: 09
            Seq primer: -28RPpOT reverse
            Class: shotgun
            High quality sequence start: 8
            High quality sequence stop: 551.
FEATURES             Location/Qualifiers
     source          1. .734
                     /organism="Brassica oleracea"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:3712"
                     /clone_lib="B.oleracea002"
                     /note="Vector: pOTw13; Whole genome shotgun library from
                     flowering buds. DNA was purified  from a crude nuclear
                     prep using Brassica oleracea TO1000DH3 buds  provided by
```

Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."
ORIGIN

Query Match 3.0%; Score 20; DB 11; Length 734;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 569 ATTTTTATAAAACTAAAATC 588
||||||||||||||||||||
Db 722 ATTTTTATAAAACTAAAATC 703

RESULT 60
DT077555/c
LOCUS DT077555 771 bp mRNA linear EST 11-AUG-2005
DEFINITION AGENCOURT_56120360 NIH_ZGC_7 Danio rerio cDNA clone IMAGE:7996947 5', mRNA sequence.
ACCESSION DT077555
VERSION DT077555.1 GI:72376945
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 771)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Len Zon, Harvard
cDNA Library Preparation: Open Biosystems
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM17154 row: h column: 01
High quality sequence start: 329
High quality sequence stop: 512.
FEATURES Location/Qualifiers
source 1. .771
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:7996947"
/tissue_type="whole body"
/lab_host="DH10B"
/clone_lib="NIH_ZGC_7"
/note="Vector: pExpress1; Site_1: NotI; Site_2: EcoRV; Bulk tissue was collected from a whole adult individual from the Tuebingen strain. 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was cloned into the Not I and EcoRV sites of pExpress-1. Library was size-selected for >1 kb fragments and normalized. A non-normalized version of this library is also available (NIH_ZGC_10). Library was constructed by Open Biosystems (Huntsville, AL)"
ORIGIN

Query Match 3.0%; Score 20; DB 10; Length 771;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 ACCATCCTGGTCCTGTTAAA 50
||||||||||||||||||||
Db 341 ACCATCCTGGTCCTGTTAAA 322

RESULT 61
CD357085/c
LOCUS CD357085 822 bp mRNA linear EST 29-MAY-2003
DEFINITION AGENCOURT_14284510 NIH_MGC_187 Homo sapiens cDNA clone IMAGE:30402141 5', mRNA sequence.
ACCESSION CD357085
VERSION CD357085.1 GI:31128496
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 822)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM183 row: p column: 22
High quality sequence stop: 252.
FEATURES Location/Qualifiers
source 1. .822
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30402141"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_187"
/note="Organ: blood vessels - aorta, basilar and artery; Vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc); Site_2: SfiI (ggccgcctcggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
ORIGIN

Query Match 3.0%; Score 20; DB 5; Length 822;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 237 AGATAAAACCAGCACAGTGG 256
||||||||||||||||||||
Db 130 AGATAAAACCAGCACAGTGG 111

RESULT 62
AQ574005
LOCUS AQ574005 855 bp DNA linear GSS 02-JUN-1999
DEFINITION nbxb0083O17f CUGI Rice BAC Library Oryza sativa (japonica cultivar-group) genomic clone nbxb0083O17f, genomic survey sequence.
ACCESSION AQ574005
VERSION AQ574005.1 GI:4973806
KEYWORDS GSS.

```
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 855)
  AUTHORS   Wing,R.A. and Dean,R.A.
  TITLE     A BAC End Sequencing Framework to Sequence the Rice Genome
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Seq primer: TAATACGACTCACTATAGGG
            Class: BAC ends
            High quality sequence stop: 408.
FEATURES             Location/Qualifiers
     source          1. .855
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="genomic DNA"
                     /cultivar="japonica"
                     /cultivar="Nipponbare"
                     /db_xref="taxon:39947"
                     /clone="nbxb0083O17f"
                     /tissue_type="Leaf"
                     /lab_host="E. coli DH10B"
                     /clone_lib="CUGI Rice BAC Library"
                     /note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                     HindIII; Rice is one of two most popular grains in the
                     world. Half of the world  population especially those
                     inhabiting highly populated areas of the  humid tropics
                     and subtropics, rely on rice as their primary source of
                     carbohydrate. Monocotyledonous rice is a diploid plant
                     (2n=24) with a  haploid genome equivalent of 431 Mbp
                     (Arumuganathan and Earle, 1991).  The relatively small
                     genome of rice, three times larger than that of
                     Arabidopsis, makes it suitable for genomic studies. In
                     order to  facilitate positional cloning, physical mapping
                     and genome sequencing  of rice, we have constructed a BAC
                     library from Oryza sativa, Nipponbare  variety. The
                     library contains 36,864 clones with an average insert size
                     of 128.5 Kb providing 10.9 haploid genome equivalents. The
                     deep  coverage allows the isolation a particular sequence
                     with a probability  of 99.9 %. Two high density filters,
                     each containing 18,432 clones  (doubly spotted), represent
                     the whole library for colony screening."
ORIGIN

  Query Match             3.0%;  Score 20;  DB 11;  Length 855;
  Best Local Similarity   100.0%;  Pred. No. 80;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        563 AACCGGATTTTTATAAAACT 582
              ||||||||||||||||||||
Db        760 AACCGGATTTTTATAAAACT 779


RESULT 63
CL868149/c
LOCUS       CL868149                875 bp    DNA     linear   GSS 26-AUG-2004
DEFINITION  Gma_01_C05_T3 Soybean Genome Shotgun Sequences Glycine max genomic,
            genomic survey sequence.
ACCESSION   CL868149
VERSION     CL868149.1  GI:51562374
KEYWORDS    GSS.
SOURCE      Glycine max (soybean)
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 875)
  AUTHORS   Jackson,S.A., Walling,J.G. and SanMiguel,P.M.
  TITLE     Molecular and cytogenetic characterization of the heterochromatic,
            gene-poor centric regions of chromosomes of Glycine max L. Merr
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Scott A. Jackson
            Jackson Laboratory
            Purdue University
            915 W. State St., West Lafayette, IN 47907, USA
            Tel: 7654963621
            Fax: 7654967255
            Email: sjackson@purdue.edu
            Plate: 01  row: C  column: 05
            Seq primer: T3
            Class: shotgun
            High quality sequence stop: 875.
FEATURES             Location/Qualifiers
     source          1. .875
                     /organism="Glycine max"
                     /mol_type="genomic DNA"
                     /cultivar="Williams 82"
                     /db_xref="taxon:3847"
                     /sex="hermaphrodite"
                     /tissue_type="Leaf"
                     /dev_stage="seedling"
                     /clone_lib="Soybean Genome Shotgun Sequences"
                     /note="Organ: Leaf; Vector: Invitrogen ToPo vector;
                     Approximately 3-kb randomly sheared inserts"
ORIGIN

  Query Match             3.0%;  Score 20;  DB 13;  Length 875;
  Best Local Similarity   100.0%;  Pred. No. 80;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        570 TTTTTATAAAACTAAAATCA 589
              ||||||||||||||||||||
Db        770 TTTTTATAAAACTAAAATCA 751


RESULT 64
CF242845
LOCUS       CF242845                912 bp    mRNA    linear   EST 05-AUG-2003
DEFINITION  AGENCOURT_15112273 NIH_MGC_192 Homo sapiens cDNA clone
            IMAGE:30512253 5', mRNA sequence.
ACCESSION   CF242845
VERSION     CF242845.1  GI:33446057
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 912)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Agencourt
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM572  row: d  column: 22
            High quality sequence stop: 705.
FEATURES             Location/Qualifiers
     source          1. .912
```

```
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:30512253"
                     /tissue_type="Brain glioblastoma"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_192"
                     /note="Vector: pExpress1; Site_1: SmaI; Site_2: NotI; The
                     library was constructed by reverse transcription of 1 ug
                     mRNA using the oligo dT primer GCGGCCGCCC(T)20 and an
                     RNaseH + MMLV reverse transcriptase. Second strand
                     synthesis was carried out by standard methods. The cDNA
                     was size selected by agarose gel for > 1.2 kb, digested
                     with Not I and directionally cloned into the vector
                     Express-1 at the SmaI/NotI sites. DNA from the primary
                     library was used for in vitro transcription from the T7
                     promoter to produce biotinylated RNA transcripts. These
                     biotinylated transcripts, along with blocking oligos to
                     the poly-A, multiple cloning site and primer regions, were
                     hybridized with single stranded circles produced by
                     phagmeid production from the primary library to a Cot
                     value of 10-20. Strepavidin/phenol extraction was utilized
                     to remove DNA:RNA hybrids leaving un-hybridized single
                     stranded circles which were repaired by primer extension
                     and transformed back into E. coli resulting in the
                     normalized library. Average insert size 2.0 kb. 3'
                     linker/adaptor sequence GCGGCCGCCC(T)20. This libary was
                     constructed by Agencourt Bioscience."
ORIGIN

  Query Match             3.0%;  Score 20;  DB 5;  Length 912;
  Best Local Similarity   100.0%;  Pred. No. 81;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         68 GTTTGGCCAGGAACCTCCCC 87
              ||||||||||||||||||||
Db        802 GTTTGGCCAGGAACCTCCCC 821


RESULT 65
BF530961/c
LOCUS       BF530961                920 bp    mRNA    linear   EST 11-DEC-2000
DEFINITION  602072472F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4215425
            5', mRNA sequence.
ACCESSION   BF530961
VERSION     BF530961.1  GI:11618324
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 920)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9790  row: p  column: 18
            High quality sequence stop: 652.
FEATURES             Location/Qualifiers
     source          1. .920
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4215425"
                     /tissue_type="anaplastic oligodendroglioma with 1p/19q
                     loss"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Brn67"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 2.3 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match             3.0%;  Score 20;  DB 7;  Length 920;
  Best Local Similarity   100.0%;  Pred. No. 81;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        533 TGACTGTGCCACAGAACTCC 552
              ||||||||||||||||||||
Db        308 TGACTGTGCCACAGAACTCC 289


RESULT 66
CL465003
LOCUS       CL465003                959 bp    DNA     linear   GSS 31-MAR-2004
DEFINITION  SAIL_1232_C07.v1 SAIL Collection Arabidopsis thaliana genomic clone
            SAIL_1232_C07.v1, genomic survey sequence.
ACCESSION   CL465003
VERSION     CL465003.1  GI:45867908
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 959)
  AUTHORS   Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D.,
            Dietrich,B., Ho,P., Bacwaden,J., Ko,C., Clarke,J.D., Cotton,D.,
            Bullis,D., Snell,J., Miguel,T., Hutchison,D., Kimmerly,B.,
            Mitzel,T., Katagiri,F., Glazebrook,J., Law,M. and Goff,S.A.
  TITLE     A high-throughput Arabidopsis reverse genetics system
  JOURNAL   Plant Cell 14 (12), 2985-2994 (2002)
   PUBMED   12468722
COMMENT     Contact: Sessions A
            Applied Trait Genetics
            Syngenta Biotechnology Inc.
            3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
            Email: allen.sessions@syngenta.com
            ABRC Stock Number CS845125; T-DNA left border flanking sequences of
            Syngenta Arabidopsis Insertion Library (SAIL) lines are available
            through the Arabidopsis Biological Resource Center (ABRC).
            Sequences represent a pool of amplified genomic regions and not
            single contiguous sequences.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .959
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /ecotype="Columbia"
                     /db_xref="taxon:3702"
                     /clone="SAIL_1232_C07.v1"
                     /clone_lib="SAIL Collection"
                     /note="T-DNA left border sequences were isolated using a
                     modified TAIL-PCR strategy"
ORIGIN

  Query Match             3.0%;  Score 20;  DB 13;  Length 959;
  Best Local Similarity   100.0%;  Pred. No. 82;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        120 CCTCAACCACTCCCAAACCC 139
              ||||||||||||||||||||
Db        590 CCTCAACCACTCCCAAACCC 609


RESULT 67
```

```
CNS01GIY
LOCUS       CNS01GIY                1035 bp    DNA     linear   GSS 01-JUN-2001
DEFINITION  Anopheles gambiae GSS T7 end of clone 06N18 of NotreDame1 library
            from strain PEST of Anopheles gambiae (African malaria mosquito),
            genomic survey sequence.
ACCESSION   AL143195
VERSION     AL143195.1  GI:7001313
KEYWORDS    GSS.
SOURCE      Anopheles gambiae (African malaria mosquito)
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Culicidae; Anophelinae; Anopheles.
REFERENCE   1  (bases 1 to 1035)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
REFERENCE   2  (bases 1 to 1035)
  AUTHORS   Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.
            Roux, Paris 75015, France
COMMENT     This clone is from an A. gambiae BAC library provided by F.H.
            Collins and sequenced by Genoscope in collaboration with the
            Laboratory of Biochem. and Biol. Molec. of Insects, Institut
            Pasteur.
FEATURES             Location/Qualifiers
     source          1. .1035
                     /organism="Anopheles gambiae"
                     /mol_type="genomic DNA"
                     /strain="PEST"
                     /db_xref="taxon:7165"
                     /clone="06N18"
                     /clone_lib="NotreDame1"
                     /note="end : T7"
ORIGIN

  Query Match             3.0%;  Score 20;  DB 14;  Length 1035;
  Best Local Similarity   100.0%;  Pred. No. 83;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        435 TGCAAAGCTGTTAATGGATC 454
              ||||||||||||||||||||
Db        308 TGCAAAGCTGTTAATGGATC 327


RESULT 68
BQ054286
LOCUS       BQ054286                1075 bp    mRNA    linear   EST 29-MAR-2002
DEFINITION  AGENCOURT_6830330 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5936368
            5', mRNA sequence.
ACCESSION   BQ054286
VERSION     BQ054286.1  GI:19813626
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1075)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2125  row: j  column: 17
            High quality sequence start: 147
            High quality sequence stop: 411.
FEATURES             Location/Qualifiers
     source          1. .1075
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5936368"
                     /tissue_type="natural killer cells, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_106"
                     /note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             3.0%;  Score 20;  DB 3;  Length 1075;
  Best Local Similarity   100.0%;  Pred. No. 83;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         68 GTTTGGCCAGGAACCTCCCC 87
              ||||||||||||||||||||
Db        797 GTTTGGCCAGGAACCTCCCC 816


RESULT 69
DT990937
LOCUS       DT990937                1321 bp    mRNA    linear   EST 22-SEP-2005
DEFINITION  CNB152-F06.x1d-t SHGC-CNB Gasterosteus aculeatus cDNA clone
            CNB152-F06 3', mRNA sequence.
ACCESSION   DT990937
VERSION     DT990937.1  GI:76114747
KEYWORDS    EST.
SOURCE      Gasterosteus aculeatus (three spined stickleback)
  ORGANISM  Gasterosteus aculeatus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
            Gasterosteidae; Gasterosteus.
REFERENCE   1  (bases 1 to 1321)
  AUTHORS   Kingsley,D.M., Peichel,C., Balabahdra,S., Grimwood,J., Dickson,M.,
            Schmutz,J. and Myers,R.M.
  TITLE     Expressed sequence tags from Gasterosteus aculeatus
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Grimwood, Jane
            Stanford Human Genome Center
            Stanford University School of Medicine
            975 S California Ave, Palo Alto, CA 94304, USA
            Tel: 650 320 5917
            Fax: 650 320 5801
            Email: jane@shgc.stanford.edu
            Plate: 152
            High quality sequence start: 18
            High quality sequence stop: 787.
FEATURES             Location/Qualifiers
     source          1. .1321
                     /organism="Gasterosteus aculeatus"
                     /mol_type="mRNA"
                     /strain="Conner Creek sticklebacks, WA USA"
                     /db_xref="taxon:69293"
                     /clone="CNB152-F06"
                     /sex="mixed male and female"
                     /tissue_type="brain"
                     /dev_stage="adult"
                     /lab_host="DH10B (T1 phage resistant)"
                     /clone_lib="SHGC-CNB"
```

```
                     /note="Vector: Express 1; Total and poly A+ RNA was
                     isolated from the indicated stickleback tissue, and a cDNA
                     library was constructed in the Express 1 plasmid vector by
                     Open Biosystems. First strand cDNA synthesis was primed
                     with an 54 bp linker primer containing an oligodT sequence
                     preceeded by a synthetic NotI site (first strand primer:
                     5'-GACTAGTTCTAGATCGCGAGCGGCCGCCC(T)25-3'). Following
                     second strand synthesis, cDNAs were made blunt at the end
                     corresponding to the original 5 prime end of mRNA, and
                     cloned directionally into the NotI and EcoRV sites of
                     Express 1. Note that the EcoRV site is typically destroyed
                     in the blunt end cloning, leaving a junction of the form
                     'xxxATC' (where is ATC is the second half of the EcoRV
                     site, and xxx is derived from the cDNA sequence). A map of
                     the Express 1 vector is available at:
                     http://www.openbiosystems.com/cdna_library_construction_fa
                     q.php#8 The primary library was transformed and amplified
                     in DH10B (T1 phage resistant) bacteria. Clones available
                     from Open Biosystems:
                     http://www.openbiosystems.com/stickleback"
ORIGIN

  Query Match             3.0%;  Score 20;  DB 10;  Length 1321;
  Best Local Similarity   100.0%;  Pred. No. 87;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        205 TCCGAAGAGATTGATCATGA 224
              ||||||||||||||||||||
Db        941 TCCGAAGAGATTGATCATGA 960


RESULT 70
CD147489/c
LOCUS       CD147489                 134 bp    mRNA    linear   EST 14-SEP-2003
DEFINITION  ML1-0007T-V098-D04-2.B ML1-0007 Schistosoma mansoni cDNA clone
            ML1-0007T-V098-D04.B, mRNA sequence.
ACCESSION   CD147489
VERSION     CD147489.1  GI:34685274
KEYWORDS    EST.
SOURCE      Schistosoma mansoni
  ORGANISM  Schistosoma mansoni
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 134)
  AUTHORS   Verjovski-Almeida,S., DeMarco,R., Martins,E.A.L., Guimaraes,P.E.M.,
            Ojopi,E.P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y. Jr.,
            Kitajima,J.P., Adamson,R.E., Ashton,P.D., Bonaldo,M.F.,
            Coulson,P.S., Dillon,G.P., Farias,L.P., Gregorio,S.P., Ho,P.L.,
            Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.A.,
            Nascimento,A.L.T.O., Ohlweiler,F.P., Reis,E.M., Ribeiro,M.A.,
            Sa,R.G., Stukart,G.C., Soares,M.B., Gargioni,C., Kawano,T.,
            Rodrigues,V., Madeira,A.M.B.N., Wilson,R.A., Menck,C.F.M.,
            Setubal,J.C., Leite,L.C.C. and Dias-Neto,E.
  TITLE     Transcriptome analysis of the acoelomate human parasite Schistosoma
            mansoni
  JOURNAL   Nat. Genet. 35 (2), 148-157 (2003)
   PUBMED   12973350
COMMENT     Other_ESTs: ML1-0007T-V098-D04-1.B
            Contact: Dr. Sergio Verjovski-Almeida
            Departamento de Bioquimica
            Instituto de Quimica - Universidade de Sao Paulo
            Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
            Brasil
            Tel: +55-11-3091-2173
            Fax: +55-11-3091-2186
            Email: verjo@iq.usp.br
            This sequence was derived from the FAPESP Schistosoma mansoni EST
            Genome Project. All sequences in the project were assembled and
            annotated. This entry and all the assembled sequences can be seen
            in the following URL http://bioinfo.iq.usp.br/schisto/
            Plate: ML1-0007T-V098  row: 4  column: D.
FEATURES             Location/Qualifiers
     source          1. .134
                     /organism="Schistosoma mansoni"
                     /mol_type="mRNA"
                     /db_xref="taxon:6183"
                     /clone="ML1-0007T-V098-D04.B"
                     /sex="mixed pool"
                     /dev_stage="miracidium"
                     /clone_lib="ML1-0007"
                     /note="Vector: pGEM T-easy"
ORIGIN

  Query Match             2.9%;  Score 19;  DB 5;  Length 134;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         48 AAACCACCTGGACCACCTC 66
              |||||||||||||||||||
Db         96 AAACCACCTGGACCACCTC 78


RESULT 71
CN094503
LOCUS       CN094503                 167 bp    mRNA    linear   EST 31-MAR-2004
DEFINITION  EC2BBA9DE06.b1 Xenopus tropicalis xtbs plasmid library Xenopus
            tropicalis cDNA clone xtbs09J12 3', mRNA sequence.
ACCESSION   CN094503
VERSION     CN094503.1  GI:45887199
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 167)
  AUTHORS   Thuret,R., Fierro,A.C., Coen,L., Perron,M., Demeneix,B., Wegnez,M.,
            Gyapay,G., Weissenbach,J., Wincker,P., Mazabraud,A. and Pollet,N.
  TITLE     Exploring the nervous system transcriptome in the model Xenopus
            tropicalis using EST analysis
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Pollet N
            Transgenese et Genetique des Amphibiens
            CNRS UMR 8080
            IBAIC bat 447, Universite Paris Sud, Orsay, F-91405, France
            Tel: +33 169157272
            Fax: +33 169156816
            Email: Nicolas.Pollet@ibaic.u-psud.fr.
FEATURES             Location/Qualifiers
     source          1. .167
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /strain="Ivory Coast"
                     /db_xref="taxon:8364"
                     /clone="xtbs09J12"
                     /tissue_type="pool of brains and spinal cords from
                     tadpoles at stages 51-52 and 61-62"
                     /dev_stage="stage 51-52 and 61-62"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Xenopus tropicalis xtbs plasmid library"
                     /note="Vector: pCMVSPORT6_xtbs; Site_1: SfiI; Site_2:
                     SfiI; Xenopus tropicalis polyA+ RNA was obtained from
                     brain and spinal cord of tadpoles at stages 51-52 and
                     61-62. cDNAs were synthesized using the SMART system of
                     CLONTECH and directionally cloned into pCMVSPORT6_xtbs, a
                     modified version of pCMVSPORT6 allowing directional
                     cloning using asymetric SfiI sites. For antisense RNA
                     synthesis, use T7 promoter and for sense RNA use SP6
                     promoter. Library constructed by Dr. L. Coen and Prof. B.
                     Demeneix (Museum National d'Histoire Naturelle and CNRS
                     UMR 5166, Paris, France)."
ORIGIN

  Query Match             2.9%;  Score 19;  DB 8;  Length 167;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy        570 TTTTTATAAAACTAAAATC 588
              ||||||||||||||||||
Db         89 TTTTTATAAAACTAAAATC 107


RESULT 72
DY151937
LOCUS       DY151937                196 bp    mRNA    linear   EST 01-FEB-2006
DEFINITION  000923BEMN018313HT BEMN Bos taurus cDNA, mRNA sequence.
ACCESSION   DY151937
VERSION     DY151937.1  GI:86346112
KEYWORDS    EST.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 196)
  AUTHORS   McCulloch,A., Wilson,T., Molenaar,A., Grigor,M., Davis,S.,
            Glenn,M., Havukkala,I., Watson,J., Crawford,A., Wheeler,T.,
            Hagemann,L., Lee,R., Hein,W., Johnstone,P., Maqbool,N., McMahon,C.,
            McCracken,J., Stelwagen,K., Farr,V., Singh,K., Whitley,J.,
            Nicholas,K., Savin,K., Mather,A., McPartlan,H., Whitley,J.,
            Wells,M., Bowman,P., Goddard,M., Langford,C., McEwan,J. and
            Atkinson,P.
  TITLE     AgResearch, Genesis and Primary Industry Victoria Bovine EST
            project
  JOURNAL   Unpublished (2006)
COMMENT     Contact: Maqbool N
            AgResearch Ltd.
            Invermay Agricultural Centre, Puddle Alley, Private Bag 50034,
            Mosgiel, New Zealand
            Email: nauman.maqbool@agresearch.co.nz.
FEATURES             Location/Qualifiers
     source          1. .196
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="Life Tech Normalised library"
                     /clone_lib="BEMN"
                     /note="Vector: pCMV-Sport6; Life Tech Normalised library"
ORIGIN

  Query Match             2.9%;  Score 19;  DB 10;  Length 196;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        404 AGATGTACCAGGTGGAGTT 422
              ||||||||||||||||||
Db        103 AGATGTACCAGGTGGAGTT 121


RESULT 73
CB438594
LOCUS       CB438594                199 bp    mRNA    linear   EST 25-MAR-2003
DEFINITION  687245 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   CB438594
VERSION     CB438594.1  GI:29222764
KEYWORDS    EST.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 199)
  AUTHORS   Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
            Wray,J.E. and Keele,J.W.
  TITLE     A second set of bovine ESTs from pooled-tissue normalized libraries
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Plate: FQY8043  row: N  column: 24
            Seq primer: GTAATACGACTCACTATAGGG.
FEATURES             Location/Qualifiers
     source          1. .199
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 6BOV"
                     /note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
                     Library made with RNA pooled from multiple tissues
                     including liver, lung, hypothalamus, pituitary, and
                     placenta/endometrium."
ORIGIN

  Query Match             2.9%;  Score 19;  DB 4;  Length 199;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        126 CCACTCCCAAACCCTGCTG 144
              ||||||||||||||||||
Db         19 CCACTCCCAAACCCTGCTG 37


RESULT 74
CR583097
LOCUS       CR583097                219 bp    mRNA    linear   EST 26-JUL-2004
DEFINITION  CR583097 XGC-tailbud-head Xenopus tropicalis cDNA clone THdA028d23
            5', mRNA sequence.
ACCESSION   CR583097
VERSION     CR583097.1  GI:50583097
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 219)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Garrett,N. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (2004)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Croning MDR
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
             TROPICALIS_SEQUENCE_ID: THdA028d23.p1kbSP6
             This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Nigel Garrett.
            Seq primer: SP6.
FEATURES             Location/Qualifiers
     source          1. .219
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="THdA028d23"
                     /dev_stage="tailbud head (stage 28-30)"
                     /lab_host="Escherichia coli DH10B."
                     /clone_lib="XGC-tailbud-head"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from tailbud
                     head. EcoRI-NotI cut cDNA was then ligated into pCS107
                     with EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

  Query Match             2.9%;  Score 19;  DB 8;  Length 219;
```

```
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        570 TTTTTATAAAACTAAAATC 588
              ||||||||||||||||||
Db        170 TTTTTATAAAACTAAAATC 188


RESULT 75
AL864786/c
LOCUS       AL864786                229 bp    mRNA    linear   EST 03-DEC-2003
DEFINITION  AL864786 XGC-egg Xenopus tropicalis cDNA clone TEgg132g06 5', mRNA
            sequence.
ACCESSION   AL864786
VERSION     AL864786.2  GI:38659459
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 229)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     On Sep 15, 2002 this sequence version replaced gi:22885051.
            Contact: Taylor R
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TEgg132g06.p1kSP6
            Sequencing primer: SP6
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from egg.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
            5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli XL1-blue.
FEATURES             Location/Qualifiers
     source          1. .229
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TEgg132g06"
                     /dev_stage="egg"
                     /lab_host="Escherichia coli XL1-blue"
                     /clone_lib="XGC-egg"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from egg.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end"
ORIGIN

  Query Match             2.9%;  Score 19;  DB 1;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         77 GGAACCTCCCCACACCCAC 95
              ||||||||||||||||||
Db         66 GGAACCTCCCCACACCCAC 48


RESULT 76
BB391337
LOCUS       BB391337                237 bp    mRNA    linear   EST 13-JUL-2000
DEFINITION  BB391337 RIKEN full-length enriched, 0 day neonate cerebellum Mus
            musculus cDNA clone C230074B09 3' similar to AB014577 Homo sapiens
            mRNA for KIAA0677 protein, mRNA sequence.
ACCESSION   BB391337
VERSION     BB391337.1  GI:9114288
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 237)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T.,
            Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
            Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
            Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
            Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C.,
            Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H.,
            Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K.,
            Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A.,
            Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watahiki,A.,
            Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A.,
            Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,
            Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length
            cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
            Okazaki,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
             Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .237
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="C230074B09"
                     /tissue_type="cerebellum"
                     /dev_stage="0 day neonate"
                     /lab_host="DH10B"
                     /clone_lib="RIKEN full-length enriched, 0 day neonate
                     cerebellum"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3']. cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 20.0 and subtraction to Rot = 479.0. Second
                     strand cDNA was prepared with the primer adapter of
                     sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC
                     3']. cDNA was cleaved with XhoI and BamHI. Vector: a
                     modified pBluescript KS(+) after bulk excision from Lambda
                     FLC I."
ORIGIN
```

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  Query Match             2.9%;  Score 19;  DB 7;  Length 237;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        404 AGATGTACCAGGTGGAGTT 422
              ||||||||||||||||||
Db         83 AGATGTACCAGGTGGAGTT 101


RESULT 77
CN094504/c
LOCUS       CN094504                242 bp    mRNA    linear   EST 31-MAR-2004
DEFINITION  EC2BBA9DE06.g1 Xenopus tropicalis xtbs plasmid library Xenopus
            tropicalis cDNA clone xtbs09J12 5', mRNA sequence.
ACCESSION   CN094504
VERSION     CN094504.1  GI:45887200
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 242)
  AUTHORS   Thuret,R., Fierro,A.C., Coen,L., Perron,M., Demeneix,B., Wegnez,M.,
            Gyapay,G., Weissenbach,J., Wincker,P., Mazabraud,A. and Pollet,N.
  TITLE     Exploring the nervous system transcriptome in the model Xenopus
            tropicalis using EST analysis
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Pollet N
            Transgenese et Genetique des Amphibiens
            CNRS UMR 8080
            IBAIC bat 447, Universite Paris Sud, Orsay, F-91405, France
            Tel: +33 169157272
            Fax: +33 169156816
            Email: Nicolas.Pollet@ibaic.u-psud.fr.
FEATURES             Location/Qualifiers
     source          1. .242
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /strain="Ivory Coast"
                     /db_xref="taxon:8364"
                     /clone="xtbs09J12"
                     /tissue_type="pool of brains and spinal cords from
                     tadpoles at stages 51-52 and 61-62"
                     /dev_stage="stage 51-52 and 61-62"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Xenopus tropicalis xtbs plasmid library"
                     /note="Vector: pCMVSPORT6_xtbs; Site_1: SfiI; Site_2:
                     SfiI; Xenopus tropicalis polyA+ RNA was obtained from
                     brain and spinal cord of tadpoles at stages 51-52 and
                     61-62. cDNAs were synthesized using the SMART system of
                     CLONTECH and directionally cloned into pCMVSPORT6_xtbs, a
                     modified version of pCMVSPORT6 allowing directional
                     cloning using asymetric SfiI sites. For antisense RNA
                     synthesis, use T7 promoter and for sense RNA use SP6
                     promoter. Library constructed by Dr. L. Coen and Prof. B.
                     Demeneix (Museum National d'Histoire Naturelle and CNRS
                     UMR 5166, Paris, France)."
ORIGIN

  Query Match             2.9%;  Score 19;  DB 8;  Length 242;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        570 TTTTTATAAAACTAAAATC 588
              ||||||||||||||||||
Db         78 TTTTTATAAAACTAAAATC 60


RESULT 78
AL640225/c
LOCUS       AL640225                247 bp    mRNA    linear   EST 07-NOV-2003
DEFINITION  AL640225 XGC-neurula Xenopus tropicalis cDNA clone TNeu002k23 5',
            mRNA sequence.
ACCESSION   AL640225
VERSION     AL640225.2  GI:38219389
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 247)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     On Nov 7, 2001 this sequence version replaced gi:16792356.
            Contact: Huckle E
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
            5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli DH10B
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TNeu002k23.p1kSP6
            Sequencing primer: SP6.
FEATURES             Location/Qualifiers
     source          1. .247
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TNeu002k23"
                     /dev_stage="neurula"
                     /lab_host="Escherichia coli DH10B"
                     /clone_lib="XGC-neurula"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from neurula.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

  Query Match             2.9%;  Score 19;  DB 1;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        570 TTTTTATAAAACTAAAATC 588
              ||||||||||||||||||
Db        101 TTTTTATAAAACTAAAATC 83


RESULT 79
BX668635
LOCUS       BX668635                247 bp    mRNA    linear   EST 07-MAY-2004
DEFINITION  BX668635 Sus Scrofa library (scac) Sus scrofa cDNA clone
            scac0028i.i.24 3prim, mRNA sequence.
ACCESSION   BX668635
VERSION     BX668635.1  GI:37977384
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 247)
  AUTHORS   Bonnet,A., Tosser-Klopp,G., Benne,F., Cabau,C., Villeger,S.,
            Soares,M., Bonaldo,F. and Hatey,F.
  TITLE     A Pig Normalised Multi-Tissue cDNA Library
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Tosser-Klopp G
            Genetique Animale
```

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            Institut National de la Recherche Agronomique
            Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
            cedex, FRANCE
            Tel: 33 (0) 5.61.28.51.14
            Fax: 33 (0) 5.61.28.53.08
            Email: tosser@toulouse.inra.fr
            Sequence cleaned of vector, adaptator and repetitions. Contact us
            at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
            sequence.
            Plate: 0028  row: i  column: 24.
FEATURES             Location/Qualifiers
     source          1. .247
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /clone="scac0028i.i.24"
                     /tissue_type="mixed"
                     /clone_lib="Sus Scrofa library (scac)"
                     /note="Vector: pT7T3D-PacI; tissues: adipose tissue,
                     brain, kidney, liver, muscle, ovary, testis,  heart,
                     hypothalamus, pancreas, skin, spleen, thymus, placenta,
                     pituitary  gland, seminal vesicle, small intestine,
                     uterus, adrenals, bulbo uretral  gland, cerebral trunk,
                     epididymis, female gonad, gall-bladder,  hippocampus,
                     large intestine, male gonad, melanocytes, stomach, udder"
ORIGIN

  Query Match             2.9%;  Score 19;  DB 4;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        284 TGAATGAGAGTTGCCTGGC 302
              ||||||||||||||||||
Db        162 TGAATGAGAGTTGCCTGGC 180


RESULT 80
BB425487/c
LOCUS       BB425487                247 bp    mRNA    linear   EST 18-JUL-2000
DEFINITION  BB425487 RIKEN full-length enriched, 12 days embryo spinal cord Mus
            musculus cDNA clone C530046M16 3', mRNA sequence.
ACCESSION   BB425487
VERSION     BB425487.1  GI:9265214
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 247)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T.,
            Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
            Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
            Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
            Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C.,
            Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H.,
            Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K.,
            Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A.,
            Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watahiki,A.,
            Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A.,
            Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,
            Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length
            cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
            Okazaki,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
             Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .247
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="C530046M16"
                     /tissue_type="spinal cord"
                     /dev_stage="12 days embryo"
                     /lab_host="DH10B"
                     /clone_lib="RIKEN full-length enriched, 12 days embryo
                     spinal cord"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. Second strand cDNA was prepared with the
                     primer adapter of sequence [5'
                     GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA
                     was cleaved with XhoI and BamHI. Vector: a modified
                     pBluescript KS(+) after bulk excision from Lambda FLC I."
ORIGIN

  Query Match             2.9%;  Score 19;  DB 7;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        578 AAACTAAAATCAAGCTCTG 596
              ||||||||||||||||||
Db        104 AAACTAAAATCAAGCTCTG 86


RESULT 81
BX714043/c
LOCUS       BX714043                255 bp    mRNA    linear   EST 18-NOV-2003
DEFINITION  BX714043 XGC-tadpole Xenopus tropicalis cDNA clone TTpA016103 5',
            mRNA sequence.
ACCESSION   BX714043
VERSION     BX714043.1  GI:38385449
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 255)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Croning MDR
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
```

```
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TTpA016103.p1kSP6
            Sequencing primer: SP6
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Nigel Garrett.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from tadpole
            embryos. EcoRI-NotI cut cDNA was then ligated into pCS107 with
            EcoRI at the 5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli DH10B.
FEATURES              Location/Qualifiers
     source           1. .255
                      /organism="Xenopus tropicalis"
                      /mol_type="mRNA"
                      /db_xref="taxon:8364"
                      /clone="TTpA016103"
                      /dev_stage="tadpole (stage 35-40)"
                      /lab_host="E. coli DH10B"
                      /clone_lib="XGC-tadpole"
                      /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                      was oligo dT primed from 5ug of poly A+ RNA from tadpole
                      embryos. EcoRI-NotI cut cDNA was then ligated into pCS107
                      with EcoRI at the 5' end and NotI at the 3' end"
ORIGIN

  Query Match             2.9%;  Score 19;  DB 4;  Length 255;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        570 TTTTTATAAAACTAAAATC 588
              ||||||||||||||||||
Db        243 TTTTTATAAAACTAAAATC 225


RESULT 82
CD190551
LOCUS       CD190551                261 bp    mRNA    linear   EST 14-SEP-2003
DEFINITION  MS1-0064U-A263-F03-U.B MS1-0064 Schistosoma mansoni cDNA clone
            MS1-0064U-A263-F03.B, mRNA sequence.
ACCESSION   CD190551
VERSION     CD190551.1  GI:34720521
KEYWORDS    EST.
SOURCE      Schistosoma mansoni
  ORGANISM  Schistosoma mansoni
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 261)
  AUTHORS   Verjovski-Almeida,S., DeMarco,R., Martins,E.A.L., Guimaraes,P.E.M.,
            Ojopi,E.P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y. Jr.,
            Kitajima,J.P., Adamson,R.E., Ashton,P.D., Bonaldo,M.F.,
            Coulson,P.S., Dillon,G.P., Farias,L.P., Gregorio,S.P., Ho,P.L.,
            Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.A.,
            Nascimento,A.L.T.O., Ohlweiler,F.P., Reis,E.M., Ribeiro,M.A.,
            Sa,R.G., Stukart,G.C., Soares,M.B., Gargioni,C., Kawano,T.,
            Rodrigues,V., Madeira,A.M.B.N., Wilson,R.A., Menck,C.F.M.,
            Setubal,J.C., Leite,L.C.C. and Dias-Neto,E.
  TITLE     Transcriptome analysis of the acoelomate human parasite Schistosoma
            mansoni
  JOURNAL   Nat. Genet. 35 (2), 148-157 (2003)
   PUBMED   12973350
COMMENT     Contact: Dr. Sergio Verjovski-Almeida
            Departamento de Bioquimica
            Instituto de Quimica - Universidade de Sao Paulo
            Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
            Brasil
            Tel: +55-11-3091-2173
            Fax: +55-11-3091-2186
            Email: verjo@iq.usp.br
            This sequence was derived from the FAPESP Schistosoma mansoni EST
            Genome Project. All sequences in the project were assembled and
            annotated. This entry and all the assembled sequences can be seen
            in the following URL http://bioinfo.iq.usp.br/schisto/
            Plate: MS1-0064U-A263  row: 3  column: F.
FEATURES              Location/Qualifiers
     source           1. .261
                      /organism="Schistosoma mansoni"
                      /mol_type="mRNA"
                      /db_xref="taxon:6183"
                      /clone="MS1-0064U-A263-F03.B"
                      /sex="mixed pool"
                      /dev_stage="schistosomulum"
                      /lab_host="in vitro culture"
                      /clone_lib="MS1-0064"
                      /note="Vector: pGEM T-easy"
ORIGIN

  Query Match             2.9%;  Score 19;  DB 5;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         48 AAACCACCTGGACCACCTC 66
              ||||||||||||||||||
Db        230 AAACCACCTGGACCACCTC 248


RESULT 83
BI703350
LOCUS       BI703350                265 bp    mRNA    linear   EST 18-SEP-2001
DEFINITION  fs85e10.x1 Zebrafish neuronal Danio rerio cDNA clone IMAGE:5076571
            3', mRNA sequence.
ACCESSION   BI703350
VERSION     BI703350.1  GI:15665979
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 265)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
            Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library constructed by S. Lin DNA Sequencing by: Washington
            University Genome Sequencing Center Clone distribution: the
            I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
            Seq primer: T7 from Gibco.
FEATURES              Location/Qualifiers
     source           1. .265
                      /organism="Danio rerio"
                      /mol_type="mRNA"
                      /db_xref="taxon:7955"
                      /clone="IMAGE:5076571"
                      /sex="mixed"
                      /dev_stage="adult"
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="Zebrafish neuronal"
                      /note="Organ: brain; Vector: pBluescript (modified);
                      Site_1: DraIII(Y); Site_2: DRAIII(X); Library is cloned
                      directionally between the DraIII(X) and DraIII(Y) sites
                      and has been amplified. Library constructed by S. Lin. "
ORIGIN

  Query Match             2.9%;  Score 19;  DB 2;  Length 265;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy        517 CTGAATGTCAACAGTGTGA 535
              ||||||||||||||||||
Db        104 CTGAATGTCAACAGTGTGA 122


RESULT 84
AV338007
LOCUS       AV338007                267 bp    mRNA    linear   EST 11-NOV-1999
DEFINITION  AV338007 RIKEN full-length enriched, adult male olfactory bulb Mus
            musculus cDNA clone 6430407D11 3', mRNA sequence.
ACCESSION   AV338007
VERSION     AV338007.1  GI:6378059
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 267)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T.,
            Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F.,
            Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I.,
            Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M.,
            Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
            Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K.,
            Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y.,
            Suzuki,H., Suzuki,H., Takahashi,F., Tateno,M., Tominaga,N.,
            Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A.,
            Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al. 1999)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
            Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
            Hayashizaki,Y.
             Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
            Okazaki,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
             Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .267
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="6430407D11"
                     /sex="male"
                     /tissue_type="olfactory brain"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="RIKEN full-length enriched, adult male
                     olfactory bulb"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 10.0 and subtraction to Rot = 100.0. Second
                     strand cDNA was prepared with the primer adapter of
                     sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC
                     3']. cDNA was cloned into the XhoI and BamHI sites.
                     Vector: a modified pBluescript KS(+) after bulk excision
                     from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
                     BamHI"
ORIGIN

  Query Match             2.9%;  Score 19;  DB 1;  Length 267;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        412 CAGGTGGAGTTCAAGGCCA 430
              ||||||||||||||||||
Db        187 CAGGTGGAGTTCAAGGCCA 205


RESULT 85
AL777805/c
LOCUS       AL777805                276 bp    mRNA    linear   EST 12-NOV-2003
DEFINITION  AL777805 XGC-neurula Xenopus tropicalis cDNA clone TNeu077117 5',
            mRNA sequence.
ACCESSION   AL777805
VERSION     AL777805.2  GI:38281824
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 276)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     On Jun 25, 2002 this sequence version replaced gi:21563509.
            Contact: Taylor R
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
            5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli DH10B
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TNeu077117.p1cSP6
            Sequencing primer: SP6.
FEATURES             Location/Qualifiers
     source          1. .276
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TNeu077117"
                     /dev_stage="neurula"
                     /lab_host="Escherichia coli DH10B"
                     /clone_lib="XGC-neurula"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from neurula.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

  Query Match             2.9%;  Score 19;  DB 1;  Length 276;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
```

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  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        570 TTTTTATAAAACTAAAATC 588
              ||||||||||||||||||
Db        117 TTTTTATAAAACTAAAATC 99


RESULT 86
BX683343
LOCUS       BX683343                280 bp    mRNA    linear   EST 14-NOV-2003
DEFINITION  BX683343 XGC-neurula Xenopus tropicalis cDNA clone TNeu077l17, mRNA
            sequence.
ACCESSION   BX683343
VERSION     BX683343.1  GI:38332463
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 280)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Croning MDR
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TNeu077l17.q1kT7
            Sequencing primer: T7
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
            5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli DH10B.
FEATURES             Location/Qualifiers
     source          1. .280
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TNeu077l17"
                     /dev_stage="neurula"
                     /lab_host="Escherichia coli DH10B"
                     /clone_lib="XGC-neurula"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from neurula.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

  Query Match             2.9%;  Score 19;  DB 4;  Length 280;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        570 TTTTTATAAAACTAAAATC 588
              ||||||||||||||||||
Db        174 TTTTTATAAAACTAAAATC 192


RESULT 87
AZ406693
LOCUS       AZ406693                283 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0176H05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0176H05 F, genomic survey sequence.
ACCESSION   AZ406693
VERSION     AZ406693.1  GI:10530706
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 283)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0176  row: H  column: 05
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 283.
FEATURES             Location/Qualifiers
     source          1. .283
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0176H05"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             2.9%;  Score 19;  DB 11;  Length 283;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        412 CAGGTGGAGTTCAAGGCCA 430
              ||||||||||||||||||
Db        179 CAGGTGGAGTTCAAGGCCA 197


RESULT 88
BQ392367
LOCUS       BQ392367                286 bp    mRNA    linear   EST 22-MAY-2002
DEFINITION  NISC_mq24a11.x1 NICHD_XGC_Emb5 Xenopus tropicalis cDNA clone
            IMAGE:5309109 3', mRNA sequence.
ACCESSION   BQ392367
VERSION     BQ392367.1  GI:21080054
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
```

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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 286)
  AUTHORS   NIH-XCG http://image.llnl.gov/image/html/xenopuslib_info.shtml.
  TITLE     National Institute of Child Health and Human Development, National
            Cancer Insitute, Xenopus Gene Collection
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation:
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
             DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC)
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            info@image.llnl.gov
            Plate: LLAM11783  row: B  column: 22
            Seq primer: -21M13 forward primer (ABI).
FEATURES              Location/Qualifiers
     source           1. .286
                      /organism="Xenopus tropicalis"
                      /mol_type="mRNA"
                      /db_xref="taxon:8364"
                      /clone="IMAGE:5309109"
                      /tissue_type="gastrula"
                      /dev_stage="embryo, stages 10-13"
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="NICHD_XGC_Emb5"
                      /note="Vector: pCMV-SPORT6.1; Site_1: NotI; Site_2: EcoRV;
                      Cloned unidirectionally. Primer: Oligo dT. Average insert
                      size 2.0 kb. Constructed by Invitrogen. Note: This is a
                      Xenopus Gene Collection (XGC) library."
ORIGIN

  Query Match             2.9%;  Score 19;  DB 3;  Length 286;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        570 TTTTTATAAAACTAAAATC 588
              ||||||||||||||||||
Db        210 TTTTTATAAAACTAAAATC 228


RESULT 89
AL643008
LOCUS       AL643008                287 bp    mRNA    linear   EST 07-NOV-2003
DEFINITION  AL643008 XGC-neurula Xenopus tropicalis cDNA clone TNeu016b16 5',
            mRNA sequence.
ACCESSION   AL643008
VERSION     AL643008.2  GI:38221579
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 287)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     On Nov 7, 2001 this sequence version replaced gi:16795133.
            Contact: Huckle E
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
            5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli DH10B
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TNeu016b16.p1kSP6
            Sequencing primer: SP6.
FEATURES              Location/Qualifiers
     source           1. .287
                      /organism="Xenopus tropicalis"
                      /mol_type="mRNA"
                      /db_xref="taxon:8364"
                      /clone="TNeu016b16"
                      /dev_stage="neurula"
                      /lab_host="Escherichia coli DH10B"
                      /clone_lib="XGC-neurula"
                      /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                      was oligo dT primed from 5ug of poly A+ RNA from neurula.
                      EcoRI-NotI cut cDNA was then ligated into pCS107 with
                      EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

  Query Match             2.9%;  Score 19;  DB 1;  Length 287;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        570 TTTTTATAAAACTAAAATC 588
              ||||||||||||||||||
Db        219 TTTTTATAAAACTAAAATC 237


RESULT 90
BI703351/c
LOCUS       BI703351                290 bp    mRNA    linear   EST 18-SEP-2001
DEFINITION  fs85e10.y1 Zebrafish neuronal Danio rerio cDNA clone IMAGE:5076571
            5', mRNA sequence.
ACCESSION   BI703351
VERSION     BI703351.1  GI:15665980
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 290)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
            Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Other_ESTs: fs85e10.x1
            Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library constructed by S. Lin DNA Sequencing by: Washington
            University Genome Sequencing Center Clone distribution: the
            I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
            Seq primer: T3 ET from Amersham.
FEATURES              Location/Qualifiers
     source           1. .290
                      /organism="Danio rerio"
                      /mol_type="mRNA"
                      /db_xref="taxon:7955"
                      /clone="IMAGE:5076571"
                      /sex="mixed"
                      /dev_stage="adult"
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="Zebrafish neuronal"
                      /note="Organ: brain; Vector: pBluescript (modified);
                      Site_1: DraIII(Y); Site_2: DRAIII(X); Library is cloned
                      directionally between the DraIII(X) and DraIII(Y) sites
```

and has been amplified. Library constructed by S. Lin. "
ORIGIN

Query Match 2.9%; Score 19; DB 2; Length 290;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 517 CTGAATGTCAACAGTGTGA 535
||||||||||||||||||
Db 172 CTGAATGTCAACAGTGTGA 154

RESULT 91
BB460815/c
LOCUS BB460815 307 bp mRNA linear EST 21-JUL-2000
DEFINITION BB460815 RIKEN full-length enriched, 12 days embryo spinal ganglion Mus musculus cDNA clone D130068N23 3', mRNA sequence.
ACCESSION BB460815
VERSION BB460815.1 GI:9356308
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 307)
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Konno,H., et al.)
JOURNAL Unpublished (2000)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
FEATURES Location/Qualifiers
source 1. .307
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="D130068N23"
/tissue_type="spinal ganglion"
/dev_stage="12 days embryo"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 12 days embryo spinal ganglion"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTTTTTTTTVN 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."
ORIGIN

Query Match 2.9%; Score 19; DB 7; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 331 GGGAGTTGCCTGGCCTCCA 349
||||||||||||||||||
Db 52 GGGAGTTGCCTGGCCTCCA 34

RESULT 92
CD183936
LOCUS CD183936 309 bp mRNA linear EST 14-SEP-2003
DEFINITION MS1-0040T-L267-G10-U.B MS1-0040 Schistosoma mansoni cDNA clone MS1-0040T-L267-G10.B, mRNA sequence.
ACCESSION CD183936
VERSION CD183936.1 GI:34714132
KEYWORDS EST.
SOURCE Schistosoma mansoni
ORGANISM Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE 1 (bases 1 to 309)
AUTHORS Verjovski-Almeida,S., DeMarco,R., Martins,E.A.L., Guimaraes,P.E.M., Ojopi,E.P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y. Jr., Kitajima,J.P., Adamson,R.E., Ashton,P.D., Bonaldo,M.F., Coulson,P.S., Dillon,G.P., Farias,L.P., Gregorio,S.P., Ho,P.L., Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.A., Nascimento,A.L.T.O., Ohlweiler,F.P., Reis,E.M., Ribeiro,M.A., Sa,R.G., Stukart,G.C., Soares,M.B., Gargioni,C., Kawano,T., Rodrigues,V., Madeira,A.M.B.N., Wilson,R.A., Menck,C.F.M., Setubal,J.C., Leite,L.C.C. and Dias-Neto,E.
TITLE Transcriptome analysis of the acoelomate human parasite Schistosoma mansoni
JOURNAL Nat. Genet. 35 (2), 148-157 (2003)
PUBMED 12973350
COMMENT Contact: Dr. Sergio Verjovski-Almeida
Departamento de Bioquimica
Instituto de Quimica - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP, Brasil
Tel: +55-11-3091-2173
Fax: +55-11-3091-2186
Email: verjo@iq.usp.br
This sequence was derived from the FAPESP Schistosoma mansoni EST Genome Project. All sequences in the project were assembled and annotated. This entry and all the assembled sequences can be seen in the following URL http://bioinfo.iq.usp.br/schisto/
Plate: MS1-0040T-L267 row: 10 column: G.
FEATURES Location/Qualifiers
source 1. .309
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="MS1-0040T-L267-G10.B"

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                     /sex="mixed pool"
                     /dev_stage="schistosomulum"
                     /lab_host="in vitro culture"
                     /clone_lib="MS1-0040"
                     /note="Vector: pGEM T-easy"
ORIGIN

  Query Match             2.9%;  Score 19;  DB 5;  Length 309;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         48 AAACCACCTGGACCACCTC 66
              ||||||||||||||||||
Db         78 AAACCACCTGGACCACCTC 96


RESULT 93
BQ392345
LOCUS       BQ392345                317 bp    mRNA    linear   EST 22-MAY-2002
DEFINITION  NISC_mq23h11.x1 NICHD_XGC_Emb5 Xenopus tropicalis cDNA clone
            IMAGE:5309444 3', mRNA sequence.
ACCESSION   BQ392345
VERSION     BQ392345.1  GI:21080032
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 317)
  AUTHORS   NIH-XCG http://image.llnl.gov/image/html/xenopuslib_info.shtml.
  TITLE     National Institute of Child Health and Human Development, National
            Cancer Insitute, Xenopus Gene Collection
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation:
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
             DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC)
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            info@image.llnl.gov
            Plate: LLAM11783  row: P  column: 21
            Seq primer: -21M13 forward primer (ABI).
FEATURES              Location/Qualifiers
     source           1. .317
                      /organism="Xenopus tropicalis"
                      /mol_type="mRNA"
                      /db_xref="taxon:8364"
                      /clone="IMAGE:5309444"
                      /tissue_type="gastrula"
                      /dev_stage="embryo, stages 10-13"
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="NICHD_XGC_Emb5"
                      /note="Vector: pCMV-SPORT6.1; Site_1: NotI; Site_2: EcoRV;
                      Cloned unidirectionally. Primer: Oligo dT. Average insert
                      size 2.0 kb. Constructed by Invitrogen. Note: This is a
                      Xenopus Gene Collection (XGC) library."
ORIGIN

  Query Match             2.9%;  Score 19;  DB 3;  Length 317;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        570 TTTTTATAAAACTAAAATC 588
              ||||||||||||||||||
Db        207 TTTTTATAAAACTAAAATC 225


RESULT 94
AG255889/c
LOCUS       AG255889                330 bp    DNA     linear   GSS 19-JUL-2003
DEFINITION  Lotus corniculatus var. japonicus DNA, clone:LjT40h03_sfi, genomic
            survey sequence.
ACCESSION   AG255889
VERSION     AG255889.1  GI:26655726
KEYWORDS    GSS.
SOURCE      Lotus corniculatus var. japonicus (Lotus japonicus)
  ORGANISM  Lotus corniculatus var. japonicus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
            Lotus.
REFERENCE   1
  AUTHORS   Sato,S., Nakamura,Y. and Tabata,S.
  TITLE     Lotus japonicus TAC End sequences
  JOURNAL   Published Only in Database (2002)
REFERENCE   2  (bases 1 to 330)
  AUTHORS   Sato,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute,
            The First Laboratory for Plant Gene Research; 2-6-7
            Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan
            (E-mail:ssato@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/,
            Tel:81-438-52-3935(ex.2336), Fax:81-438-52-3934)
FEATURES              Location/Qualifiers
     source           1. .330
                      /organism="Lotus corniculatus var. japonicus"
                      /mol_type="genomic DNA"
                      /strain="Miyakojima MG-20"
                      /variety="japonicus"
                      /db_xref="taxon:34305"
                      /clone="LjT40h03_sfi"
                      /clone_lib="genomic TAC library"
                      /note="VECTOR:pYLTAC7
                      synonym: Lotus japonicus"
ORIGIN

  Query Match             2.9%;  Score 19;  DB 14;  Length 330;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        569 ATTTTTATAAAACTAAAAT 587
              ||||||||||||||||||
Db        243 ATTTTTATAAAACTAAAAT 225


RESULT 95
BQ392422
LOCUS       BQ392422                334 bp    mRNA    linear   EST 22-MAY-2002
DEFINITION  NISC_mq24d03.x1 NICHD_XGC_Emb5 Xenopus tropicalis cDNA clone
            IMAGE:5309237 3', mRNA sequence.
ACCESSION   BQ392422
VERSION     BQ392422.1  GI:21080109
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 334)
  AUTHORS   NIH-XCG http://image.llnl.gov/image/html/xenopuslib_info.shtml.
  TITLE     National Institute of Child Health and Human Development, National
            Cancer Insitute, Xenopus Gene Collection
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation:
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
             DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC)
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            info@image.llnl.gov
            Plate: LLAM11783  row: H  column: 6
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           Seq primer: -21M13 forward primer (ABI).
FEATURES             Location/Qualifiers
     source          1. .334
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="IMAGE:5309237"
                     /tissue_type="gastrula"
                     /dev_stage="embryo, stages 10-13"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NICHD_XGC_Emb5"
                     /note="Vector: pCMV-SPORT6.1; Site_1: NotI; Site_2: EcoRV;
                     Cloned unidirectionally. Primer: Oligo dT. Average insert
                     size 2.0 kb. Constructed by Invitrogen. Note: This is a
                     Xenopus Gene Collection (XGC) library."
ORIGIN

  Query Match             2.9%;  Score 19;  DB 3;  Length 334;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        570 TTTTTATAAAACTAAAATC 588
              ||||||||||||||||||
Db        171 TTTTTATAAAACTAAAATC 189


RESULT 96
AL849698/c
LOCUS       AL849698                335 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AL849698 XGC-egg Xenopus tropicalis cDNA clone TEgg003k15 5', mRNA
            sequence.
ACCESSION   AL849698
VERSION     AL849698.2  GI:38560935
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 335)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     On Sep 15, 2002 this sequence version replaced gi:22869920.
            Contact: Taylor R
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TEgg003k15.p1kSP6
            Sequencing primer: SP6
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from egg.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
            5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli XL1-blue.
FEATURES             Location/Qualifiers
     source          1. .335
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TEgg003k15"
                     /dev_stage="egg"
                     /lab_host="Escherichia coli XL1-blue"
                     /clone_lib="XGC-egg"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from egg.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end"
ORIGIN

  Query Match             2.9%;  Score 19;  DB 1;  Length 335;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        570 TTTTTATAAAACTAAAATC 588
              ||||||||||||||||||
Db        189 TTTTTATAAAACTAAAATC 171


RESULT 97
AG265393/c
LOCUS       AG265393                348 bp    DNA     linear   GSS 22-JUL-2003
DEFINITION  Lotus corniculatus var. japonicus DNA, clone:LjT62n06_not, genomic
            survey sequence.
ACCESSION   AG265393
VERSION     AG265393.1  GI:26665232
KEYWORDS    GSS.
SOURCE      Lotus corniculatus var. japonicus (Lotus japonicus)
  ORGANISM  Lotus corniculatus var. japonicus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
            Lotus.
REFERENCE   1
  AUTHORS   Sato,S., Nakamura,Y. and Tabata,S.
  TITLE     Lotus japonicus TAC End sequences
  JOURNAL   Published Only in Database (2002)
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Sato,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute,
            The First Laboratory for Plant Gene Research; 2-6-7
            Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan
            (E-mail:ssato@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/,
            Tel:81-438-52-3935(ex.2336), Fax:81-438-52-3934)
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Lotus corniculatus var. japonicus"
                     /mol_type="genomic DNA"
                     /strain="Miyakojima MG-20"
                     /variety="japonicus"
                     /db_xref="taxon:34305"
                     /clone="LjT62n06_not"
                     /clone_lib="genomic TAC library"
                     /note="VECTOR:pYLTAC7
                     synonym: Lotus japonicus"
ORIGIN

  Query Match             2.9%;  Score 19;  DB 14;  Length 348;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         58 GACCACCTCAGTTTGGCCA 76
              ||||||||||||||||||
Db        131 GACCACCTCAGTTTGGCCA 113


RESULT 98
CX358439
LOCUS       CX358439                350 bp    mRNA    linear   EST 28-SEP-2005
DEFINITION  JGI_XZT28.rev NIH_XGC_tropTad5 Xenopus tropicalis cDNA clone XZT28
            3', mRNA sequence.
ACCESSION   CX358439
VERSION     CX358439.1  GI:57126998
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 350)
  AUTHORS   Richardson,P., Lucas,S., Rokhsar,D., Detter,J.C., Ng,D.C.,
            Brokstein,P. and Lindquist,E.A.
```

```
  TITLE     DOE Joint Genome Institute Xenopus tropicalis EST project
  JOURNAL   Unpublished (2004)
COMMENT     Other_ESTs: JGI_XZT28.fwd
            Contact: Lindquist,E.A., Richardson,P.
            DOE Joint Genome Institute
            2800 Mitchell Drive, Walnut Creek, CA 94598, USA
            Tel: 925 296 5600
            Fax: 925 296 5710
            Email: cdna@jgi-psf.org
            Tissue Procurement: Richard M. Harland Laboratory, University of
            California, Berkeley: http://tropicalis.berkeley.edu/home
            cDNA Library Preparation: Richard M. Harland Laboratory, University
            of California, Berkeley
            cDNA Library Arrayed by: DOE Joint Genome Institute:
            http://www.jgi.doe.gov
            DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
            Clone Unavailable: The master plate for this cDNA clone no longer
            exists.
            Naming Conventions: EST name is generated by the concatenation of
            the JGI Clone Id and the direction of sequencing. The suffix '.rev'
            indicates a reverse sequencing read of the insert. It does not
            necessarily reflect the orientation of the insert.
            Poly-A: Based upon the presence of a run of 14 or more T residues
            at the beginning of the sequence, this clone was polyadenylated.
            The resulting Poly-T sequence has been removed.
            Small Insert: Based upon one or more sequencing reads of this clone
            where vector sequence was present at both ends, this clone has been
            determined to contain a cDNA insert on the order of 600-1000 bases.
            Plate: XZT 0001  row: g  column: 7
            High quality sequence stop: 171
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .350
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="XZT28"
                     /tissue_type="whole embryo"
                     /dev_stage="Tadpole (st. 36-41)"
                     /lab_host="E. coli XL1-Blue derivative, Stratagene
                     ElectroTen-Blue"
                     /clone_lib="NIH_XGC_tropTad5"
                     /note="Vector: pCS108; Site_1: SalI; Site_2: NotI; Tadpole
                     library constructed by Russell B. Fletcher in R. Harland's
                     lab using poly A RNA and oligo dT primers (Invitrogen
                     SuperScript Plasmid System for cDNA Synthesis and
                     Cloning). SalI (5' end) -NotI (3' end) cDNA was inserted
                     into vector pCS108
                     (http://mcb.berkeley.edu/labs/harland/pages/plasmids.html)
                     ."
ORIGIN

  Query Match             2.9%;  Score 19;  DB 9;  Length 350;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        570 TTTTTATAAAACTAAAATC 588
              ||||||||||||||||||||
Db         11 TTTTTATAAAACTAAAATC 29


RESULT 99
BX708129
LOCUS       BX708129                351 bp    mRNA    linear   EST 17-NOV-2003
DEFINITION  BX708129 XGC-tadpole Xenopus tropicalis cDNA clone TTpA002b09 3',
            mRNA sequence.
ACCESSION   BX708129
VERSION     BX708129.1  GI:38370336
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 351)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Croning MDR
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TTpA002b09.q1kT7
            Sequencing primer: T7
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Nigel Garrett.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from tadpole
            embryos. EcoRI-NotI cut cDNA was then ligated into pCS107 with
            EcoRI at the 5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli DH10B.
FEATURES             Location/Qualifiers
     source          1. .351
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TTpA002b09"
                     /dev_stage="tadpole (stage 35-40)"
                     /lab_host="E. coli DH10B"
                     /clone_lib="XGC-tadpole"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from tadpole
                     embryos. EcoRI-NotI cut cDNA was then ligated into pCS107
                     with EcoRI at the 5' end and NotI at the 3' end"
ORIGIN

  Query Match             2.9%;  Score 19;  DB 4;  Length 351;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        570 TTTTTATAAAACTAAAATC 588
              ||||||||||||||||||||
Db        181 TTTTTATAAAACTAAAATC 199


RESULT 100
CN106168
LOCUS       CN106168                354 bp    mRNA    linear   EST 31-MAR-2004
DEFINITION  EC2CAA29AC03.b1 Xenopus tropicalis xthr plasmid library Xenopus
            tropicalis cDNA clone xthr29E05 3', mRNA sequence.
ACCESSION   CN106168
VERSION     CN106168.1  GI:45898864
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 354)
  AUTHORS   Thuret,R., Fierro,A.C., Coen,L., Perron,M., Demeneix,B., Wegnez,M.,
            Gyapay,G., Weissenbach,J., Wincker,P., Mazabraud,A. and Pollet,N.
  TITLE     Exploring the nervous system transcriptome in the model Xenopus
            tropicalis using EST analysis
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Pollet N
            Transgenese et Genetique des Amphibiens
            CNRS UMR 8080
            IBAIC bat 447, Universite Paris Sud, Orsay, F-91405, France
            Tel: +33 169157272
            Fax: +33 169156816
            Email: Nicolas.Pollet@ibaic.u-psud.fr.
FEATURES             Location/Qualifiers
     source          1. .354
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
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/strain="Ivory Coast"
/db_xref="taxon:8364"
/clone="xthr29E05"
/tissue_type="pool of heads and retinas from tailbud stages 25-35"
/dev_stage="stage 25-35"
/lab_host="E.coli DH10B"
/clone_lib="Xenopus tropicalis xthr plasmid library"
/note="Vector: pCMVSPORT6_xthr; Site_1: SfiI; Site_2: SfiI; Xenopus tropicalis polyA+ RNA was obtained from pool of heads and retinas from tailbud stages 25-35 cDNAs were synthesized using the SMART system of CLONTECH and directionally cloned into pCMVSPORT6_xthr, a modified version of pCMVSPORT6 allowing directional cloning using asymetric SfiI sites. For antisense RNA synthesis, use T7 promoter and for sense RNA use SP6 promoter. Library constructed by Drs. N. Pollet, M. Perron, M. Wegnez, A. Mazabraud (CNRS UMR 8080, Universite Paris Sud, Orsay, France)."

ORIGIN

Query Match 2.9%; Score 19; DB 8; Length 354;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        570 TTTTTATAAAACTAAAATC 588
              |||||||||||||||||||
Db         87 TTTTTATAAAACTAAAATC 105
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Search completed: June 10, 2006, 14:53:32
Job time : 4094.83 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 10, 2006, 15:46:40 ; Search time 26.5748 Seconds
(without alignments)
7321.729 Million cell updates/sec

Title: US-10-821-670A-43
Perfect score: 1533
Sequence: 1 atatgggaactggagaaaaa.....tgagctatctgaatgcttcc 1533

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 253354 seqs, 63461778 residues

Total number of hits satisfying chosen parameters: 506708

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	36.8	2.4	3401	6	US-10-196-749-411	Sequence 411, App
	2	35	2.3	2487	6	US-10-471-571A-3681	Sequence 3681, Ap
	3	34.8	2.3	3166	7	US-11-293-697-739	Sequence 739, App
c	4	34.4	2.2	1438	6	US-10-953-349-20792	Sequence 20792, A
	5	34.4	2.2	2268	7	US-11-217-529-1612	Sequence 1612, Ap
	6	33.8	2.2	1287	7	US-11-217-529-80999	Sequence 80999, A
	7	33.8	2.2	1948	6	US-10-508-063A-4	Sequence 4, Appli
	8	33.2	2.2	1710	7	US-11-217-529-79541	Sequence 79541, A
	9	33.2	2.2	2513	7	US-11-293-697-145	Sequence 145, App
	10	32.4	2.1	2152	6	US-10-953-349-38921	Sequence 38921, A
	11	32.4	2.1	2338	7	US-11-293-697-1600	Sequence 1600, Ap
	12	32	2.1	620	6	US-10-953-349-32903	Sequence 32903, A
	13	32	2.1	2024	7	US-11-293-697-1253	Sequence 1253, Ap
	14	31.8	2.1	1404	6	US-10-471-571A-5411	Sequence 5411, Ap
c	15	31.8	2.1	1906	6	US-10-953-349-22720	Sequence 22720, A
c	16	31.4	2.0	654	6	US-10-488-619-2605	Sequence 2605, Ap
c	17	31.4	2.0	1636	6	US-10-953-349-22635	Sequence 22635, A
c	18	31.4	2.0	6051	7	US-11-313-450-9	Sequence 9, Appli
	19	31.2	2.0	1286	7	US-11-145-307A-72	Sequence 72, Appl
c	20	31.2	2.0	1532	6	US-10-196-749-121	Sequence 121, App
c	21	31	2.0	1617	6	US-10-953-349-30783	Sequence 30783, A
	22	31	2.0	2843	7	US-11-293-697-1498	Sequence 1498, Ap
	23	30.8	2.0	588	6	US-10-953-349-2851	Sequence 2851, Ap
c	24	30.8	2.0	855	6	US-10-953-349-2895	Sequence 2895, Ap
c	25	30.8	2.0	992	6	US-10-953-349-31065	Sequence 31065, A
	26	30.8	2.0	1212	6	US-10-471-571A-4253	Sequence 4253, Ap
	27	30.8	2.0	2630	7	US-11-293-697-1769	Sequence 1769, Ap
	28	30.8	2.0	2640	6	US-10-527-411-29	Sequence 29, Appl
c	29	30.8	2.0	2920	7	US-11-293-697-683	Sequence 683, App
	30	30.8	2.0	3930	7	US-11-217-529-76026	Sequence 76026, A
	31	30.6	2.0	979	6	US-10-953-349-34412	Sequence 34412, A
	32	30.6	2.0	1210	6	US-10-953-349-23356	Sequence 23356, A
	33	30.6	2.0	1761	6	US-10-953-349-22246	Sequence 22246, A
	34	30.6	2.0	2619	7	US-11-302-678-18	Sequence 18, Appl
	35	30.6	2.0	3232	7	US-11-302-678-16	Sequence 16, Appl
c	36	30.4	2.0	296	7	US-11-301-554-517	Sequence 517, App
	37	30.4	2.0	444	7	US-11-217-529-79558	Sequence 79558, A
c	38	30.4	2.0	1467	7	US-11-217-529-79610	Sequence 79610, A
c	39	30.4	2.0	2249	7	US-11-293-697-442	Sequence 442, App
c	40	30.4	2.0	3294	7	US-11-293-697-1397	Sequence 1397, Ap
c	41	30.2	2.0	924	7	US-11-217-529-1898	Sequence 1898, Ap
c	42	30.2	2.0	1422	6	US-10-953-349-31587	Sequence 31587, A
	43	30.2	2.0	1491	6	US-10-953-349-10993	Sequence 10993, A
	44	30.2	2.0	1848	6	US-10-519-335-5	Sequence 5, Appli
	45	30.2	2.0	1878	6	US-10-519-335-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-10-196-749-411
; Sequence 411, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 411
; LENGTH: 3401
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-196-749-411

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  Query Match             2.4%;  Score 36.8;  DB 6;  Length 3401;
  Best Local Similarity   46.5%;  Pred. No. 0.22;
  Matches  119;  Conservative    0;  Mismatches  137;  Indels    0;  Gaps    0;

Qy        474 CAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTG 533
              ||  ||  || ||  | |  | |  |||| |   ||||| ||     | || || ||   |
Db        130 CACCGTCTACTACGTGCACAACATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAG 189

Qy        534 CCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAA 593
              || | | | |    | |   | |  ||     |    ||| | |  |   |||| ||
Db        190 CCTGACGGGCTACCGCACCTACCGCTGTGCCCACCCCCTGGCCACACTCTTCAAGATCCT 249

Qy        594 GTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAA 653
              |      |||||  ||||    || || ||   | | |||||     | || |||
Db        250 GGCGTCCTTCTACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCATGTACACACTGTG 309

Qy        654 GAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCC 713
              |    ||| || |    |  | || || |    |  || |    | |   |||   |
Db        310 GTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTTGAGTCGATCCGTGAGGAGAGCAG 369

Qy        714 TGACACCTGGAGCACC 729
                ||| |   | | ||
Db        370 CTACAGCGACATCCCC 385


RESULT 2
US-10-471-571A-3681
; Sequence 3681, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 3681
;   LENGTH: 2487
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-3681

  Query Match             2.3%;  Score 35;  DB 6;  Length 2487;
  Best Local Similarity   46.2%;  Pred. No. 0.65;
  Matches  116;  Conservative    0;  Mismatches  135;  Indels    0;  Gaps    0;

Qy       1270 AAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGG 1329
              || ||  | | | || |   || |    ||||   |||| |  ||| | | | ||  |
Db       2144 AATATAAAACGGTTGAATCACAGGAATCTGAAGCTAAAGATAGTAAGGAAACATACGACA 2203

Qy       1330 CAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAAT 1389
              ||    ||   | ||    ||| | ||  |   ||  ||       |  ||   | |
Db       2204 CAACCTTTAAAGTATATCCACAAGGTGCAACAAATGTATCGAAACATCAAGATGCACATG 2263

Qy       1390 GTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACT 1449
              | ||| |   ||    | | | || |||      |  ||  |  | ||| |   || |
Db       2264 GGCAAGATGATGCACATTCAATAGTACTAGATGATAAAACGATGGCATTGTACCAAGAAG 2323

Qy       1450 AAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGA 1509
                || ||          | ||| |  | |||  |  || | |  |  ||  |||| | |
Db       2324 TGAAACAGCAATCAGCAAGTTCATTGTTCTTATATGATGCTTTAATAGATTATCAAAACA 2383

Qy       1510 ATGATGAGCTA 1520
              |  || | |||
Db       2384 AGCATCAACTA 2394


RESULT 3
US-11-293-697-739
; Sequence 739, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 739
;   LENGTH: 3166
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-739

  Query Match             2.3%;  Score 34.8;  DB 7;  Length 3166;
  Best Local Similarity   49.5%;  Pred. No. 0.89;
  Matches   90;  Conservative    0;  Mismatches   92;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              || ||||| || ||  |  || ||||| |     ||      | |    |  ||| |   |
Db       1418 GGACAGAGAGGTCAGAAATGAATATAACATCACCATCACCGTGACCGACTTGGGGACACC 1477

Qy        531 CTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCT 590
              | | | |    ||||| | | | || || |    |||   |  | | |    ||   |
Db       1478 CAGGCTGAAAACCGAGCACAACATAACCGTGCTGGTCTCCGACGTCAATGACAACGCCCC 1537

Qy        591 CAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACC 650
              ||  | |    |  | ||  || | | ||| || | || | || ||  || | ||  |
Db       1538 CATCTTCACCCAAACCTCCTACACCCTGTTCGTCCGCGAGAACAACAGCCCCGCCCTGCA 1597

Qy        651 CA 652
              ||
Db       1598 CA 1599


RESULT 4
US-10-953-349-20792/c
; Sequence 20792, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20792
;   LENGTH: 1438
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-20792

  Query Match             2.2%;  Score 34.4;  DB 6;  Length 1438;
  Best Local Similarity   50.0%;  Pred. No. 0.7;
  Matches   86;  Conservative    0;  Mismatches   86;  Indels    0;  Gaps    0;

Qy        177 ATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTT 236
              ||  ||| |||   || | ||  |||     | | |||    |      ||| ||  | |
Db       1331 ATAGGCACATGGAAGCAATTACTCCTTCACCATATGAGAACAACACTGGAGTCAAGCATG 1272

Qy        237 CCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAA 296
              |||| || ||| |     |||  ||    |     ||| || | || || | | ||   ||
Db       1271 GATCCTAATCCACTAGTTCGAAACTGTGTTAAACTCCTCTCAAATTTTCATGCAATCTAA 1212

Qy        297 AGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGA 348
                  ||   |||| |||||| | |     | | | ||    ||| |   ||
Db       1211 CTGTAACACTGATAACATCTTTTTTACCCCTTATGTAATACTTTACTGCTGA 1160
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RESULT 5
US-11-217-529-1612
; Sequence 1612, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1612
; LENGTH: 2268
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1612

Query Match 2.2%; Score 34.4; DB 7; Length 2268;
Best Local Similarity 59.0%; Pred. No. 0.95;
Matches 59; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

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Qy          84 CAATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGG 143
               |||||| |||||||| ||||||      ||| | | |    | ||   ||  |   |
Db        1869 CAATACCCCTGAAGAAAATGACACTGAGGGGAAGTATAATACAATCAAGAAAAGCTCGGA 1928

Qy         144 CTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCA 183
                | || | || |||  | ||   |  ||||||||||  ||
Db        1929 TTATGATGAATCTCATATCACGAATATCAAAGAATTACCA 1968
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RESULT 6
US-11-217-529-80999
; Sequence 80999, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80999
; LENGTH: 1287
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-80999

Query Match 2.2%; Score 33.8; DB 7; Length 1287;
Best Local Similarity 53.4%; Pred. No. 1;
Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

```
Qy        1380 GGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTT 1439
               | || |||||         ||||  | |  ||    ||| ||| ||  | ||| ||| |||
Db         327 GCCCATGAATAGATCAGATGTGGATTTAACAATATACTACTCTTTTAATGAAACGGTTTT 386

Qy        1440 TTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGAC 1499
                 | ||  | || ||     |   |   | || |||| | |  |   || |  ||| | |
Db         387 AGAGAACCCAAATATAGGTCAAAGTGCAGTTTTTCAGGATGGCTACATCCAAGCATTAGC 446

Qy        1500 CATCAATAGAATG 1512
               ||||| |  | ||
Db         447 CATCAGTCCAGTG 459
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RESULT 7
US-10-508-063A-4
; Sequence 4, Application US/10508063A
; Publication No. US20060088832A1
; GENERAL INFORMATION:
; APPLICANT: Deutsches Krebsforschungszentrum
; APPLICANT: ANGEL, Peter
; APPLICANT: FURSTENBERGER, Gerhard
; APPLICANT: BREITENBACH, Ute
; APPLICANT: RICHTER, Harmut
; APPLICANT: HESS, Jochen
; APPLICANT: TUCKERMAN, Jan
; TITLE OF INVENTION: TAP-70, A NOVEL MARKER FOR EPITHELIAL TUMORS
; FILE REFERENCE: 31304-701.831
; CURRENT APPLICATION NUMBER: US/10/508,063A
; CURRENT FILING DATE: 2004-09-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 1948
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-508-063A-4

Query Match 2.2%; Score 33.8; DB 6; Length 1948;
Best Local Similarity 52.4%; Pred. No. 1.3;
Matches 99; Conservative 0; Mismatches 87; Indels 3; Gaps 1;

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Qy         429 CCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAG 488
               | ||| ||  | | | | ||    ||   |||  |  | |  || || ||     | |
Db        1111 CAAAGTGGCCAATGGGGCAGAGATGAAGATCTTGGGTGTGTGGGACACAGAAATTAGCCT 1170

Qy         489 GGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGA 548
               ||   | |  |||   |  |  |||| || || || ||  ||| ||   || |  ||||
Db        1171 GGGCAAGACAAAGCTGAAGGCCGAGTTTCTGGTGGCCAACGCCAGC---GCAGAAGAGGC 1227

Qy         549 GAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACAC 608
                 |   |   ||  || ||| ||  ||||   | |  |  |||  | | |||| ||  |||
Db        1228 TATTATTGGCACAGACGTCTTGCAGGACCACAATGCCGTGCTGGACTTCGAACACCGCAC 1287

Qy         609 CAGCAGCTT 617
               | ||| | |
Db        1288 CTGCACCCT 1296
```

RESULT 8
US-11-217-529-79541
; Sequence 79541, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 79541
; LENGTH: 1710
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1692)..(1692)
; OTHER INFORMATION: a, c, g, t, unknown, or other
US-11-217-529-79541

Query Match 2.2%; Score 33.2; DB 7; Length 1710;
Best Local Similarity 55.1%; Pred. No. 1.9;
Matches 65; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

Qy 1019 TCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAG 1078
Db 290 TCAAGAACGATCTTCAAAATTTCATGAAGAATGTAGGATTTGACCAACACAAACTCGAAG 349

Qy 1079 AGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACC 1136
Db 350 ATGTAGACGATGACGATATAGAAGAAGAATCCACTAGCTCCAAAGAATCTAAAATACC 407

RESULT 9
US-11-293-697-145
; Sequence 145, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 145
; LENGTH: 2513
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-145

Query Match 2.2%; Score 33.2; DB 7; Length 2513;
Best Local Similarity 52.1%; Pred. No. 2.4;
Matches 74; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy 561 TGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTT 620
Db 973 TGAAATGGCCCTGGATGCTGAGTTCCTGGACGTGTACAAGAACTGCAACGGGGTGGTCAT 1032

Qy 621 CATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAA 680
Db 1033 GATGTTCGACATTACCAAGCAGTGGACCTTCAATTACATTCTCCGGGAGCTTCCAAAAGT 1092

Qy 681 TTCTCGGCATGTGGAAGTGAGC 702
Db 1093 GCCCACCCACGTGCCAGTGTGC 1114

RESULT 10
US-10-953-349-38921
; Sequence 38921, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 38921
; LENGTH: 2152
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
US-10-953-349-38921

Query Match 2.1%; Score 32.4; DB 6; Length 2152;
Best Local Similarity 47.9%; Pred. No. 3.9;
Matches 93; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

Qy 458 TCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTC 517
Db 475 TCTCGGCCGAGGAGATCAGCTCCATGATCCTGAACAAGATGAAGGAGACGGCCGAGGCTT 534

Qy 518 AGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACG 577
Db 535 ACCTCGGCACCACCATCAAGAACGCTGTCGTCACCGTCCCGGCCTACTTCAACGACTCCC 594

Qy 578 CTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCA 637
Db 595 AGCGCCAGGCCACCAAGGACGCCGGCGTCATCTCCGGCCTCAACGTCATGCGCATCATCA 654

Qy 638 AACCGGACCCACCC 651
Db 655 ACGAGCCCACCGCC 668

RESULT 11
US-11-293-697-1600
; Sequence 1600, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1600
; LENGTH: 2338
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-1600

Query Match 2.1%; Score 32.4; DB 7; Length 2338;
Best Local Similarity 49.4%; Pred. No. 4.2;
Matches 84; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

Qy 1246 CTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCA 1305
Db 1001 CTCAGGCGGAGCAAAGTGTCCATTGAGATGTACCAGTCGCAGGTGGCAAAGCTGGAGGAT 1060

Qy 1306 AAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATT 1365
Db 1061 GATATCTACAAAGAGGCCGAAGAGAAGGCCCTGCTGAAGGAGGCCCTGGAGCGCATGGAG 1120

Qy 1366 GATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAA 1415
Db 1121 CACCAGCTGTGCCAGGAGAAGAGGGTCAACAGGGCCATCCGGCAGCAGAA 1170

RESULT 12
US-10-953-349-32903
; Sequence 32903, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2

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;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32903
;   LENGTH: 620
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-32903

  Query Match             2.1%;  Score 32;  DB 6;  Length 620;
  Best Local Similarity   47.1%;  Pred. No. 2.3;
  Matches   98;  Conservative    0;  Mismatches  110;  Indels    0;  Gaps    0;

Qy        508 GTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTC 567
              |||||||      | |    ||     || |||||| | |  |    |  ||    |   ||
Db         90 GTGGAGTTGGCAAAAGCTCATGAGATCCAGGCTGCTGTGCTGTTGCACCCTTCTTTTGTT 149

Qy        568 GTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGG 627
                || |||| |||   |   || |||||| || ||   |  | |  | |        ||
Db        150 ACCGTTGACGATATCAAAGAGGTCAAGTGCGCAATTTCTATCCTCGGAGCTGAGATTGAC 209

Qy        628 GACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGG 687
               | ||    |  |||||| | |  |||| |  |  | | |    |  |      || ||  ||
Db        210 AAAATGTCCCCACCGGAGCTAATCAAGCAGTTCGAGCAGGTCCTTTCTTTGAACTCAGGG 269

Qy        688 CATGTGGAAGTGAGCTGGGAATACCCTG 715
               ||    |  |    |  |   | |||||
Db        270 GTTGGCCACTTCGTCAAGATCTTCCCTG 297


RESULT 13
US-11-293-697-1253
; Sequence 1253, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1253
;   LENGTH: 2024
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1253

  Query Match             2.1%;  Score 32;  DB 7;  Length 2024;
  Best Local Similarity   50.7%;  Pred. No. 5.1;
  Matches   77;  Conservative    0;  Mismatches   75;  Indels    0;  Gaps    0;

Qy        144 CTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTG 203
              |||||  |  |||  |  ||     |||    | |   | | |   |||       |||| ||
Db        496 CTCTGTTGAAAGTTTGTTTCACCAGCAAATACTTTCTTCTTGTGCCAAAAGCTATAACTT 555

Qy        204 TCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGG 263
              | || ||    |  |||| | |  ||||| |   | || |  ||  || |||||   |
Db        556 TGATCAATATAGGAAGGTCTTTACTCATTCATCATTGCTTAATCAACAAGAGGAAATAGA 615

Qy        264 AATTTGGTCCACTGATATCTTAAGGGAACAGA 295
              ||||||   |   ||  | ||   ||  | |
Db        616 TATTTGGGGAAAACATCACATATATGATAAAA 647


RESULT 14
US-10-471-571A-5411
; Sequence 5411, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 5411
;   LENGTH: 1404
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-5411

  Query Match             2.1%;  Score 31.8;  DB 6;  Length 1404;
  Best Local Similarity   57.6%;  Pred. No. 4.6;
  Matches   57;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy        262 GGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTA 321
              | |||||  |  |   |  | |  | |  || ||  ||| |||   ||   ||||  ||| ||
Db         11 GTAATTTTTTAAATGTAGAGTTAATAGGTACTAAAATAATAACAATGGAAGACTTTTATA 70

Qy        322 AAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              |||||   |   ||||||| ||||  |  | | | || |
Db         71 AAATGAAGGAAGAAGAATTTTTCTTAAAATCTAAGCTAC 109


RESULT 15
US-10-953-349-22720/c
; Sequence 22720, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22720
;   LENGTH: 1906
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-22720

  Query Match             2.1%;  Score 31.8;  DB 6;  Length 1906;
  Best Local Similarity   61.4%;  Pred. No. 5.6;
  Matches   51;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy        160 ACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAG 219
              || ||||||||||  ||  |||||| | |       ||   | ||||||      | |
Db        918 ACTATCCAAGTCACTGACATTGCAGTTCCCATTATTTAACGCAGTCATATCTATAGAGGA 859

Qy        220 GTTCTGAGCCATTCGTTCCTCCT 242
              || |||||||  |  ||||||||
Db        858 ATTTTGAGCCAATGCTTCCTCCT 836


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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 12, 2006, 15:14:42 ; Search time 6929 Seconds
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Title: US-10-821-670A-44
Perfect score: 2687
Sequence: 1 IWELEKNVYVVELDWHPDAP.....HAFRIRAVTINRMMSYLNAS 511

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

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Listing first 45 summaries

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-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss06h
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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5: gb_pr:*
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10: gb_vi:*
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12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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c	2	2687	100.0	1533	2	AR595960	AR595960 Sequence
	3	2687	100.0	1599	2	AR595956	AR595956 Sequence
c	4	2687	100.0	1599	2	AR595957	AR595957 Sequence
	5	2546	94.8	1533	2	AR595973	AR595973 Sequence
c	6	2546	94.8	1533	2	AR595974	AR595974 Sequence
	7	2546	94.8	1599	2	AR595971	AR595971 Sequence
c	8	2546	94.8	1599	2	AR595972	AR595972 Sequence
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	10	2320.5	86.4	1560	2	AR091395	AR091395 Sequence
	11	2320.5	86.4	1623	2	AR091394	AR091394 Sequence
	12	2320.5	86.4	6139	2	AR091393	AR091393 Sequence
	13	1671	62.2	5252	2	CQ803341	CQ803341 Sequence
	14	1671	62.2	9049	2	CQ803350	CQ803350 Sequence
	15	1671	62.2	10633	2	CQ803349	CQ803349 Sequence
	16	1671	62.2	11746	2	CQ803348	CQ803348 Sequence
	17	1671	62.2	38246	2	CQ803351	CQ803351 Sequence
	18	1666	62.0	2438	2	CQ812173	CQ812173 Sequence
	19	1658	61.7	1669	8	AF411293	AF411293 Synthetic
	20	1646	61.3	921	2	AR595948	AR595948 Sequence
c	21	1646	61.3	921	2	AR595949	AR595949 Sequence
	22	1646	61.3	1006	14	FCIL12P40	Y07762 Felis catus
	23	1640	61.0	4522	2	AX076209	AX076209 Sequence
	24	1640	61.0	4522	2	AX076476	AX076476 Sequence
	25	1639	61.0	921	2	AR242436	AR242436 Sequence
	26	1639	61.0	921	2	AR242437	AR242437 Sequence
	27	1639	61.0	921	2	AR280204	AR280204 Sequence
	28	1639	61.0	921	2	AR280205	AR280205 Sequence
	29	1639	61.0	921	2	AR322419	AR322419 Sequence
	30	1639	61.0	921	2	AR322420	AR322420 Sequence
	31	1639	61.0	987	2	AR595950	AR595950 Sequence
c	32	1639	61.0	987	2	AR595951	AR595951 Sequence
	33	1639	61.0	990	2	AX076200	AX076200 Sequence
	34	1639	61.0	990	2	AX076482	AX076482 Sequence
	35	1639	61.0	2193	2	AR242435	AR242435 Sequence
	36	1639	61.0	2193	2	AR280203	AR280203 Sequence
	37	1639	61.0	2193	2	AR322418	AR322418 Sequence
	38	1635	60.8	985	2	AR595967	AR595967 Sequence
c	39	1635	60.8	985	2	AR595968	AR595968 Sequence
	40	1634	60.8	990	14	FCU83184	U83184 Felis catus
	41	1547	57.6	1015	14	CFU49100	U49100 Canis famil
	42	1546	57.5	921	2	AR595965	AR595965 Sequence
c	43	1546	57.5	921	2	AR595966	AR595966 Sequence
	44	1546	57.5	987	2	AR595969	AR595969 Sequence
c	45	1546	57.5	987	2	AR595970	AR595970 Sequence

ALIGNMENTS

RESULT 1
AR595959
LOCUS AR595959 1533 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 43 from patent US 6818444.
ACCESSION AR595959
VERSION AR595959.1 GI:56646940
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1533)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 43 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .1533
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.: 7.14e-284 Length: 1533
Score: 2687.00 Matches: 511
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0

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DB:                    2              Gaps:          0

US-10-821-670A-44 (1-511) x AR595959 (1-1533)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
              |||||||||||||||||||||||||||||||
Db       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533

RESULT 2
AR595960/c
LOCUS       AR595960               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 45 from patent US 6818444.
ACCESSION   AR595960
VERSION     AR595960.1  GI:56646941
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 45 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              7.14e-284      Length:         1533
Score:                  2687.00        Matches:        511
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-44 (1-511) x AR595960 (1-1533)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414
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Qy        41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy       101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy       121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy       141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy       161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy       221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy       241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy       261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy       281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy       301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       633 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy       321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       573 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy       341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy       361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy       381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy       401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy       421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy       441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy       461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy       481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy       501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
             |||||||||||||||||||||||||||||||||
Db        33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 3
AR595956
LOCUS       AR595956               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 38 from patent US 6818444.
ACCESSION   AR595956
VERSION     AR595956.1  GI:56646937
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 38 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              7.63e-284       Length:         1599
Score:                  2687.00         Matches:        511
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-44 (1-511) x AR595956 (1-1599)

Qy         1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy        21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1086

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1146

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1147 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1266

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1267 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1326

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1327 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1386

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1387 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1446

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1506

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1566

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
              |||||||||||||||||||||||||||||||||
Db       1567 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599

RESULT 4
AR595957/c
LOCUS       AR595957               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 40 from patent US 6818444.
ACCESSION   AR595957
VERSION     AR595957.1  GI:56646938
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 40 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              7.63e-284       Length:         1599
Score:                  2687.00         Matches:        511
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-44 (1-511) x AR595957 (1-1599)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
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Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180

Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200

Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220

Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240

Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260

Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280

Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300

Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320

Db        633 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340

Db        573 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360

Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380

Db        453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400

Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420

Db        333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440

Db        273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460

Db        213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480

Db        153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500

Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
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Db         33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
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RESULT 5
AR595973

LOCUS	AR595973	1533 bp	DNA	linear	PAT 15-DEC-2004

DEFINITION Sequence 66 from patent US 6818444.
ACCESSION AR595973
VERSION AR595973.1 GI:56646954
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1533)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 66 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .1533
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Alignment Scores:

Pred. No.:	2.07e-268	Length:	1533
Score:	2546.00	Matches:	482
Percent Similarity:	96.7%	Conservative:	12
Best Local Similarity:	94.3%	Mismatches:	17
Query Match:	94.8%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-44 (1-511) x AR595973 (1-1533)

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Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20

Db          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40

Db         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60

Db        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80

Db        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100

Db        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120

Db        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140

Db        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160

Db        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180

Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540

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Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600
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Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
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Db        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||   :::|||   ||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              |||||||||||||||||||||||   |||||||||||||||||||||||||||||||||||
Db        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
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Db        961 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 1020

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
              |||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 1080

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
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Db       1081 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1200

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
              ||||||||||||||   |||   ||||||||||||   ||||||||||||||||||||||
Db       1201 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1260

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1320

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
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Db       1321 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 1380

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
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Db       1381 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1440

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1500

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
              |||||||||||||||||||||||:::|||
Db       1501 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1533

RESULT 6
AR595974/c
LOCUS       AR595974               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 68 from patent US 6818444.
ACCESSION   AR595974
VERSION     AR595974.1  GI:56646955
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 68 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                2.07e-268      Length:          1533
Score:                    2546.00        Matches:         482
Percent Similarity:       96.7%          Conservative:    12
Best Local Similarity:    94.3%          Mismatches:      17
Query Match:              94.8%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-44 (1-511) x AR595974 (1-1533)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
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Db       1473 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||:::|||||||||   |||   |||||||
Db       1353 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||
Db       1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||:::|||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||   ||||||||||||||||   ||||||||||||||:::|||||||||
Db       1113 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
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Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
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Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
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Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
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Db        873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||   :::|||   ||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754
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Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||    |||||||||||||||||||||||||||||||||
Db        753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 634

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        573 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 514

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
              ||||||||||||||||||||||||||||||||||    ||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 454

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 334

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
              ||||||||||||||    |||   ||||||||||||   ||||||||||||||||||||
Db        333 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 274

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
              ||||||||||||||||||:::|||||||||||||||||||||||||||||||||||||||
Db        273 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 214

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 154

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
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Db        153 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 94

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 34

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
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Db         33 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1
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RESULT 7
AR595971
LOCUS       AR595971               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 61 from patent US 6818444.
ACCESSION   AR595971
VERSION     AR595971.1  GI:56646952
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 61 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
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ORIGIN
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Alignment Scores:
Pred. No.:              2.21e-268       Length:         1599
Score:                  2546.00         Matches:        482
Percent Similarity:     96.7%           Conservative:   12
Best Local Similarity:  94.3%           Mismatches:     17
Query Match:            94.8%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-44 (1-511) x AR595971 (1-1599)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||:::|||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||:::|||||||||   |||   |||
Db        247 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db        307 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||:::|||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||   ||||||||||||   ||||||||||||||:::|||||||||
Db        487 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 606

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 726

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 786

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||   :::|||   ||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 846

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||    |||||||||||||||||||||||||||||||||
Db        847 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 966

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
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Db        967 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db       1027 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 1086

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
              |||||||||||||||||||||||||||||||||||    ||||||||||||||||||||
Db       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 1146

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1147 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1266

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
              ||||||||||||||    |||    ||||||||||||    ||||||||||||||||||||
Db       1267 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1326

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db       1327 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1386

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1387 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 1446

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
              |||||||||    ||||||||||||||||||||    ||||||||||||||||||||||
Db       1447 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1506

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1566

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
              |||||||||||||||||||||||||:::|||
Db       1567 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1599

RESULT 8
AR595972/c
LOCUS       AR595972               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 63 from patent US 6818444.
ACCESSION   AR595972
VERSION     AR595972.1  GI:56646953
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 63 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.21e-268      Length:         1599
Score:                  2546.00        Matches:        482
Percent Similarity:     96.7%          Conservative:   12
Best Local Similarity:  94.3%          Mismatches:     17
Query Match:            94.8%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-44 (1-511) x AR595972 (1-1599)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||:::|||||||||    |||    |||
Db       1353 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||
Db       1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||    ||||||||||||||||    ||||||||||||||:::|||||||||
Db       1113 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||    :::|||    ||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||    ||||||||||||||||||||||||||||||||||
Db        753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 634

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        573 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 514

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
              |||||||||||||||||||||||||||||||||||    ||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 454

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 334

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
                |||||||||||||||   |||   ||||||||||||   ||||||||||||||||||||
Db        333 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 274

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
                ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db        273 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 214

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 154

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
                |||||||||   ||||||||||||||||||||   ||||||||||||||||||||||||
Db        153 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 94

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 34

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
                |||||||||||||||||||||||||:::|||
Db         33 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1

RESULT 9
AF401989
LOCUS       AF401989                1626 bp    mRNA    linear   SYN 14-FEB-2002
DEFINITION  Synthetic construct single chain interleukin-12 mRNA, complete cds.
ACCESSION   AF401989
VERSION     AF401989.1  GI:18656516
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 1626)
  AUTHORS   McMonagle,E.L.J., Taylor,S., van Zuilekom,H., Sanders,L.,
            Scholtes,N., Keanie,L.J., Hopkins,C.A., Logan,N.A., Bain,D.,
            Argyle,D.J., Onions,D.E., Schijns,V.E. and Nicolson,L.
  TITLE     Production of biologically active equine interleukin 12 through
            expression of p35, p40 and single chain IL-12 in mammalian and
            baculovirus expression systems
  JOURNAL   Equine Vet. J. 33 (7), 693-698 (2001)
   PUBMED   11770992
REFERENCE   2  (bases 1 to 1626)
  AUTHORS   McMonagle,L.J., Taylor,S., Keanie,L.J., Hopkins,C.A., Logan,N.A.,
            Argyle,D.J., Onions,D.E. and Nicolson,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUL-2001) Veterinary Pathology, Glasgow Veterinary
            School, Bearsden Rd, Glasgow G61 1QH, UK
FEATURES             Location/Qualifiers
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                     GSSDPRGVTCGAATLSAERVSVDDREYKKYTVECQEGSACPAAEESLPIEIVVDAVHK
                     LKYENYTSGFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPETWSTPHSYFSLTFSI
                     QVQGKNKKERKDRLFMDETSATVTCHKDGQIRVQARDRYYSSSWSEWASVSCSGGGGS
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     misc_feature    1033. .1611
                     /note="interleukin-12 p35 sequence"
     primer_bind     complement(1612. .1626)
ORIGIN

Alignment Scores:
Pred. No.:                9.33e-248      Length:          1626
Score:                    2358.00        Matches:         444
Percent Similarity:       91.1%          Conservative:    29
Best Local Similarity:    85.5%          Mismatches:      38
Query Match:              87.8%          Indels:          8
DB:                       8              Gaps:            1

US-10-821-670A-44 (1-511) x AF401989 (1-1626)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||:::||||||||||||||||||||||||:::||||||||||||||
Db         67 ATATGGGAACTGGAGAAAGATGTGTATGTTGTAGAATTGGATTGGTACCCTGATGCCCCT 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||:::   ||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACCCCTGAAGAAGAAGGCATCACCTGGACCTCG 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
                 ||||||:::||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GCCCAGAGCAATGAGGTCTTAGGCTCTGGCAAAACCTTGACCATCCAAGTCAAAGAGTTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
                 |||||||||   ||||||||||||||||||||||||||||||||||||   |||
Db        247 GGAGATGCTGGCTGGTACACCTGTCACAAAGGAGGCGAGGTTCTGAGCCATTCTCACCTG 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              |||:::||||||||||||||||||||||||||||||||||||||:::::::|||||||||
Db        307 CTGCTTCACAAGAAGGAAGATGGAATTTGGTCCACTGACATTTTAAAAGACCAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGACCTTTCTAAAATGTGAGGCAAAGAATTATTCCGGACGTTTCACATGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db        427 TGGTGGCTGACAGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGCAGCAGAGGTTCC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||:::   ||||||||||||||||||||||||||||||:::|||   |||
Db        487 TCTGACCCCCGAGGGGTGACGTGTGGAGCAGCGACACTCTCCGCAGAGAGGGTCAGCGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              |||:::|||:::||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACGACAGGGAGTATAAGAAGTACACGGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCC 606

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||:::||||||||||||:::||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTGCCCATTGAGATCGTGGTGGATGCTGTTCACAAGCTCAAGTATGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCGGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACCTG 726

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||   ||||||||||||||||||||:::|||
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Db        727 CAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCCGAGACC 786

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||   :::|||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTCTCTATTCAGGTCCAGGGCAAGAAC 846

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
                 :::|||:::|||||||||||||   :::|||:::|||||||||   |||   ||||||
Db        847 AAGAAGGAAAGGAAAGACAGACTCTTCATGGATGAGACTTCAGCCACAGTCACATGCCAC 906

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||   :::|||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGGCCAGATCCGTGTCCAAGCCAGGGACCGCTACTACAGCTCATCCTGGAGCGAA 966

Qy        301 TrpAlaSerValSerCysSerGlyGly----------------------GlyGlyGly 312
              |||||||||||||||||||||||||||                      |||||||||
Db        967 TGGGCATCCGTATCCTGCAGTGGTGGCGGTGGCTCGGGCGGTGGTGGATCCGGTGGCGGC 1026

Qy        313 GlySerArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHis 332
              ||||||||||||||||||    ||||||   ||||||||||||||||||||||||||||||
Db       1027 GGATCTAGGAACCTCCCCACAGCCACACCAGGCCCAGGAATGTTCCAGTGCCTCAACCAC 1086

Qy        333 SerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGlu 352
              ||||||   |||||||||   :::|||||||||||||||||||||||||||||||||||||
Db       1087 TCCCAAAACCTGCTGAGGACCGTCAGCAACACGCTTCAGAAGGCCAGGCAAACCCTAGAA 1146

Qy        353 PheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSer 372
              |||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||
Db       1147 TTCTACTCCTGCACTTCTGAAGAGATCGATCATGAGGATATCACAAAAGACAAGAGCAGC 1206

Qy        373 ThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArg 392
              ||||||   ||||||||||||||||||||      ||||||||||||||||||||||
Db       1207 ACCGTGGCGGCCTGCCTCCCCCTGGAACTCGCCCCGAACGAGAGTTGCCTGGCTTCCAGA 1266

Qy        393 GluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThr 412
              |||||||||   ||||||||||||||||||||        |||   |||   |||
Db       1267 GAGATCTCTTTCATAACTAATGGGAGTTGCCTGACCCCCGGAAAGGCCTCTTCTATGATG 1326

Qy        413 ThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAla 432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1327 ACGCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCC 1386

Qy        433 MetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 452
              ||||||||||||||||||:::||||||:::|||||||||||||||||:::|||||||||
Db       1387 ATGAATGCCAAGCTGTTGATAGATCCTCAGAGGCAGATCTTTCTGGATGAGAACATGCTG 1446

Qy        453 ThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsn 472
              ||||||||||:::|||:::||||||||||||   ||||||   ||||||||||||
Db       1447 ACAGCCATTGACAAGCTGATGCAGGCCCTGAACTTCAACAGTGAGACTGTGCCACAAAAG 1506

Qy        473 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 492
                 |||||||||      ||||||||||||||||||:::||||||||||||||||||||
Db       1507 CCCTCCCTTGAAGGACTGGATTTTTATAAAACTAAAGTCAAGCTCTGCATCCTTCTTCAT 1566

Qy        493 AlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 511
              |||||||||||||||||||||||||||||||||||||||   |||||||||||||||
Db       1567 GCCTTCAGAATCCGCGCAGTGACCATCAACAGGATGATGGGCTATCTGAATGCTTCC 1623

RESULT 10
AR091395
LOCUS       AR091395               1560 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 11 from patent US 5994104.
ACCESSION   AR091395
VERSION     AR091395.1  GI:10018150
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1560)
  AUTHORS   Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
  TITLE     Interleukin-12 fusion protein
  JOURNAL   Patent: US 5994104-A 11 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .1560
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.13e-243      Length:          1560
Score:                  2320.50        Matches:         441
Percent Similarity:     90.2%          Conservative:    27
Best Local Similarity:  85.0%          Mismatches:      42
Query Match:            86.4%          Indels:          9
DB:                     2              Gaps:            2

US-10-821-670A-44 (1-511) x AR091395 (1-1560)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              |||||||||||||:::|||:::|||||||||||||||||||||||||:::|||||||||||||
Db          4 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 63

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              |||||||||||||||||||||||||:::|||||||||||||||   ||||||||||||
Db         64 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 123

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 183

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        184 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 243

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              |||:::|||||||||||||||||||||||||||||||||||||||:::::::|||||||||
Db        244 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 303

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              |||||||||   |||||||:::|||||||||||||||||||||||||||||||||||||
Db        304 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 363

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||   ||||||||||||||   |||:::||||||||||||||||||||||
Db        364 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 423

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||   ||||||||||||||||||||||||||||||:::||||||
Db        424 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 483

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||::::::|||   :::|||:::||||||||||||||   ||||||||||||||||
Db        484 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              |||||||||||||||||||||||||||:::|||||||||:::|||||||||||||||||||
Db        541 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        661 CAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||   |||||||||||||||||||:::
Db        721 TGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||:::      |||||||||||||||   |||:::|||
Db        781 AAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              |||:::|||   |||   |||:::|||:::|||||||||||||||||||||||||||||
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Db        841 AAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAA 900

Qy        301 TrpAlaSerValSerCysSerGlyGly-----------------------GlyGlyGly 312
              |||||||||||||   ||||||||||||                      |||||||||
Db        901 TGGGCATCTGTGCCCTGCAGTGGTGGCGGTGGAAGCGGCGGTGGCGGAAGCGGCGGTGGC 960

Qy        313 GlySerArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHis 332
              |||||||||||||||||      ||||||   ||||||||||||   ||||||:::|||
Db        961 GGCAGCAGAAACCTCCCCCTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCAC 1020

Qy        333 SerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGlu 352
              ||||||   ||||||||||||:::||||||   ||||||||||||||||||||||||||
Db       1021 TCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAA 1080

Qy        353 PheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSer 372
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGC 1140

Qy        373 ThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArg 392
              ||||||||||||||||||||||||||||||   ||||||||||||||   ||||||
Db       1141 ACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGA 1200

Qy        393 GluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThr 412
              |||   |||   ||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATG 1260

Qy        413 ThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAla 432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACC 1320

Qy        433 MetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 452
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTG 1380

Qy        453 ThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsn 472
              |||||||||||||:::||||||||||||   ||||||   ||||||||||||
Db       1381 GCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAA 1440

Qy        473 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1500

Qy        493 AlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 511
              |||||||||||||||||||||||||:::||:::   ||||||||||||||||||
Db       1501 GCTTTCAGAATTCGGGCAGTGACTATTGACAGAGTGACGAGCTATCTGAATGCTTCC 1557

RESULT 11
AR091394
LOCUS       AR091394               1623 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 9 from patent US 5994104.
ACCESSION   AR091394
VERSION     AR091394.1  GI:10018149
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1623)
  AUTHORS   Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
  TITLE     Interleukin-12 fusion protein
  JOURNAL   Patent: US 5994104-A 9 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .1623
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.2e-243        Length:         1623
Score:                  2320.50         Matches:        441
Percent Similarity:     90.2%           Conservative:   27
Best Local Similarity:  85.0%           Mismatches:     42
Query Match:            86.4%           Indels:         9
DB:                     2               Gaps:           2
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US-10-821-670A-44 (1-511) x AR091394 (1-1623)

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Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              |||||||||||:::|||:::||||||||||||||||||||||||:::||||||||||||
Db         67 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||:::|||||||||||||||   ||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        247 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              |||:::|||||||||||||||||||||||||||||||||||||:::::::|||||||||
Db        307 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              |||||||||   ||||||:::||||||||||||||||||||||||||||||||||||||
Db        367 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||   ||||||||||||||||   |||:::||||||||||||||||||
Db        427 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||   ||||||||||||||||||||||||||||||:::||||||
Db        487 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||::::::|||   :::|||:::||||||||||||||   ||||||||||||||
Db        547 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 603

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||:::|||||||||:::||||||||||||||
Db        604 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAA 663

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTG 723

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        724 CAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACC 783

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              |||||||||||||||||||||||||||||||||||   |||||||||||||||||||:::
Db        784 TGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGC 843

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||:::      ||||||||||||||   |||:::|||
Db        844 AAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGC 903

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              |||:::|||   |||   |||:::|||:::|||||||||||||||||||||||||||
Db        904 AAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAA 963

Qy        301 TrpAlaSerValSerCysSerGlyGly-----------------------GlyGlyGly 312
              |||||||||||||   ||||||||||                      |||||||||
Db        964 TGGGCATCTGTGCCCTGCAGTGGTGGCGGTGGAAGCGGCGGTGGCGGAAGCGGCGGTGGC 1023

Qy        313 GlySerArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHis 332
              ||||||||||||||||||      ||||||   ||||||||||||   ||||||:::|||
Db       1024 GGCAGCAGAAACCTCCCCCTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCAC 1083

Qy        333 SerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGlu 352
              ||||||   ||||||||||||:::||||||   ||||||||||||||||||||||||||
Db       1084 TCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAA 1143
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Db       1084 TCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAA 1143

Qy        353 PheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSer 372

Db       1144 TTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGC 1203

Qy        373 ThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArg 392

Db       1204 ACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGA 1263

Qy        393 GluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThr 412

Db       1264 GAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATG 1323

Qy        413 ThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAla 432

Db       1324 GCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACC 1383

Qy        433 MetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 452

Db       1384 ATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTG 1443

Qy        453 ThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsn 472

Db       1444 GCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAA 1503

Qy        473 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 492

Db       1504 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1563

Qy        493 AlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 511

Db       1564 GCTTTCAGAATTCGGGCAGTGACTATTGACAGAGTGACGAGCTATCTGAATGCTTCC 1620
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RESULT 12
AR091393
LOCUS AR091393 6139 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 7 from patent US 5994104.
ACCESSION AR091393
VERSION AR091393.1 GI:10018148
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 6139)
AUTHORS Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
TITLE Interleukin-12 fusion protein
JOURNAL Patent: US 5994104-A 7 30-NOV-1999;
FEATURES Location/Qualifiers
source 1. .6139
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Alignment Scores:

Pred. No.:	9.72e-243	Length:	6139
Score:	2320.50	Matches:	441
Percent Similarity:	90.2%	Conservative:	27
Best Local Similarity:	85.0%	Mismatches:	42
Query Match:	86.4%	Indels:	9
DB:	2	Gaps:	2

US-10-821-670A-44 (1-511) x AR091393 (1-6139)

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Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20

Db       3288 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 3347

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40

Db       3348 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 3407

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60

Db       3408 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 3467

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80

Db       3468 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 3527

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100

Db       3528 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 3587

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120

Db       3588 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 3647

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140

Db       3648 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 3707

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160

Db       3708 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 3767

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180

Db       3768 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 3824

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200

Db       3825 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAA 3884

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220

Db       3885 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTG 3944

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240

Db       3945 CAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACC 4004

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260

Db       4005 TGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGC 4064

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280

Db       4065 AAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGC 4124

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300

Db       4125 AAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAA 4184

Qy        301 TrpAlaSerValSerCysSerGlyGly----------GlyGlyGly 312

Db       4185 TGGGCATCTGTGCCCTGCAGTGGTGGCGGTGGAAGCGGCGGTGGCGGAAGCGGCGGTGGC 4244

Qy        313 GlySerArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHis 332

Db       4245 GGCAGCAGAAACCTCCCCCTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCAC 4304

Qy        333 SerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGlu 352

Db       4305 TCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAA 4364

Qy        353 PheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSer 372

Db       4365 TTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGC 4424

Qy        373 ThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArg 392

Db       4425 ACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGA 4484

Qy        393 GluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThr 412
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Db       4485 GAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATG 4544

Qy        413 ThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAla 432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4545 GCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACC 4604

Qy        433 MetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 452
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4605 ATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTG 4664

Qy        453 ThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsn 472
              ||||||||||||:::||||||||||||    ||||||    ||||||||||||
Db       4665 GCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAA 4724

Qy        473 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4725 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 4784

Qy        493 AlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 511
              |||||||||||||||||||||||||:::|||:::   ||||||||||||||||||
Db       4785 GCTTTCAGAATTCGGGCAGTGACTATTGACAGAGTGACGAGCTATCTGAATGCTTCC 4841

RESULT 13
CQ803341
LOCUS       CQ803341               5252 bp    DNA     linear   PAT 10-MAY-2004
DEFINITION  Sequence 1 from Patent WO2004035799.
ACCESSION   CQ803341
VERSION     CQ803341.1  GI:47110207
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Waehler,R. and Schnieders,F.
  TITLE     Viral vectors and the use of the same for gene therapy
  JOURNAL   Patent: WO 2004035799-A 1 29-APR-2004;
            Universitaetsklinikum Hamburg-Eppendorf (DE)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Vektor mit tricistronischer Expressionskassette als
                     Insert"
ORIGIN

Alignment Scores:
Pred. No.:              1.26e-171      Length:         5252
Score:                  1671.00        Matches:        327
Percent Similarity:     74.2%          Conservative:   66
Best Local Similarity:  61.7%          Mismatches:     109
Query Match:            62.2%          Indels:         28
DB:                     2              Gaps:           6

US-10-821-670A-44 (1-511) x CQ803341 (1-5252)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              :::|||||||||||||||:::|||||||||||||||:::||||||   ||||||||||||
Db        679 ATGTGGGAGCTGGAGAAAGACGTTTATGTTGTAGAGGTGGACTGGACTCCCGATGCCCCT 738

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||   |||   |||||||||:::||||||||||||||||||||||||||||||||
Db        739 GGAGAAACAGTGAACCTCACCTGTGACACGCCTGAAGAAGATGACATCACCTGGACCTCA 798

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||         |||:::|||||||||||||||||||||   ||||||||||||
Db        799 GACCAGAGACATGGAGTCATAGGCTCTGGAAAGACCCTGACCATCACTGTCAAAGAGTTT 858

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||   ||||||||||||   |||
Db        859 CTAGATGCTGGCCAGTACACCTGCCACAAAGGAGGCGAGACTCTGAGCCACTCACATCTG 918

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              |||:::|||||||||||:::|||||||||||||||:::||||||         |||
Db        919 CTGCTCCACAAGAAGGAAAATGGAATTTGGTCCACTGAAATTTTA---------AAAAAT 969

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              |||||||||   ||||||||||||||||||    ||||||||||||||||||||||||
Db        970 TTCAAAAACAAGACTTTCCTGAAGTGTGAAGCACCAAATTACTCCGGACGGTTCACGTGC 1029

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||         :::   ||||||||||||   :::|||||||||       |||
Db       1030 TCATGGCTGGTGCAAAGAAACATGGACTTGAAGTTCAACATCAAGAGCAGTAGCAGTTCC 1089

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||   :::   ||||||||||||   |||:::||||||||||||||||   :::
Db       1090 CCTGACTCTCGGGCAGTGACATGTGGAATGGCGTCTCTGTCTGCAGAGAAGGTCACACTG 1149

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              |||   |||||||||:::||||||:::|||   |||||||||         ||||||
Db       1150 GACCAAAGGGACTATGAGAAGTATTCAGTGTCCTGCCAGGAGGATGTCACCTGCCCAACT 1209

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              |||||||||:::||||||||||||:::   ::::::|||      :::   |||||||||
Db       1210 GCCGAGGAGACCCTGCCCATTGAACTGGCGTTGGAAGCACGGCAGCAGAATAAATATGAG 1269

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||::::::||||||||||||||||||||||||||||||||||||||||||||||||
Db       1270 AACTACAGCACCAGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTG 1329

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              |||:::|||||||||||||||||:::   ||||||||||||||||||||||||||:::
Db       1330 CAGATGAAGCCTTTGAAGAACTCACAG---GTGGAGGTCAGCTGGGAGTACCCTGACTCC 1386

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||   |||   |||::::::|||   |||
Db       1387 TGGAGCACTCCCCATTCCTACTTCTCCCTCAAGTTCTTTGTTCGAATCCAGCGCAAGAAA 1446

Qy        261 AsnArgGluLys----------------------LysAspArgLeuSerValAspLys 272
              :::   |||                      |||           |||:::|||
Db       1447 GAAAAGATGAAGGAGACAGAGGAGGGGGTGTAACCAGAAAGGTGCGTTCCTCGTAGAGAAG 1506

Qy        273 ThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaArgAspArg 292
              ||||||   :::|||   |||   |||         :::   ||||||||:::||||||
Db       1507 ACATCTACCGAAGTCCAATGC---AAAGGCGGGAATGTCTGCGTGCAAGCTCAGGATCGC 1563

Qy        293 TyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys------------------ 306
              ||||||:::||||||   |||   ||||||   |||   |||
Db       1564 TATTACAATTCCTCATGCAGCAAGTGGGCATGTGTTCCCTGCAGGGTCCGATCCGGTGGC 1623

Qy        307 --------------SerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrProThr 321
                           |||   ||||||||||||||||   :::|||
Db       1624 GGTGGCTCGGGCGGTGGTGGGTCGGGTGGCGGCGGATCTAGGGTCATTCCAGTCTCTGGA 1683

Qy        322 ProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSer 341
              |||:::            :::|||||:::   |||:::   ||||||:::
Db       1684 CCTGCC------------AGGTGTCTTAGCCAGTCCCGAAACCTGCTGAAGACCACAGAT 1731

Qy        342 AsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIle 361
              :::   :::::   ||||||:::   |||:::   |||||||||||||:::|||:::|||
Db       1732 GACATGGTGAAGACGGCCAGAGAAAAGCTGAAACATTATTCCTGCACTGCTGAAGACATC 1791

Qy        362 AspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGlu 381
              ||||||||||||||||||:::|||:::|||||||||::::::   ||||||||||||||
Db       1792 GATCATGAAGACATCACACGGGACCAAACCAGCACATTGAAGACCTGTTTACCACTGGAA 1851

Qy        382 LeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySer 401
              |||       ||||||||||||||||||:::||||||   |||       |||   ||||||
Db       1852 CTACACAAGAACGAGAGTTGCCTGGCTACTAGAGAGACTTCTTCCACAACAAGAGGGAGC 1911

Qy        402 CysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGlu 421
              ||||||      :::|||||||||   |||   ||||||||||||   ||||||||||||
Db       1912 TGCCTGCCCCCACAGAAGACGTCTTTGATGATGACCCTGTGCCTTGGTAGCATCTATGAG 1971

Qy        422 AspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspPro 441
              ||||||||||||||||||   |||||||:::|||:::||||||   |||
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Db       1972 GACTTGAAGATGTACCAGACAGAGTTCCAGGCCATCAACGCAGCACTTCAGAATCACAAC 2031

Qy        442 LysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAla 461

Db       2032 CATCAGCAGATCATTCTAGACAAGGGCATGCTGGTGGCCATCGATGAGCTGATGCAGTCT 2091

Qy        462 LeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyr 481

Db       2092 CTGAATCATAATGGCGAGACTCTGCGCCAGAAACCTCCTGTGGGAGAAGCAGACCCTTAC 2151

Qy        482 LysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIle 501

Db       2152 AGAGTGAAAATGAAGCTCTGCATCCTGCTTCACGCCTTCAGCACCCGCGTCGTGACCATC 2211

Qy        502 AsnArgMetMetSerTyrLeuAsnAlaSer 511

Db       2212 AACAGGGTGATGGGCTATCTGAGCTCCGCC 2241

RESULT 14
CQ803350
LOCUS       CQ803350                9049 bp    DNA     linear   PAT 10-MAY-2004
DEFINITION  Sequence 10 from Patent WO2004035799.
ACCESSION   CQ803350
VERSION     CQ803350.1  GI:47110216
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Waehler,R. and Schnieders,F.
  TITLE     Viral vectors and the use of the same for gene therapy
  JOURNAL   Patent: WO 2004035799-A 10 29-APR-2004;
            Universitaetsklinikum Hamburg-Eppendorf (DE)
FEATURES             Location/Qualifiers
     source          1. .9049
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     misc_feature    1. .9049
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ORIGIN

Alignment Scores:
Pred. No.:              2.96e-171       Length:         9049
Score:                  1671.00         Matches:        327
Percent Similarity:     74.2%           Conservative:   66
Best Local Similarity:  61.7%           Mismatches:     109
Query Match:            62.2%           Indels:         28
DB:                     2               Gaps:           6

US-10-821-670A-44 (1-511) x CQ803350 (1-9049)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20

Db       1070 ATGTGGGAGCTGGAGAAAGACGTTTATGTTGTAGAGGTGGACTGGACTCCCGATGCCCCT 1129

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40

Db       1130 GGAGAAACAGTGAACCTCACCTGTGACACGCCTGAAGAAGATGACATCACCTGGACCTCA 1189

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60

Db       1190 GACCAGAGACATGGAGTCATAGGCTCTGGAAAGACCCTGACCATCACTGTCAAAGAGTTT 1249

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80

Db       1250 CTAGATGCTGGCCAGTACACCTGCCACAAAGGAGGCGAGACTCTGAGCCACTCACATCTG 1309

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100

Db       1310 CTGCTCCACAAGAAGGAAAATGGAATTTGGTCCACTGAAATTTTA---------AAAAAT 1360

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120

Db       1361 TTCAAAAACAAGACTTTCCTGAAGTGTGAAGCACCAAATTACTCCGGACGGTTCACGTGC 1420

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140

Db       1421 TCATGGCTGGTGCAAAGAAACATGGACTTGAAGTTCAACATCAAGAGCAGTAGCAGTTCC 1480

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160

Db       1481 CCTGACTCTCGGGCAGTGACATGTGGAATGGCGTCTCTGTCTGCAGAGAAGGTCACACTG 1540

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180

Db       1541 GACCAAAGGGACTATGAGAAGTATTCAGTGTCCTGCCAGGAGGATGTCACCTGCCCAACT 1600

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Db       1601 GCCGAGGAGACCCTGCCCATTGAACTGGCGTTGGAAGCACGGCAGCAGAATAAATATGAG 1660

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220

Db       1661 AACTACAGCACCAGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTG 1720

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240

Db       1721 CAGATGAAGCCTTTGAAGAACTCACAG---GTGGAGGTCAGCTGGGAGTACCCTGACTCC 1777

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260

Db       1778 TGGAGCACTCCCCATTCCTACTTCTCCCTCAAGTTCTTTGTTCGAATCCAGCGCAAGAAA 1837

Qy        261 AsnArgGluLys----------LysAspArgLeuSerValAspLys 272

Db       1838 GAAAAGATGAAGGAGACAGAGGAGGGGTGTAACCAGAAAGGTGCGTTCCTCGTAGAGAAG 1897

Qy        273 ThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaArgAspArg 292

Db       1898 ACATCTACCGAAGTCCAATGC---AAAGGCGGGAATGTCTGCGTGCAAGCTCAGGATCGC 1954

Qy        293 TyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys---------- 306

Db       1955 TATTACAATTCCTCATGCAGCAAGTGGGCATGTGTTCCCTGCAGGGTCCGATCCGGTGGC 2014

Qy        307 ----------SerGlyGlyGlyGlyGlySerArgAsnLeuProThrProThr 321

Db       2015 GGTGGCTCGGGCGGTGGTGGGTCGGGTGGCGGCGGATCTAGGGTCATTCCAGTCTCTGGA 2074

Qy        322 ProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSer 341

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Qy        402 CysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGlu 421

Db       2303 TGCCTGCCCCCACAGAAGACGTCTTTGATGATGACCCTGTGCCTTGGTAGCATCTATGAG 2362

Qy        422 AspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspPro 441

Db       2363 GACTTGAAGATGTACCAGACAGAGTTCCAGGCCATCAACGCAGCACTTCAGAATCACAAC 2422

Qy        442 LysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAla 461
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Qy        462 LeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyr 481

Db       2483 CTGAATCATAATGGCGAGACTCTGCGCCAGAAACCTCCTGTGGGAGAAGCAGACCCTTAC 2542

Qy        482 LysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIle 501

Db       2543 AGAGTGAAAATGAAGCTCTGCATCCTGCTTCACGCCTTCAGCACCCGCGTCGTGACCATC 2602

Qy        502 AsnArgMetMetSerTyrLeuAsnAlaSer 511

Db       2603 AACAGGGTGATGGGCTATCTGAGCTCCGCC 2632

RESULT 15
CQ803349
LOCUS       CQ803349               10633 bp    DNA     linear   PAT 10-MAY-2004
DEFINITION  Sequence 9 from Patent WO2004035799.
ACCESSION   CQ803349
VERSION     CQ803349.1  GI:47110215
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Waehler,R. and Schnieders,F.
  TITLE     Viral vectors and the use of the same for gene therapy
  JOURNAL   Patent: WO 2004035799-A 9 29-APR-2004;
            Universitaetsklinikum Hamburg-Eppendorf (DE)
FEATURES             Location/Qualifiers
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     misc_feature    1. .10633
                     /note="#N# = #A#, #C#, #G# or #T#"
ORIGIN

Alignment Scores:
Pred. No.:              3.82e-171      Length:         10633
Score:                  1671.00        Matches:        327
Percent Similarity:     74.2%          Conservative:   66
Best Local Similarity:  61.7%          Mismatches:     109
Query Match:            62.2%          Indels:         28
DB:                     2              Gaps:           6

US-10-821-670A-44 (1-511) x CQ803349 (1-10633)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20

Db       1070 ATGTGGGAGCTGGAGAAAGACGTTTATGTTGTAGAGGTGGACTGGACTCCCGATGCCCCT 1129

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40

Db       1130 GGAGAAACAGTGAACCTCACCTGTGACACGCCTGAAGAAGATGACATCACCTGGACCTCA 1189

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60

Db       1190 GACCAGAGACATGGAGTCATAGGCTCTGGAAAGACCCTGACCATCACTGTCAAAGAGTTT 1249

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80

Db       1250 CTAGATGCTGGCCAGTACACCTGCCACAAAGGAGGCGAGACTCTGAGCCACTCACATCTG 1309

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100

Db       1310 CTGCTCCACAAGAAGGAAAATGGAATTTGGTCCACTGAAATTTTA---------AAAAAT 1360

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120

Db       1361 TTCAAAAACAAGACTTTCCTGAAGTGTGAAGCACCAAATTACTCCGGACGGTTCACGTGC 1420

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140

Db       1421 TCATGGCTGGTGCAAAGAAACATGGACTTGAAGTTCAACATCAAGAGCAGTAGCAGTTCC 1480

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160

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Db       1541 GACCAAAGGGACTATGAGAAGTATTCAGTGTCCTGCCAGGAGGATGTCACCTGCCCAACT 1600

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200

Db       1601 GCCGAGGAGACCCTGCCCATTGAACTGGCGTTGGAAGCACGGCAGCAGAATAAATATGAG 1660

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220

Db       1661 AACTACAGCACCAGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTG 1720

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240

Db       1721 CAGATGAAGCCTTTGAAGAACTCACAG---GTGGAGGTCAGCTGGGAGTACCCTGACTCC 1777

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260

Db       1778 TGGAGCACTCCCCATTCCTACTTCTCCCTCAAGTTCTTTGTTCGAATCCAGCGCAAGAAA 1837

Qy        261 AsnArgGluLys----------------------LysAspArgLeuSerValAspLys 272

Db       1838 GAAAAGATGAAGGAGACAGAGGAGGGGTGTAACCAGAAAGGTGCGTTCCTCGTAGAGAAG 1897

Qy        273 ThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaArgAspArg 292

Db       1898 ACATCTACCGAAGTCCAATGC---AAAGGCGGGAATGTCTGCGTGCAAGCTCAGGATCGC 1954

Qy        293 TyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys------------------ 306

Db       1955 TATTACAATTCCTCATGCAGCAAGTGGGCATGTGTTCCCTGCAGGGTCCGATCCGGTGGC 2014

Qy        307 --------------SerGlyGlyGlyGlyGlySerArgAsnLeuProThrProThr 321

Db       2015 GGTGGCTCGGGCGGTGGTGGGTCGGGTGGCGGCGGATCTAGGGTCATTCCAGTCTCTGGA 2074

Qy        322 ProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSer 341

Db       2075 CCTGCC------------AGGTGTCTTAGCCAGTCCCGAAACCTGCTGAAGACCACAGAT 2122

Qy        342 AsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIle 361

Db       2123 GACATGGTGAAGACGGCCAGAGAAAAGCTGAAACATTATTCCTGCACTGCTGAAGACATC 2182

Qy        362 AspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGlu 381

Db       2183 GATCATGAAGACATCACACGGGACCAAACCAGCACATTGAAGACCTGTTTACCACTGGAA 2242

Qy        382 LeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySer 401

Db       2243 CTACACAAGAACGAGAGTTGCCTGGCTACTAGAGAGACTTCTTCCACAACAAGAGGGAGC 2302

Qy        402 CysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGlu 421

Db       2303 TGCCTGCCCCCACAGAAGACGTCTTTGATGATGACCCTGTGCCTTGGTAGCATCTATGAG 2362

Qy        422 AspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspPro 441

Db       2363 GACTTGAAGATGTACCAGACAGAGTTCCAGGCCATCAACGCAGCACTTCAGAATCACAAC 2422

Qy        442 LysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAla 461

Db       2423 CATCAGCAGATCATTCTAGACAAGGGCATGCTGGTGGCCATCGATGAGCTGATGCAGTCT 2482
```

```
Qy        462 LeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyr 481
              ||||||   |||      |||:::   |||         :::   |||   |||   |||
Db       2483 CTGAATCATAATGGCGAGACTCTGCGCCAGAAACCTCCTGTGGGAGAAGCAGACCCTTAC 2542

Qy        482 LysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIle 501
              :::   |||:::|||||||||||||||||||||||||||      |||   |||||||||
Db       2543 AGAGTGAAAATGAAGCTCTGCATCCTGCTTCACGCCTTCAGCACCCGCGTCGTGACCATC 2602

Qy        502 AsnArgMetMetSerTyrLeuAsnAlaSer 511
              ||||||:::|||   ||||||:::::::::
Db       2603 AACAGGGTGATGGGCTATCTGAGCTCCGCC 2632


Search completed: June 13, 2006, 03:26:33
Job time : 6966 secs
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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 9, 2006, 23:43:41 ; Search time 1090.81 Seconds
(without alignments)
4899.317 Million cell updates/sec

Title: US-10-821-670A-44
Perfect score: 2687
Sequence: 1 IWELEKNVYVVELDWHPDAP.....HAFRIRAVTINRMMSYLNAS 511

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/abss/ABSSWEB_spool/US10821670/runat_07062006_110100_26141/app_query.fasta_1
-DB=N_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05h
-USER=US10821670_@CGN_1_1_2027_@runat_07062006_110100_26141 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
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8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	2687	100.0	1533	6	ABK98954	Abk98954 Feline in
	2	2687	100.0	1533	6	ABK98953	Abk98953 Feline in
c	3	2687	100.0	1533	14	ADV34697	Adv34697 Feline si
	4	2687	100.0	1533	14	ADV34695	Adv34695 Feline si
	5	2687	100.0	1599	6	ABK98950	Abk98950 Feline in
c	6	2687	100.0	1599	6	ABK98951	Abk98951 Feline in
	7	2687	100.0	1599	14	ADV34691	Adv34691 Feline si
c	8	2687	100.0	1599	14	ADV34693	Adv34693 Feline si
	9	2546	94.8	1533	6	ABK98967	Abk98967 Canine in
c	10	2546	94.8	1533	6	ABK98968	Abk98968 Canine in
c	11	2546	94.8	1533	14	ADV34718	Adv34718 Canine si
	12	2546	94.8	1533	14	ADV34716	Adv34716 Canine si
	13	2546	94.8	1599	6	ABK98965	Abk98965 Canine in
c	14	2546	94.8	1599	6	ABK98966	Abk98966 Canine in
c	15	2546	94.8	1599	14	ADV34715	Adv34715 Canine si
	16	2546	94.8	1599	14	ADV34713	Adv34713 Canine si
	17	2335.5	86.9	11569	10	ADG25150	Adg25150 Vector pA
	18	2330.5	86.7	11453	10	ADG25152	Adg25152 Vector pS
	19	2320.5	86.4	6139	3	AAZ40023	Aaz40023 Interleuk
	20	2314	86.1	8608	6	AAD31548	Aad31548 pIRES-hB7
	21	2314	86.1	8629	6	AAD31552	Aad31552 pIRES-IL1
	22	2311.5	86.0	8623	6	AAD31547	Aad31547 pIRES-hB7
	23	2311.5	86.0	8644	6	AAD31551	Aad31551 pIRES-IL1
	24	2309	85.9	8638	6	AAD31549	Aad31549 pIRES-hB7
	25	2309	85.9	8659	6	AAD31550	Aad31550 pIRES-IL1
	26	2280	84.9	8578	6	AAD31546	Aad31546 pIRES-hB7
	27	2280	84.9	8578	6	AAD31545	Aad31545 pIRES-hB7
	28	1671	62.2	5252	12	ADO07652	Ado07652 Tricistro
	29	1671	62.2	9049	12	ADO07661	Ado07661 Viral vec
	30	1671	62.2	10633	12	ADO07660	Ado07660 Viral vec
	31	1671	62.2	11458	10	ADG25151	Adg25151 Vector pA
	32	1671	62.2	11746	12	ADO07659	Ado07659 Viral vec
	33	1671	62.2	38246	12	ADO07662	Ado07662 Viral vec
	34	1666	62.0	2438	12	ADO43004	Ado43004 DNA encod
	35	1646	61.3	921	6	ABK98942	Abk98942 Feline in
c	36	1646	61.3	921	6	ABK98943	Abk98943 Feline in
c	37	1646	61.3	921	14	ADV34681	Adv34681 Feline si
	38	1646	61.3	921	14	ADV34679	Adv34679 Feline si
	39	1640	61.0	4522	4	AAF26076	Aaf26076 Feline IL
	40	1640	61.0	4522	4	AAF26094	Aaf26094 Plasmid p
	41	1639	61.0	921	2	AAV56627	Aav56627 Feline FL
	42	1639	61.0	921	2	AAV56626	Aav56626 Feline FL
	43	1639	61.0	987	6	ABK98944	Abk98944 Feline in
c	44	1639	61.0	987	6	ABK98945	Abk98945 Feline in
	45	1639	61.0	987	14	ADV34682	Adv34682 Feline si

ALIGNMENTS

RESULT 1
ABK98954/c
ID ABK98954 standard; cDNA; 1533 BP.
XX
AC ABK98954;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12-1533 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX

PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 66-67; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.17e-223	Length:	1533
Score:	2687.00	Matches:	511
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-44 (1-511) x ABK98954 (1-1533)

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Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
              |||||||||||||||||||||||||||||||||
Db         33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
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RESULT 2
ABK98953
ID ABK98953 standard; cDNA; 1533 BP.
XX
AC ABK98953;
XX

DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12-1533 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69307.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 63-64; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.17e-223	Length:	1533
Score:	2687.00	Matches:	511
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-44 (1-511) x ABK98953 (1-1533)

```
Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320
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Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
              |||||||||||||||||||||||||||||||||
Db       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
```

RESULT 3
ADV34697/c
ID ADV34697 standard; DNA; 1533 BP.
XX
AC ADV34697;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain IL-12 complementary DNA, nFeIL-12 1533.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Felis catus.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 3; SEQ ID NO 45; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain IL-12 complementary DNA.
XX
SQ Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.17e-223	Length:	1533
Score:	2687.00	Matches:	511
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-44 (1-511) x ADV34697 (1-1533)

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Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy         381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy         401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy         421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy         441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy         461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy         481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy         501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
                |||||||||||||||||||||||||||||||||
Db          33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
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RESULT 4
ADV34695
ID   ADV34695 standard; cDNA; 1533 BP.
XX
AC   ADV34695;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1533
FT                   /*tag=  a
FT                   /product= "PFeIL-12 511 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34696.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 43; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;
```

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Alignment Scores:
Pred. No.:              4.17e-223       Length:         1533
Score:                  2687.00         Matches:        511
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-44 (1-511) x ADV34695 (1-1533)

Qy           1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy          21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy          41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy          61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy          81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy         101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy         121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy         141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy         161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy         181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy         201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy         221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy         241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
              |||||||||||||||||||||||||||||||||
Db       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
```

```
RESULT 5
ABK98950
ID   ABK98950 standard; cDNA; 1599 BP.
XX
AC   ABK98950;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1599 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69306.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 58-60; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.:              4.41e-223       Length:         1599
Score:                  2687.00         Matches:        511
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-44 (1-511) x ABK98950 (1-1599)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
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Qy       141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
Db       487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy       161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
Db       547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
Db       607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
Db       667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy       221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
Db       727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy       241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
Db       787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy       261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
Db       847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy       281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
Db       907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy       301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
Db       967 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026

Qy       321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
Db      1027 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1086

Qy       341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
Db      1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1146

Qy       361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
Db      1147 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206

Qy       381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
Db      1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1266

Qy       401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
Db      1267 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1326

Qy       421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
Db      1327 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1386

Qy       441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
Db      1387 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1446

Qy       461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
Db      1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1506

Qy       481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
Db      1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1566

Qy       501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
Db      1567 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
```

RESULT 6
ABK98951/c
ID ABK98951 standard; cDNA; 1599 BP.
XX
AC ABK98951;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12-1599 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 61-62; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.41e-223	Length:	1599
Score:	2687.00	Matches:	511
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-44 (1-511) x ABK98951 (1-1599)

```
Qy         1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
Db      1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy        21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
Db      1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414
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Qy        41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy       101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy       121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy       141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy       161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy       221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy       241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy       261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy       281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy       301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       633 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy       321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       573 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy       341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy       361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy       381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy       401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy       421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy       441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy       461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy       481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy       501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
             |||||||||||||||||||||||||||||||
Db        33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
```

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RESULT 7
ADV34691
ID   ADV34691 standard; cDNA; 1599 BP.
XX
AC   ADV34691;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1599
FT                   /*tag=  a
FT                   /product= "PFeIL-12p533 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34692.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 38; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
```

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CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              4.41e-223       Length:         1599
Score:                  2687.00         Matches:        511
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-44 (1-511) x ADV34691 (1-1599)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1086

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1146

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1147 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1266

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1267 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1326

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1327 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1386

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1387 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1446

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1506

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1566

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
              |||||||||||||||||||||||||||||||
Db       1567 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599

RESULT 8
ADV34693/c
ID   ADV34693 standard; DNA; 1599 BP.
XX
AC   ADV34693;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 complementary DNA, nFeIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
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XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 40; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 complementary DNA.
XX
SQ   Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              4.41e-223       Length:         1599
Score:                  2687.00         Matches:        511
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-44 (1-511) x ADV34693 (1-1599)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
              ||||||||||||||||||||||||||||||||
Db         33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 9
ABK98967
ID   ABK98967 standard; cDNA; 1533 BP.
XX
AC   ABK98967;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1533 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
```

KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69314.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 83-85; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1533 BP; 446 A; 368 C; 369 G; 350 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	7.13e-211	Length:	1533
Score:	2546.00	Matches:	482
Percent Similarity:	96.7%	Conservative:	12
Best Local Similarity:	94.3%	Mismatches:	17
Query Match:	94.8%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-44 (1-511) x ABK98967 (1-1533)

```
Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||:::|||||||||   |||   |||
Db        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||
Db        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||:::|||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||   ||||||||||||||   ||||||||||||||:::||||||||||
Db        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||   :::|||   ||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        781 AATAGAGAAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        961 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 1020

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 1080

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1200

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
              ||||||||||||||   |||   ||||||||||   ||||||||||||||||||||
Db       1201 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1260

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db       1261 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1320

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 1380

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
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Db       1381 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1440

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500

Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1500

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511

Db       1501 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1533

RESULT 10
ABK98968/c
ID   ABK98968 standard; cDNA; 1533 BP.
XX
AC   ABK98968;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1533 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 86-87; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              7.13e-211      Length:          1533
Score:                  2546.00        Matches:         482
Percent Similarity:     96.7%          Conservative:    12
Best Local Similarity:  94.3%          Mismatches:      17
Query Match:            94.8%          Indels:          0
DB:                     6              Gaps:            0

US-10-821-670A-44 (1-511) x ABK98968 (1-1533)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20

Db       1533 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40

Db       1473 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60

Db       1413 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80

Db       1353 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100

Db       1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120

Db       1233 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140

Db       1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160

Db       1113 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180

Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200

Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220

Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240

Db        873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260

Db        813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280

Db        753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300

Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 634

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320

Db        633 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340

Db        573 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 514

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360

Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 454
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Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 334

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
              |||||||||||||||   |||   ||||||||||||   ||||||||||||||||||||
Db        333 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 274

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db        273 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 214

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuGluGln 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 154

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
              |||||||||   ||||||||||||||||||||   ||||||||||||||||||||||||
Db        153 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 94

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 34

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
              |||||||||||||||||||||||:::|||
Db         33 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1
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RESULT 11
ADV34718/c
ID ADV34718 standard; DNA; 1533 BP.
XX
AC ADV34718;
XX
DT 24-FEB-2005 (first entry)
XX
DE Canine single chain IL-12 complementary DNA, nCaIL-12 1533.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Canis familiaris.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 4; SEQ ID NO 68; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the canine single chain IL-12 complementary DNA.
XX
SQ Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	7.13e-211	Length:	1533
Score:	2546.00	Matches:	482
Percent Similarity:	96.7%	Conservative:	12
Best Local Similarity:	94.3%	Mismatches:	17
Query Match:	94.8%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-44 (1-511) x ADV34718 (1-1533)

```
Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||:::|||||||||   |||   |||
Db       1353 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||
Db       1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||   ||||||||||||||   ||||||||||||||:::|||||||||
Db       1113 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||   :::|||   ||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
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```
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 634

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320

Db        633 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340

Db        573 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 514

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360

Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 454

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380

Db        453 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400

Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 334

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420

Db        333 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 274

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440

Db        273 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 214

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460

Db        213 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 154

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480

Db        153 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 94

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500

Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 34

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511

Db         33 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1

RESULT 12
ADV34716
ID   ADV34716 standard; cDNA; 1533 BP.
XX
AC   ADV34716;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12 protein cDNA, nCaIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1533
FT                   /*tag=  a
FT                   /product= "PCaIL-12 511 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34717.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 66; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1533 BP; 446 A; 368 C; 369 G; 350 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              7.13e-211      Length:          1533
Score:                  2546.00        Matches:         482
Percent Similarity:     96.7%          Conservative:    12
Best Local Similarity:  94.3%          Mismatches:      17
Query Match:            94.8%          Indels:          0
DB:                     14             Gaps:            0

US-10-821-670A-44 (1-511) x ADV34716 (1-1533)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20

Db          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40

Db         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60

Db        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80

Db        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100

Db        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120

Db        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140

Db        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160

Db        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
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Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||:::|||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        961 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 1020

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 1080

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1200

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
              ||||||||||||||   |||   ||||||||||||   ||||||||||||||||||||||
Db       1201 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1260

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db       1261 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1320

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 1380

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
              |||||||||   ||||||||||||||||||||   ||||||||||||||||||||||||
Db       1381 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1440

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1500

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
              |||||||||||||||||||||||||:::|||
Db       1501 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1533

RESULT 13
ABK98965
ID   ABK98965 standard; cDNA; 1599 BP.
XX
AC   ABK98965;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1599 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69313.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 79-80; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 452 A; 392 C; 383 G; 372 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              7.55e-211       Length:         1599
Score:                  2546.00         Matches:        482
Percent Similarity:     96.7%           Conservative:   12
Best Local Similarity:  94.3%           Mismatches:     17
Query Match:            94.8%           Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-44 (1-511) x ABK98965 (1-1599)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
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Qy        61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
             ||||||||||||||||||||||||||||||||||:::|||||||||   |||   |||
Db       247 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 306

Qy        81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
             ||||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||
Db       307 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 366

Qy       101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       367 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 426

Qy       121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
             ||||||||||||||||||||||||||||||||:::|||||||||||||||||||
Db       427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486

Qy       141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
             ||||||||||||   ||||||||||||||   ||||||||||||||:::|||||||||
Db       487 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 546

Qy       161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db       547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 606

Qy       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db       667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 726

Qy       221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       727 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 786

Qy       241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
             ||||||||||||||||||||||||||||||||||||   :::|||   ||||||||||||
Db       787 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 846

Qy       261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
             ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db       847 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy       281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db       907 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 966

Qy       301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       967 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026

Qy       321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db      1027 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 1086

Qy       341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
             ||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db      1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 1146

Qy       361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1147 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206

Qy       381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1266

Qy       401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
             ||||||||||||||   |||   ||||||||||||   ||||||||||||||||||||
Db      1267 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1326

Qy       421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
             ||||||||||||||||||||:::|||||||||||||||||||||||||||||||||||||
Db      1327 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1386

Qy       441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1387 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 1446

Qy       461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerLeuGluGluProAspPhe 480
             |||||||||   ||||||||||||||||||||   ||||||||||||||||||||||
Db      1447 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1506

Qy       481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1566

Qy       501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
             ||||||||||||||||||||||||||:::|||
Db      1567 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1599
```

RESULT 14
ABK98966/c
ID ABK98966 standard; cDNA; 1599 BP.
XX
AC ABK98966;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12-1599 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 82-83; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1599 BP; 372 A; 383 C; 392 G; 452 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	7.55e-211	Length:	1599
Score:	2546.00	Matches:	482
Percent Similarity:	96.7%	Conservative:	12
Best Local Similarity:	94.3%	Mismatches:	17
Query Match:	94.8%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-44 (1-511) x ABK98966 (1-1599)

```
Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||:::|||||||||   |||   |||||
Db       1353 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db       1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||   ||||||||||||||   ||||||||||||||:::||||||||||||
Db       1113 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||   :::|||   ||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 634

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574
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Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        573 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 514

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 454

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 334

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
              ||||||||||||||   |||   ||||||||||||   ||||||||||||||||||||||
Db        333 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 274

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db        273 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 214

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 154

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
              |||||||||   ||||||||||||||||||||   ||||||||||||||||||||||||
Db        153 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 94

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 34

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
              ||||||||||||||||||||||||||||:::|||
Db         33 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1
```

RESULT 15
ADV34715/c
ID ADV34715 standard; DNA; 1599 BP.
XX
AC ADV34715;
XX
DT 24-FEB-2005 (first entry)
XX
DE Canine single chain IL-12 complementary DNA, nCaIL-12 1599.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Canis familiaris.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a

```
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 63; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 complementary DNA.
XX
SQ   Sequence 1599 BP; 372 A; 383 C; 392 G; 452 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              7.55e-211       Length:         1599
Score:                  2546.00         Matches:        482
Percent Similarity:     96.7%           Conservative:   12
Best Local Similarity:  94.3%           Mismatches:     17
Query Match:            94.8%           Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-44 (1-511) x ADV34715 (1-1599)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
                 ||||||||||||||||||||||||||||||||||:::|||||||||    |||   |||
Db       1353 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||
Db       1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||:::|||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||   ||||||||||||||||   ||||||||||||||:::|||||||||
Db       1113 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||   :::|||   ||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 634

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        573 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 514

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 454

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 334

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
              ||||||||||||||   |||   ||||||||||||   ||||||||||||||||||||
Db        333 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 274

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        273 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 214

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 154

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
              |||||||||   ||||||||||||||||||||   ||||||||||||||||||||||||
Db        153 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 94

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 34

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
              ||||||||||||||||||||||||||:::|||
Db         33 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1

Search completed: June 10, 2006, 01:17:24
Job time : 1116.81 secs
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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 10, 2006, 00:20:47 ; Search time 6263.17 Seconds
(without alignments)
6843.525 Million cell updates/sec

Title: US-10-821-670A-44
Perfect score: 2687
Sequence: 1 IWELEKNVYVVELDWHPDAP.....HAFRIRAVTINRMMSYLNAS 511

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10821670/runat_07062006_110104_26172/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
-USER=US10821670_@CGN_1_1_27300_@runat_07062006_110104_26172 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1100.5	41.0	1839	6	AK162981	AK162981 Mus muscu
	2	1087.5	40.5	2908	6	AK155593	AK155593 Mus muscu
	3	1028.5	38.3	735	5	CD559605	CD559605 AGENCOURT
	4	1028.5	38.3	756	5	CK130264	CK130264 AGENCOURT
	5	1015.5	37.8	747	5	CD559607	CD559607 AGENCOURT
	6	1001	37.3	772	5	CD559604	CD559604 AGENCOURT
c	7	957	35.6	785	5	CD559448	CD559448 AGENCOURT
c	8	955.5	35.6	736	5	CD559453	CD559453 AGENCOURT
c	9	952.5	35.4	772	5	CD559450	CD559450 AGENCOURT
c	10	947.5	35.3	762	5	CD559451	CD559451 AGENCOURT
	11	898.5	33.4	745	5	CD559602	CD559602 AGENCOURT
c	12	898.5	33.4	766	5	CD559449	CD559449 AGENCOURT
c	13	890.5	33.1	754	5	CD559452	CD559452 AGENCOURT
	14	890	33.1	762	14	DQ033872	DQ033872 Homo sapi
	15	877	32.6	762	14	DQ033873	DQ033873 Pan trogl
	16	862.5	32.1	1136	4	CD013915	CD013915 90138132
c	17	816	30.4	725	5	CD559454	CD559454 AGENCOURT
	18	816	30.4	935	4	CD013914	CD013914 90138124
	19	755.5	28.1	1938	6	BC035571	BC035571 Homo sapi
	20	700	26.1	724	5	CD559603	CD559603 AGENCOURT
	21	696	25.9	1042	5	CD559606	CD559606 AGENCOURT
	22	683.5	25.4	649	5	CJ134671	CJ134671 CJ134671
	23	670	24.9	863	4	CD013916	CD013916 90138296
	24	519.5	19.3	475	7	BF704417	BF704417 MI-P-E6-a
	25	460	17.1	1299	6	AK153729	AK153729 Mus muscu
	26	431.5	16.1	417	8	CO949904	CO949904 UMC-pd12c
	27	419.5	15.6	812	2	BG702253	BG702253 602683459
	28	418.5	15.6	563	3	BU698113	BU698113 LL2in1206
	29	404	15.0	589	1	AI050362	AI050362 ub30a07.r
	30	386	14.4	387	4	BY167742	BY167742 BY167742
	31	378	14.1	535	11	AZ441303	AZ441303 1M0232M24
	32	377	14.0	432	4	BY154173	BY154173 BY154173
c	33	374.5	13.9	1099	2	BI523344	BI523344 603175938
	34	357	13.3	700	12	CE093997	CE093997 tigr-gss-
c	35	355	13.2	778	1	AJ820622	AJ820622 AJ820622
	36	353	13.1	423	4	BY218447	BY218447 BY218447
c	37	351	13.1	569	11	AZ853726	AZ853726 2M0157M01
	38	349.5	13.0	561	3	BU699383	BU699383 LL2in1157
	39	345	12.8	373	7	BF552757	BF552757 UI-R-C0-i
	40	344	12.8	692	5	CJ137697	CJ137697 CJ137697
	41	338.5	12.6	252	10	DV799576	DV799576 est_t_tru
	42	337	12.5	375	4	BY222535	BY222535 BY222535
	43	331	12.3	346	4	BY164658	BY164658 BY164658
	44	324	12.1	832	2	BI523569	BI523569 603175938
	45	321	11.9	456	10	DT913216	DT913216 S13.1426

ALIGNMENTS

RESULT 1
AK162981
LOCUS AK162981 1839 bp mRNA linear HTC 21-SEP-2005
DEFINITION Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430014H12 product:interleukin 12b, full insert sequence.
ACCESSION AK162981
VERSION AK162981.1 GI:74188061
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,

Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

PUBMED 11076861

REFERENCE 4

AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

CONSRTM RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409 (6821), 685-690 (2001)

PUBMED 11217851

REFERENCE 5

AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420 (6915), 563-573 (2002)

PUBMED 12466851

REFERENCE 6

AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE The transcriptional landscape of the mammalian genome

JOURNAL Science 309 (5740), 1559-1563 (2005)

PUBMED 16141072

REFERENCE 7

AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.

CONSRTM RIKEN Genome Exploration Research Group

TITLE Antisense transcription in the mammalian transcriptome

JOURNAL Science 309 (5740), 1564-1566 (2005)

PUBMED 16141073

REFERENCE 8 (bases 1 to 1839)

AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

```
     source          1. .1839
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM_DB:A430014H12"
                     /db_xref="taxon:10090"
                     /clone="A430014H12"
                     /tissue_type="thymus"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="0 day neonate"
     CDS             58. .1065
                     /note="unnamed protein product; interleukin 12b
                     (MGD|MGI:96540 GB|M86671, evidence: BLASTN, 100%,
                     match=1816)
                     putative"
                     /codon_start=1
                     /protein_id="BAE37146.1"
                     /db_xref="GI:74188062"
                     /translation="MCPQKLTISWFAIVLLVSPLMAMWELEKDVYVVEVDWTPDAPGE
                     TVNLTCDTPEEDDITWTSDQRHGVIGSGKTLTITVKEFLDAGQYTCHKGGETLSHSHL
                     LLHKKENGIWSTEILKNFKNKTFLKCEAPNYSGRFTCSWLVQRNMDLKFNIKSSSSSP
                     DSRAVTCGMASLSAEKVTLDQRDYEKYSVSCQEDVTCPTAEETLPIELALEARQQNKY
                     ENYSTSFFIRDIIKPDPPKNLQMKPLKNSQVEVSWEYPDSWSTPHSYFSLKFFVRIQR
                     KKEKMKETEEGCNQKGAFLVEKTSTEVQCKGGNVCVQAQDRYYNSSCSKWACVPCRVR
                     S"
ORIGIN

Alignment Scores:
Pred. No.:              1.44e-102       Length:         1839
Score:                  1100.50         Matches:        211
Percent Similarity:     77.7%           Conservative:   33
Best Local Similarity:  67.2%           Mismatches:     57
Query Match:            41.0%           Indels:         13
DB:                     6               Gaps:           4

US-10-821-670A-44 (1-511) x AK162981 (1-1839)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              :::|||||||||||||||||:::|||||||||||||||||:::||||||   ||||||||||||
Db        124 ATGTGGGAGCTGGAGAAAGACGTTTATGTTGTAGAGGTGGACTGGACTCCCGATGCCCCT 183

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||   |||   |||||||||:::||||||||||||||||||||||||||||||||
Db        184 GGAGAAACAGTGAACCTCACCTGTGACACGCCTGAAGAAGATGACATCACCTGGACCTCA 243

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||         |||:::|||||||||||||||||||||||   ||||||||||||
Db        244 GACCAGAGACATGGAGTCATAGGCTCTGGAAAGACCCTGACCATCACTGTCAAAGAGTTT 303

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||   ||||||||||||   |||
Db        304 CTAGATGCTGGCCAGTACACCTGCCACAAAGGAGGCGAGACTCTGAGCCACTCACATCTG 363

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              |||:::|||||||||||:::|||||||||||||||:::||||||         |||
Db        364 CTGCTCCACAAGAAGGAAAATGGAATTTGGTCCACTGAAATTTTA---------AAAAAT 414

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              |||||||||   ||||||||||||||||||   ||||||||||||||||||||||||||||
Db        415 TTCAAAAACAAGACTTTCCTGAAGTGTGAAGCACCAAATTACTCCGGACGGTTCACGTGC 474

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
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Db        475 TCATGGCTGGTGCAAAGAAACATGGACTTGAAGTTCAACATCAAGAGCAGTAGCAGTTCC 534

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||   :::   ||||||||||||   |||:::|||||||||||||||||   :::
Db        535 CCTGACTCTCGGGCAGTGACATGTGGAATGGCGTCTCTGTCTGCAGAGAAGGTCACACTG 594

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              |||   |||||||||:::||||||:::|||   |||||||||          ||||||
Db        595 GACCAAAGGGACTATGAGAAGTATTCAGTGTCCTGCCAGGAGGATGTCACCTGCCCAACT 654

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              |||||||||:::|||||||||||||:::   ::::::|||      :::   |||||||||
Db        655 GCCGAGGAGACCCTGCCCATTGAACTGGCGTTGGAAGCACGGCAGCAGAATAAATATGAG 714

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||::::::|||||||||||||||||||||||||||||||||||||||||||||||
Db        715 AACTACAGCACCAGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTG 774

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              |||:::|||||||||||||||:::   |||||||||||||||||||||||||||||:::
Db        775 CAGATGAAGCCTTTGAAGAACTCACAG---GTGGAGGTCAGCTGGGAGTACCCTGACTCC 831

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              |||||||||||||||||||||||||||   |||   |||::::::|||   |||
Db        832 TGGAGCACTCCCCATTCCTACTTCTCCCTCAAGTTCTTTGTTCGAATCCAGCGCAAGAAA 891

Qy        261 AsnArgGluLys----------------------LysAspArgLeuSerValAspLys 272
                 :::   |||                     |||           |||:::|||
Db        892 GAAAAGATGAAGGAGACAGAGGAGGGGTGTAACCAGAAAGGTGCGTTCCTCGTAGAGAAG 951

Qy        273 ThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaArgAspArg 292
              ||||||   :::|||   |||   |||         :::   ||||||||||:::||||||
Db        952 ACATCTACCGAAGTCCAATGC---AAAGGCGGGAATGTCTGCGTGCAAGCTCAGGATCGC 1008

Qy        293 TyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 306
              ||||||:::||||||   |||   ||||||   |||   |||
Db       1009 TATTACAATTCCTCATGCAGCAAGTGGGCATGTGTTCCCTGC 1050

RESULT 2
AK155593
LOCUS       AK155593               2908 bp    mRNA    linear   HTC 21-SEP-2005
DEFINITION  Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN
            full-length enriched library, clone:F730005O03 product:interleukin
            12b, full insert sequence.
ACCESSION   AK155593
VERSION     AK155593.1  GI:74212721
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
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Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

CONSRTM RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409 (6821), 685-690 (2001)

PUBMED 11217851

REFERENCE 5

AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420 (6915), 563-573 (2002)

PUBMED 12466851

REFERENCE 6

AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE The transcriptional landscape of the mammalian genome

JOURNAL Science 309 (5740), 1559-1563 (2005)

PUBMED 16141072

REFERENCE 7

AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.

CONSRTM RIKEN Genome Exploration Research Group

TITLE Antisense transcription in the mammalian transcriptome

JOURNAL Science 309 (5740), 1564-1566 (2005)

PUBMED 16141073

REFERENCE 8 (bases 1 to 2908)

AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

source 1. .2908
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:F730005O03"
/db_xref="taxon:10090"
/clone="F730005O03"
/cell_type="B6-derived CD11 +ve dendritic cells"
/clone_lib="RIKEN full-length enriched mouse cDNA library"

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putative"

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ORIGIN

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Score:                  1087.50         Matches:        211
Percent Similarity:     77.5%           Conservative:   33
Best Local Similarity:  67.0%           Mismatches:     57
Query Match:            40.5%           Indels:         14
DB:                     6               Gaps:           4

US-10-821-670A-44 (1-511) x AK155593 (1-2908)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              :::|||||||||||||||||:::|||||||||||||||:::||||||   ||||||||||||
Db        527 ATGTGGGAGCTGGAGAAAGACGTTTATGTTGTAGAGGTGGACTGGACTCCCGATGCCCCT 586

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||   |||   |||||||||:::|||||||||||||||||||||||||||||||||
Db        587 GGAGAAACAGTGAACCTCACCTGTGACACGCCTGAAGAAGATGACATCACCTGGACCTCA 646

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||         |||:::|||||||||||||||||||||||   ||||||||||||
Db        647 GACCAGAGACATGGAGTCATAGGCTCTGGAAAGACCCTGACCATCACTGTCAAAGAGTTT 706

Qy         61 AlaAspAlaGlyGln-TyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLe 80
              ||||||||||||| ||||||||||||||||||||||   ||||||||||||   ||
Db        707 CTAGATGCTGGCCAGCTACACCTGCCACAAAGGAGGCGAGACTCTGAGCCACTCACATCT 766

Qy         80 uLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGl 100
              ||||:::|||||||||||:::|||||||||||||||:::||||||         |||
Db        767 GCTGCTCCACAAGAAGGAAAATGGAATTTGGTCCACTGAAATTTTA---------AAAAA 817

Qy        100 uSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCy 120
              |||||||||   ||||||||||||||||||   ||||||||||||||||||||||||||
Db        818 TTTCAAAAACAAGACTTTCCTGAAGTGTGAAGCACCAAATTACTCCGGACGGTTCACGTG 877

Qy        120 sTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySe 140
              |   ||||||         :::   ||||||||||||   :::||||||||||      ||
Db        878 CTCATGGCTGGTGCAAAGAAACATGGACTTGAAGTTCAACATCAAGAGCAGTAGCAGTTC 937

Qy        140 rSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVa 160
              |   |||   :::   ||||||||||||   |||:::||||||||||||||||||   ::
Db        938 CCCTGACTCTCGGGCAGTGACATGTGGAATGGCGTCTCTGTCTGCAGAGAAGGTCACACT 997

Qy        160 lAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAl 180
              :|||   |||||||||:::||||||:::|||   |||||||||         ||||||
Db        998 GGACCAAAGGGACTATGAGAAGTATTCAGTGTCCTGCCAGGAGGATGTCACCTGCCCAAC 1057

Qy        180 aAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGl 200
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Db       1058 TGCCGAGGAGACCCTGCCCATTGAACTGGCGTTGGAAGCACGGCAGCAGAATAAATATGA 1117

Qy        200 uAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLe 220
              |||||||::::::|||||||||||||||||||||||||||||||||||||||||||||||
Db       1118 GAACTACAGCACCAGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTT 1177

Qy        220 uGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspTh 240
              ||||:::|||||||||||||||:::   |||||||||||||||||||||||||||::
Db       1178 GCAGATGAAGCCTTTGAAGAACTCACAG---GTGGAGGTCAGCTGGGAGTACCCTGACTC 1234

Qy        240 rTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAs 260
              :|||||||||||||||||||||||||||   |||   |||::::::|||   |||
Db       1235 CTGGAGCACTCCCCATTCCTACTTCTCCCTCAAGTTCTTTGTTCGAATCCAGCGCAAGAA 1294

Qy        260 nAsnArgGluLys----------------------LysAspArgLeuSerValAspLy 272
                 :::   |||                        |||            |||:::||
Db       1295 AGAAAAGATGAAGGAGACAGAGGAGGGGGTGTAACCAGAAAGGTGCGTTCCTCGTAGAAA 1354

Qy        272 sThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaArgAspAr 292
              |||||||   :::|||   |||   |||         :::   |||||||||:::|||||
Db       1355 GACATCTACCGAAGTCCAATGC---AAAGGCGGGAATGTCTGCGTGCAAGCTCAGGATCG 1411

Qy        292 gTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 306
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              |||||||:::||||||   |||   ||||||   |||   |||
Db       1412 CTATTACAATTCCTCATGCAGCAAGTGGGCATGTGTTCCCTGC 1454

RESULT 3
CD559605
LOCUS       CD559605                735 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496534 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971870 5', mRNA sequence.
ACCESSION   CD559605
VERSION     CD559605.2  GI:38558937
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 735)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585673.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 01
            High quality sequence stop: 709.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:6971870"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
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                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              1.03e-95        Length:         735
Score:                  1028.50         Matches:        190
Percent Similarity:     94.5%           Conservative:   16
Best Local Similarity:  87.2%           Mismatches:     11
Query Match:            38.3%           Indels:         1
DB:                     5               Gaps:           1

US-10-821-670A-44 (1-511) x CD559605 (1-735)
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Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||:::|||:::|||||||||||||||||||||||:::||||||||||||
Db         83 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 142

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
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Db        143 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 202

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 262

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        263 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 322

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              |||:::|||||||||||||||||||||||||||||||||||||||||||:::::|||||||||
Db        323 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 382

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||   ||||||:::|||||||||||||||||||||||||||||||||||||||
Db        383 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 442

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||   ||||||||||||||   |||:::|||||||||||||||||||||||
Db        443 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAGAGCAGCAGAGGCTCT 502

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
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Db        503 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 562

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||:::::|||   :::|||:::||||||||||||||   ||||||||||||||||
Db        563 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 619

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
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Db        620 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAA 679

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 218
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        680 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 733

RESULT 4
CK130264
LOCUS       CK130264                 756 bp    mRNA    linear   EST 02-DEC-2003
DEFINITION  AGENCOURT_14496566 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971871 5', mRNA sequence.
ACCESSION   CK130264
VERSION     CK130264.1  GI:38622200
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 756)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 02
            High quality sequence start: 5
            High quality sequence stop: 731.
FEATURES              Location/Qualifiers
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                      loxP-HindIII; Clones from this library have been
                      PCR-amplified using gene-specific primers to contain the
                      complete open reading frame (based on known gene sequences
                      available from NCBI's RefSeq). Template for PCR is cDNA
                      derived from either pooled cytoplasmic polyA RNA from 30
                      cells lines or pooled total RNA from 10 different tissues
                      (from BD Biosciences/Clontech and Washington University).
                      PCR products are directionally cloned into the loxP sites
                      of the pDNR-Dual vector. Library constructed by Dr.
                      Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                      Expression Laboratory, Research Technology Program, SAIC
                      Frederick, NCI-Frederick, Frederick, MD 21702). For
                      information on which gene each clone represents, please
                      visit our anonymous ftp site at
                      ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                      a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:                1.08e-95        Length:          756
Score:                    1028.50         Matches:         190
Percent Similarity:       94.1%           Conservative:    16
Best Local Similarity:    86.8%           Mismatches:      12
Query Match:              38.3%           Indels:          1
DB:                       5               Gaps:            1

US-10-821-670A-44 (1-511) x CK130264 (1-756)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
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Db        100 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 159

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||:::|||||||||||||   ||||||||||||
Db        160 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 219

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 279

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        280 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 339

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              |||:::|||||||||||||||||||||||||||||||||||||||||||:::::|||||||||
Db        340 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 399

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||   ||||||:::|||||||||||||||||||||||||||||||||||||||
Db        400 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 459

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
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Db        460 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 519

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||   ||||||||||||||||||||||||||||||:::||||||
Db        520 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 579
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Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||::::::|||   :::|||:::||||||||||||||||   ||||||||||||||||
Db        580 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 636

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||:::||||||||:::||||||||||||||||||
Db        637 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAA 696

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsn 219
              |||||||||||||||||||||||||||||||||  ||||||||||||||||
Db        697 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCNAACCTGACCCACCCAAGAAC 753

RESULT 5
CD559607
LOCUS       CD559607                747 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14497061 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971868 5', mRNA sequence.
ACCESSION   CD559607
VERSION     CD559607.2  GI:38558941
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 747)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585675.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: g  column: 11
            High quality sequence start: 14
            High quality sequence stop: 671.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:6971868"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN
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Alignment Scores:
Pred. No.:              2.36e-94        Length:         747
Score:                  1015.50         Matches:        187
Percent Similarity:     93.6%           Conservative:   17
Best Local Similarity:  85.8%           Mismatches:     13
Query Match:            37.8%           Indels:         1
DB:                     5               Gaps:           1

US-10-821-670A-44 (1-511) x CD559607 (1-747)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||:::|||:::|||||||||||||||||||||||:::||||||||||||
Db         95 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 154

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||:::|||||||||||||||   ||||||||||||
Db        155 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 214

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        215 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 274

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        275 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 334

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              |||:::|||||||||||||||||||||||||||||||||||||:::::|||||||||
Db        335 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 394

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
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Db        395 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 454

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||   ||||||||||||||||   |||:::||||||||||||||||||||
Db        455 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 514

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||   ||||||||||||||||||||||||||||:::||||||
Db        515 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 574

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||::::::|||   :::|||:::||||||||||||||||   ||||||||||||||||
Db        575 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 631

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||:::||||||   :::||||||||||:::||||||
Db        632 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATTGCGTTCACAAGCTCCAGTATGAA 691

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 218
              |||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        692 AACTACACCCGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAA 745

RESULT 6
CD559604
LOCUS       CD559604                772 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496598 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971872 5', mRNA sequence.
ACCESSION   CD559604
VERSION     CD559604.2  GI:38558934
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 772)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585672.
            Contact: Daniela S. Gerhard, Ph.D.
```

```
           Office of Cancer Genomics
           National Cancer Institute / NIH
           Bldg. 31 Rm10A07 Bethesda, MD 20892
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: IRBK2  row: h  column: 03
           High quality sequence start: 13
           High quality sequence stop: 750.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971872"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:                7.97e-93        Length:          772
Score:                    1001.00         Matches:         188
Percent Similarity:       93.6%           Conservative:    16
Best Local Similarity:    86.2%           Mismatches:      13
Query Match:              37.3%           Indels:          2
DB:                       5               Gaps:            1

US-10-821-670A-44 (1-511) x CD559604 (1-772)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
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Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||:::|||||||||||||||   ||||||||||||
Db        164 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 223

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 GACCAGAGCAGTGAGGTCCTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 283

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        284 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 343

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              |||:::|||||||||||||||||||||||||||||||||||||||:::::|||||||||
Db        344 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 403

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              |||||||||   ||||||:::|||||||||||||||||||||||||||||||||||||||
Db        404 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 463

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
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Db        464 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 523

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||   ||||||||||||||||||||||||||||||:::||||||
Db        524 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 583

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||::::::|||   :::|||:::|||||||||||||||   ||||||||||||||||
Db        584 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 640

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
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Db        641 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAA 700

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 218
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Db        701 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAA-CCTGACCAACCCAAA 753

RESULT 7
CD559448/c
LOCUS       CD559448                785 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496712 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971874 5', mRNA sequence.
ACCESSION   CD559448
VERSION     CD559448.2  GI:38453466
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 785)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585516.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 05
            High quality sequence stop: 696.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
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                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
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of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	3.03e-88	Length:	785
Score:	957.00	Matches:	186
Percent Similarity:	89.5%	Conservative:	18
Best Local Similarity:	81.6%	Mismatches:	23
Query Match:	35.6%	Indels:	3
DB:	5	Gaps:	1

US-10-821-670A-44 (1-511) x CD559448 (1-785)

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Qy        100 GluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThr 119
Db        713 GAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACC 654

Qy        120 CysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGly 139
Db        653 TGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGC 594

Qy        140 SerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArg 159
Db        593 TCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGA 534

Qy        160 ValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysPro 179
Db        533 GGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCA 477

Qy        180 AlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyr 199
Db        476 GCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTAT 417

Qy        200 GluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsn 219
Db        416 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAAC 357

Qy        220 LeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAsp 239
Db        356 TTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGAC 297

Qy        240 ThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLys 259
Db        296 ACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAG 237

Qy        260 AsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCys 279
Db        236 AGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGC 177

Qy        280 HisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSer 299
Db        176 CGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGC 117

Qy        300 AsnTrpAlaSerValSerCysSer 307
Db        116 GAATGGGCATCTGTGCCCTGCAGT 93
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RESULT 8
CD559453/c
LOCUS CD559453 736 bp mRNA linear EST 19-NOV-2003
DEFINITION AGENCOURT_14497154 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971869 5', mRNA sequence.
ACCESSION CD559453
VERSION CD559453.2 GI:38453475
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 736)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585521.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: g column: 12
High quality sequence stop: 683.

FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971869"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	3.93e-88	Length:	736
Score:	955.50	Matches:	181
Percent Similarity:	90.8%	Conservative:	17
Best Local Similarity:	83.0%	Mismatches:	19
Query Match:	35.6%	Indels:	2
DB:	5	Gaps:	1

US-10-821-670A-44 (1-511) x CD559453 (1-736)

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Qy         90 TrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCys 109
Db        727 TGGTCCACTGATAT-TTAAAGGACCAGAAAGAACCCAAAAATAAGACCTTTCTAAGATGC 669

Qy        110 GluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAsp 129
Db        668 GAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGACAATCAGTACTGAT 609
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Qy        130 LeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGluValThrCysGly 149
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Qy        150 AlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThr 169
              ||||||||||||||||||||:::||||||   ||||||::::::|||   :::|||:::
Db        548 GCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAACAAGGAGTAT---GAGTACTCA 492

Qy        170 ValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluVal 189
              ||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        491 GTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTC 432

Qy        190 ValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArg 209
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Qy        210 AspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
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Db        371 GACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 312

Qy        230 HisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSer 249
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Db        311 CAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACATTCCTACTTCTCC 252

Qy        250 LeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSer 269
              ||||||||   ||||||||||||||||:::   ||||||||||||||||:::
Db        251 CTGACATTCTGCGTTCAGGTCCAGGGCAAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTC 192

Qy        270 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 289
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Db        191 ACGGACAAGACCTCAGCCACGGTCATCTGCCGCAAAAATGCCAGCATTAGCGTGCGGGCC 132

Qy        290 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSer 307
              :::|||||||||||||||||||||||||||   ||||||||||||   ||||||
Db        131 CAGGACCGCTACTATAGCTCATCTTGGAGCGAATGGGCATCTGTGCCCTGCAGT 78

RESULT 9
CD559450/c
LOCUS       CD559450                772 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496612 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971872 5', mRNA sequence.
ACCESSION   CD559450
VERSION     CD559450.2  GI:38453469
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 772)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585518.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 03
            High quality sequence start: 2
            High quality sequence stop: 753.
FEATURES             Location/Qualifiers
     source          1. .772
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971872"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              8.67e-88        Length:         772
Score:                  952.50          Matches:        184
Percent Similarity:     90.2%           Conservative:   18
Best Local Similarity:  82.1%           Mismatches:     21
Query Match:            35.4%           Indels:         3
DB:                     5               Gaps:           1

US-10-821-670A-44 (1-511) x CD559450 (1-772)

Qy         84 LysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsn 103
              :::||||||||   |||   |||||||||   |||::::::|||||||||   ||||||
Db        768 CAAAAGGAAGATGA-ATTNGGTCCACTGATAT-TTAAAGGACCAGAAAGAACCCAAAAAT 711

Qy        104 LysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeu 123
              |||   ||||||:::|||||||||||||||||||||||||||||||||||||||||||||
Db        710 AAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTG 651

Qy        124 ThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSerAspPro 143
              |||   ||||||||||||||   |||:::|||||||||||||||||||||||||||||
Db        650 ACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCTGACCCC 591

Qy        144 GlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArg 163
              |||   |||||||||||||||||||||||||||||:::||||||   ||||||:::
Db        590 CAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAACAAG 531

Qy        164 AspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGlu 183
              :::|||   :::|||:::|||||||||||||||   ||||||||||||||||||||||
Db        530 GAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCTGAGGAG 474

Qy        184 SerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThr 203
              ||||||||||||||||||:::|||||||||:::||||||||||||||||||||||||||
Db        473 AGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACC 414

Qy        204 SerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGlnLeuLys 223
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 AGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAG 354

Qy        224 ProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThrTrpSerThr 243
              ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        353 CCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACT 294

Qy        244 ProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGlu 263
              ||||||||||||||||||||||||   ||||||||||||||||||:::   ||||||
Db        293 CCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGCAAGAGAGAA 234

Qy        264 LysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHisLysAspAla 283
              ||||||||||:::      ||||||||||||||   |||:::|||   |||:::|||
Db        233 AAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGCAAAAATGCC 174
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Qy        284 LysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSer 303
              |||   |||:::|||:::|||||||||||||||||||||||||||||   |||||||||
Db        173 AGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAATGGGCATCT 114

Qy        304 ValSerCysSer 307
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Db        113 GTGCCCTGCAGT 102
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RESULT 10
CD559451/c
LOCUS CD559451 762 bp mRNA linear EST 19-NOV-2003
DEFINITION AGENCOURT_14496580 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971871 5', mRNA sequence.
ACCESSION CD559451
VERSION CD559451.2 GI:38453471
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 762)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585519.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: IRBK2 row: h column: 02
High quality sequence start: 38
High quality sequence stop: 761.

FEATURES Location/Qualifiers
source 1. .762
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971871"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 2.81e-87 Length: 762
Score: 947.50 Matches: 183

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Percent Similarity:     90.1%          Conservative:  17
Best Local Similarity:  82.4%          Mismatches:    21
Query Match:            35.3%          Indels:        3
DB:                     5              Gaps:          1

US-10-821-670A-44 (1-511) x CD559451 (1-762)

Qy         86 GluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIle 105
              |||||||||   ||||||||||||   |||::::::|||||||||   |||||||||
Db        759 GAAGATGGAAT-TGGTCCACTGATAT-TTAAAGGACCAGAAAGAACCCAAAAATAAGACC 702

Qy        106 PheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAla 125
              |||:::|||||||||||||||||||||||||||||||||||||||||||||||||||
Db        701 TCTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGACA 642

Qy        126 IleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlu 145
              |||||||||||||||   |||:::|||||||||||||||||||||||||||||||||
Db        641 ATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGG 582

Qy        146 ValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyr 165
              |||||||||||||||||||||||||||||||:::||||||   ||||||::::::|||
Db        581 GTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAACAAGGAGTAT 522

Qy        166 LysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeu 185
                 :::|||:::|||||||||||||||   |||||||||||||||||||||||||||||
Db        521 ---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCTGAGGAGAGTCTG 465

Qy        186 ProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSer 205
              ||||||||||||:::||||||||||:::||||||||||||||||||||||||||||||||
Db        464 CCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACCAGCAGC 405

Qy        206 PhePheIleArgAspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeu 225
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Db        404 TTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTA 345

Qy        226 LysAsnSerArgHisValGluValSerTrpGluTyrProAspThrTrpSerThrProHis 245
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db        344 AAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACAT 285

Qy        246 SerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLys 265
              ||||||||||||||||||||   ||||||||||||||||||:::   ||||||||||||
Db        284 TCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGCAAGAGAGAAAAGAAA 225

Qy        266 AspArgLeuSerValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIle 285
              ||||||:::     |||||||||||||||   |||:::|||   |||:::|||   |||
Db        224 GATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGCAAAAATGCCAGCATT 165

Qy        286 ArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSer 305
              |||:::|||:::|||||||||||||||||||||||||   ||||||||||||
Db        164 AGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAATGGGCATCTGTGCCC 105

Qy        306 CysSer 307
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Db        104 TGCAGT 99
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RESULT 11
CD559602
LOCUS CD559602 745 bp mRNA linear EST 26-NOV-2003
DEFINITION AGENCOURT_14496684 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971874 5', mRNA sequence.
ACCESSION CD559602
VERSION CD559602.2 GI:38558930
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 745)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585670.

```
           Contact: Daniela S. Gerhard, Ph.D.
           Office of Cancer Genomics
           National Cancer Institute / NIH
           Bldg. 31 Rm10A07 Bethesda, MD 20892
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: IRBK2  row: h  column: 05
           High quality sequence start: 2
           High quality sequence stop: 644.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971874"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              3.32e-82        Length:         745
Score:                  898.50          Matches:        173
Percent Similarity:     89.8%           Conservative:   21
Best Local Similarity:  80.1%           Mismatches:     19
Query Match:            33.4%           Indels:         4
DB:                     5               Gaps:           3

US-10-821-670A-44 (1-511) x CD559602 (1-745)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||:::|||:::|||||||||||||||||||||||:::||||||||||||
Db         72 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 131

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||:::|||||||||||||||    ||||||||||||
Db        132 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 191

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 251

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        252 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 311

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              |||:::||||||||||||||||||||||||||||||||||||:::::|||||||||||
Db        312 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 371

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              |||||||||   ||||||:::||||||||||||||||||||||||||||||||||||||
Db        372 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 431

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||   ||||||||||||||||   |||:::||||||||||||||||||||
Db        432 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 491

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||   ||||||||||||||||||||||||||||||:::||||||
Db        492 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 551

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||::::::|||   :::|||:::||||||||||||||   ||||||||||||||||
Db        552 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 608

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||:::|||||||||   |||||||||      :::
Db        609 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGT-CACAAGCTCATGTTGAAA 667

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspPro 216
                 :::         ||||||:::   :::   ::::::   ||||||
Db        668 ATACAC---CACGGCTTCTTTCTCTGAAAT---CTTCAATCTGACCCA 709

RESULT 12
CD559449/c
LOCUS       CD559449                 766 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496649 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971873 5', mRNA sequence.
ACCESSION   CD559449
VERSION     CD559449.2  GI:38453467
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 766)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585517.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 04
            High quality sequence stop: 641.
FEATURES             Location/Qualifiers
     source          1. .766
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971873"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
```

PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	3.47e-82	Length:	766
Score:	898.50	Matches:	168
Percent Similarity:	90.6%	Conservative:	15
Best Local Similarity:	83.2%	Mismatches:	18
Query Match:	33.4%	Indels:	1
DB:	5	Gaps:	1

US-10-821-670A-44 (1-511) x CD559449 (1-766)

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Qy        106 PheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAla 125
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Db        693 TTTCTAAGATGCGAGGCCAAGAAGTATTCTGGACGTTTCACCTGGTGGTGGCTGACGACA 634

Qy        126 IleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlu 145
              ||||||||||||||||   |||:::|||||||||||||||||||||||||||||||||||
Db        633 ATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGG 574

Qy        146 ValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyr 165
              ||||||||||||||||||||||||||||||:::||||||   ||||||::::::|||
Db        573 GTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAACAAGGAGTAT 514

Qy        166 LysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeu 185
                 :::|||:::|||||||||||||||   ||||||||||||||||||||||||||||||
Db        513 ---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCTGAGGAGAGTCTG 457

Qy        186 ProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSer 205
              ||||||||||||:::|||||||||:::|||||||||||||||||||||||||||||||||
Db        456 CCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACCAGCAGC 397

Qy        206 PhePheIleArgAspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeu 225
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Db        396 TTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTA 337

Qy        226 LysAsnSerArgHisValGluValSerTrpGluTyrProAspThrTrpSerThrProHis 245
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db        336 AAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACAT 277

Qy        246 SerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLys 265
              ||||||||||||||||||||   ||||||||||||||||:::   ||||||||||||
Db        276 TCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGCAAGAGAGAAAAGAAA 217

Qy        266 AspArgLeuSerValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIle 285
              ||||||:::      ||||||||||||||   |||:::|||   |||:::|||   |||
Db        216 GATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGCAAAAATGCCAGCATT 157

Qy        286 ArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSer 305
              |||:::|||:::|||||||||||||||||||||||||||||   ||||||||||||
Db        156 AGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAATGGGCATCTGTGCCC 97

Qy        306 CysSer 307
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Db         96 TGCAGT 91
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RESULT 13
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            IMAGE:6971870 5', mRNA sequence.
ACCESSION   CD559452
VERSION     CD559452.2  GI:38453473
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 754)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585520.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 01
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                      /clone_lib="NIH_MGC_195"
                      /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                      loxP-HindIII; Clones from this library have been
                      PCR-amplified using gene-specific primers to contain the
                      complete open reading frame (based on known gene sequences
                      available from NCBI's RefSeq). Template for PCR is cDNA
                      derived from either pooled cytoplasmic polyA RNA from 30
                      cells lines or pooled total RNA from 10 different tissues
                      (from BD Biosciences/Clontech and Washington University).
                      PCR products are directionally cloned into the loxP sites
                      of the pDNR-Dual vector. Library constructed by Dr.
                      Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                      Expression Laboratory, Research Technology Program, SAIC
                      Frederick, NCI-Frederick, Frederick, MD 21702). For
                      information on which gene each clone represents, please
                      visit our anonymous ftp site at
                      ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                      a Note: this is a NIH_MGC Library."
ORIGIN
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Alignment Scores:

Pred. No.:	2.29e-81	Length:	754
Score:	890.50	Matches:	171
Percent Similarity:	85.8%	Conservative:	17
Best Local Similarity:	78.1%	Mismatches:	30
Query Match:	33.1%	Indels:	2
DB:	5	Gaps:	1

US-10-821-670A-44 (1-511) x CD559452 (1-754)

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Qy         89 IleTrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLys 108
              |||||||||   |||   |||::::::|||||||||   |||||||||   ||||||:::
Db        750 ATTTGGTCCAATGATAT-TTAAAGGACCAGAAAGAACCCAAAAATAAGACCTTTCTAAGA 692

Qy        109 CysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThr 128
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Db        691 TGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGACAATCAGTACT 632

Qy        129 AspLeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGluValThrCys 148
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Qy        149 GlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyr 168

Db        571 GGAGCTGCTACACTCTTTGCAGAGAGAGTCAGAGGGGACAACAAGGAGTAT---GAGTAC 515

Qy        169 ThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGlu 188

Db        514 TCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGGTGAGGAGAGTTTGCCCATTGAG 455

Qy        189 ValValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIle 208

Db        454 GTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACCAGCAGGTTTTTCATC 395

Qy        209 ArgAspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSer 228

Db        394 AGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCT 335

Qy        229 ArgHisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPhe 248

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Qy        249 SerLeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeu 268

Db        274 TCCCTGACATTTTGCGTTCAGGTTCAGGGCAAGAGCAAGAGAGAAAAGAAAGATAGAGTT 215

Qy        269 SerValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGln 288

Db        214 TTCACGGACAAGACCTTAGCCACGGTCATTTGCCGCAAAAATGCCAGCATTAGCGTGCGG 155

Qy        289 AlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSer 307

Db        154 GCCCAGGACCGGTACTATAGCTCATTTTGGAGCGAATGGGCATTTGTGCCCTGCAGT 98

RESULT 14
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DEFINITION  Homo sapiens IL12A gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   DQ033872
VERSION     DQ033872.1  GI:66885081
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     A Scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
  JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
   PUBMED   15869325
REFERENCE   2  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.  Translation starts at the beginning of
            alignment.
FEATURES             Location/Qualifiers
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Score:                  890.00          Matches:        187
Percent Similarity:     80.4%           Conservative:   10
Best Local Similarity:  76.3%           Mismatches:     34
Query Match:            33.1%           Indels:         15
DB:                     14              Gaps:           3

US-10-821-670A-44 (1-511) x DQ033872 (1-762)

Qy        267 ArgLeuSerValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArg 286

Db         68 CGGCTCGCCCTGTGTCCCTGCAGTGCCGGCTCAGCATGT---------------------- 106

Qy        287 ValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 306

Db        107 GTCCAG---------CGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCTCCTGGACCACC 157

Qy        307 SerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrProThrProSerProGlyMet 326

Db        158 TCA------------GTTTG-GCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATG 204

Qy        327 PheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLys 346

Db        205 TTCCCATGCCTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAG 264

Qy        347 AlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIle 366

Db        265 GCCAGACAAACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATC 324

Qy        367 ThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGlu 386

Db        325 ACAAAAGATAAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAG 384

Qy        387 SerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArg 406

Db        385 AGTTGCCTAAATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGA 444

Qy        407 LysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyr 426

Db        445 AAGACCTCTTTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTAC 504

Qy        427 GlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePhe 446

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Qy        447 LeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSer 466

Db        565 CTAGATCAAAACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGT 624

Qy        467 ValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLys 486

Db        625 GAGACTGTGCCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAG 684

Qy        487 LeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSer 506

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RESULT 15
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DEFINITION  Pan troglodytes IL12A gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   DQ033873
VERSION     DQ033873.1  GI:66885082
KEYWORDS    GSS.
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SOURCE      Pan troglodytes (chimpanzee)
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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     A Scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
  JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
   PUBMED   15869325
REFERENCE   2  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.  Translation starts at the beginning of
            alignment.
FEATURES             Location/Qualifiers
     source          1. .762
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     gene            <1. .>762
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ORIGIN

Alignment Scores:
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Score:                  877.00          Matches:        176
Percent Similarity:     86.0%           Conservative:   8
Best Local Similarity:  82.2%           Mismatches:     23
Query Match:            32.6%           Indels:         8
DB:                     14              Gaps:           1

US-10-821-670A-44 (1-511) x DQ033873 (1-762)

Qy        298 TrpSerAsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeu 317
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Db        140 TGGTCCTCCTGGACCAC-CTCAGTTTG--------------------GCCAGAAACCTC 177

Qy        318 ProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeu 337
              |||      ||||||   ||||||||||||   ||||||:::|||||||||   ||||||
Db        178 CCCGTGGCCACCCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCCAAAACCTGCTG 237

Qy        338 ArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThr 357
              ||||||:::||||||   ||||||||||||||||||||||||||||||   ||||||
Db        238 AGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTTTACCCTTGCACT 297

Qy        358 SerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCys 377
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Db        298 TCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGT 357

Qy        378 LeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIle 397
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Db        358 TTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGAGAGACCTCTTTCATA 417

Qy        398 ThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSer 417
              ||||||||||||||||||||||||||||||||||||||||||||      ||||||||||||
Db        418 ACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATGGCCCTGTGCCTTAGT 477

Qy        418 SerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeu 437
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Db        478 AGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAATGCAAAGCTT 537

Qy        438 LeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGlu 457
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Db        538 CTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCAGTTATTGACGAG 597

Qy        458 LeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGlu 477
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Qy        478 ProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArg 497
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Db        658 CTGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGG 717

Qy        498 AlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 511
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 10, 2006, 01:16:39 ; Search time 263.906 Seconds
(without alignments)
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Title: US-10-821-670A-44
Perfect score: 2687
Sequence: 1 IWELEKNVYVVELDWHPDAP.....HAFRIRAVTINRMMSYLNAS 511

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	3	2687	100.0	1599	3	US-09-917-265A-38	Sequence 38, Appl
c	4	2687	100.0	1599	3	US-09-917-265A-40	Sequence 40, Appl
	5	2546	94.8	1533	3	US-09-917-265A-66	Sequence 66, Appl
c	6	2546	94.8	1533	3	US-09-917-265A-68	Sequence 68, Appl
	7	2546	94.8	1599	3	US-09-917-265A-61	Sequence 61, Appl
c	8	2546	94.8	1599	3	US-09-917-265A-63	Sequence 63, Appl
	9	2320.5	86.4	1560	2	US-08-751-767A-11	Sequence 11, Appl
	10	2320.5	86.4	1623	2	US-08-751-767A-9	Sequence 9, Appli
	11	2320.5	86.4	6139	2	US-08-751-767A-7	Sequence 7, Appli
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	17	1639	61.0	921	3	US-09-302-495-7	Sequence 7, Appli
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	19	1639	61.0	921	3	US-10-079-616-7	Sequence 7, Appli
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c	21	1639	61.0	987	3	US-09-917-265A-31	Sequence 31, Appl
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	24	1639	61.0	2193	3	US-10-079-616-5	Sequence 5, Appli
	25	1635	60.8	985	3	US-09-917-265A-55	Sequence 55, Appl
c	26	1635	60.8	985	3	US-09-917-265A-57	Sequence 57, Appl
	27	1546	57.5	921	3	US-09-917-265A-52	Sequence 52, Appl
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	32	1546	57.5	990	3	US-09-390-729-11	Sequence 11, Appl
	33	1546	57.5	2267	3	US-09-917-265A-107	Sequence 107, App
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	36	1533	57.1	990	3	US-09-390-729-1	Sequence 1, Appli
	37	1439.5	53.6	1389	3	US-09-634-368-4	Sequence 4, Appli
	38	1418.5	52.8	987	2	US-08-186-529-1	Sequence 1, Appli
	39	1418.5	52.8	987	2	US-08-640-386A-1	Sequence 1, Appli
	40	1418.5	52.8	1018	2	US-08-184-009-194	Sequence 194, App
	41	1418.5	52.8	1018	2	US-08-458-356-194	Sequence 194, App
	42	1418.5	52.8	1018	3	US-08-460-736-194	Sequence 194, App
	43	1418.5	52.8	1018	3	US-09-535-370-194	Sequence 194, App
	44	1418.5	52.8	1018	3	US-09-663-667-194	Sequence 194, App
	45	1418.5	52.8	1399	2	US-08-751-767A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-917-265A-43
; Sequence 43, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)
US-09-917-265A-43

Alignment Scores:

Pred. No.:	7.69e-290	Length:	1533
Score:	2687.00	Matches:	511
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-44 (1-511) x US-09-917-265A-43 (1-1533)

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Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
              ||||||||||||||||||||||||||||||||
Db       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
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RESULT 2
US-09-917-265A-45/c
; Sequence 45, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265A-45

Alignment Scores:

Pred. No.:	7.69e-290	Length:	1533
Score:	2687.00	Matches:	511
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-44 (1-511) x US-09-917-265A-45 (1-1533)

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Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
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Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414
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Qy        41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy       101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy       121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy       141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy       161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy       221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy       241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy       261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy       281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy       301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       633 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy       321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       573 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy       341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy       361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy       381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy       401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy       421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy       441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy       461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy       481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy       501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
             ||||||||||||||||||||||||||||||||
Db        33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
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RESULT 3
US-09-917-265A-38
; Sequence 38, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1599)
US-09-917-265A-38

Alignment Scores:

Pred. No.:	8.24e-290	Length:	1599
Score:	2687.00	Matches:	511
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-44 (1-511) x US-09-917-265A-38 (1-1599)

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Qy         1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy        21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1086

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1146

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1147 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1266

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1267 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1326

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1327 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1386

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1387 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1446

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1506

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1566

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
              |||||||||||||||||||||||||||||||||
Db       1567 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599

RESULT 4
US-09-917-265A-40/c
; Sequence 40, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-40

Alignment Scores:
Pred. No.:              8.24e-290       Length:         1599
Score:                  2687.00         Matches:        511
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-44 (1-511) x US-09-917-265A-40 (1-1599)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174
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Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
              |||||||||||||||||||||||||||||||||
Db         33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
```

RESULT 5
US-09-917-265A-66
; Sequence 66, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)
US-09-917-265A-66

Alignment Scores:

Pred. No.:	4.39e-274	Length:	1533
Score:	2546.00	Matches:	482
Percent Similarity:	96.7%	Conservative:	12
Best Local Similarity:	94.3%	Mismatches:	17
Query Match:	94.8%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-44 (1-511) x US-09-917-265A-66 (1-1533)

```
Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||:::|||||||||    |||   |||
Db        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||:::||||||||||||||
Db        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||  ||||||||||||||||  ||||||||||||||:::|||||||||||
Db        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480
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Qy       161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
Db       481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540

Qy       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
Db       541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
Db       601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660

Qy       221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
Db       661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720

Qy       241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
Db       721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780

Qy       261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
Db       781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy       281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
Db       841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900

Qy       301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
Db       901 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy       321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
Db       961 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 1020

Qy       341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
Db      1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 1080

Qy       361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
Db      1081 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy       381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
Db      1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1200

Qy       401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
Db      1201 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1260

Qy       421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
Db      1261 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1320

Qy       441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
Db      1321 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 1380

Qy       461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
Db      1381 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1440

Qy       481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
Db      1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1500

Qy       501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
Db      1501 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1533
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RESULT 6
US-09-917-265A-68/c
; Sequence 68, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-68

Alignment Scores:
Pred. No.:              4.39e-274       Length:         1533
Score:                  2546.00         Matches:        482
Percent Similarity:     96.7%           Conservative:   12
Best Local Similarity:  94.3%           Mismatches:     17
Query Match:            94.8%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-44 (1-511) x US-09-917-265A-68 (1-1533)

Qy         1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
Db      1533 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy        21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
Db      1473 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1414

Qy        41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
Db      1413 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
Db      1353 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1294

Qy        81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
Db      1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

Qy       101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
Db      1233 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy       121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
Db      1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy       141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
Db      1113 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1054

Qy       161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
Db      1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 994

Qy       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
Db       993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
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Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240

Db        873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260

Db        813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280

Db        753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300

Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 634

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320

Db        633 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340

Db        573 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 514

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360

Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 454

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380

Db        453 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400

Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 334

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420

Db        333 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 274

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440

Db        273 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 214

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460

Db        213 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 154

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480

Db        153 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 94

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500

Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 34

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511

Db         33 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1

RESULT 7
US-09-917-265A-61
; Sequence 61, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-09-917-265A-61

Alignment Scores:
Pred. No.:              4.71e-274       Length:         1599
Score:                  2546.00         Matches:        482
Percent Similarity:     96.7%           Conservative:   12
Best Local Similarity:  94.3%           Mismatches:     17
Query Match:            94.8%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-44 (1-511) x US-09-917-265A-61 (1-1599)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20

Db         67 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40

Db        127 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60

Db        187 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80

Db        247 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100

Db        307 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120

Db        367 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140

Db        427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160

Db        487 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180

Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 606

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200

Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220

Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 726

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240

Db        727 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 786
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Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||   :::|||   ||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 846

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        847 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 966

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db       1027 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 1086

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 1146

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1147 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1266

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
              ||||||||||||||||  |||  ||||||||||||  ||||||||||||||||||||||
Db       1267 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1326

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db       1327 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1386

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1387 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 1446

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
              |||||||||  ||||||||||||||||||||  ||||||||||||||||||||||||||
Db       1447 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1506

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1566

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
              |||||||||||||||||||||||||:::|||
Db       1567 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1599

RESULT 8
US-09-917-265A-63/c
; Sequence 63, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-63

Alignment Scores:
Pred. No.:              4.71e-274       Length:         1599
Score:                  2546.00         Matches:        482
Percent Similarity:     96.7%           Conservative:   12
Best Local Similarity:  94.3%           Mismatches:     17
Query Match:            94.8%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-44 (1-511) x US-09-917-265A-63 (1-1599)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||:::|||||||||  |||  |||
Db       1353 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||
Db       1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||  ||||||||||||||||  ||||||||||||||:::||||||||||
Db       1113 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
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Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 634

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        573 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 514

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
              |||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 454

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 334

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
              ||||||||||||||   |||   ||||||||||||   ||||||||||||||||||||||
Db        333 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 274

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        273 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 214

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 154

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
              |||||||||   ||||||||||||||||||||||   ||||||||||||||||||||||||
Db        153 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 94

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 34

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
              |||||||||||||||||||||||||:::|||
Db         33 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1

RESULT 9
US-08-751-767A-11
; Sequence 11, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1560 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1557
US-08-751-767A-11

Alignment Scores:
Pred. No.:              7.16e-249       Length:         1560
Score:                  2320.50         Matches:        441
Percent Similarity:     90.2%           Conservative:   27
Best Local Similarity:  85.0%           Mismatches:     42
Query Match:            86.4%           Indels:         9
DB:                     2               Gaps:           2

US-10-821-670A-44 (1-511) x US-08-751-767A-11 (1-1560)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||:::|||:::|||||||||||||||||||||||:::||||||||||||
Db          4 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 63

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||:::|||||||||||||||   ||||||||||||
Db         64 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 123

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 183

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        184 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 243

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              |||:::|||||||||||||||||||||||||||||||||||||:::::::||||||||||
Db        244 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 303

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              |||||||||   ||||||:::|||||||||||||||||||||||||||||||||||||||
Db        304 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 363

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||   ||||||||||||||||   |||:::||||||||||||||||||||
Db        364 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 423

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||   ||||||||||||||||||||||||||||||:::||||||
Db        424 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 483

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||:::::::|||   :::|||:::||||||||||||||   ||||||||||||||||
Db        484 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              |||||||||||||||||||||||||:::|||||||||:::|||||||||||||||||||
Db        541 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
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Db        661 CAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260

Db        721 TGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280

Db        781 AAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300

Db        841 AAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAA 900

Qy        301 TrpAlaSerValSerCysSerGlyGly----------GlyGlyGly 312

Db        901 TGGGCATCTGTGCCCTGCAGTGGTGGCGGTGGAAGCGGCGGTGGCGGAAGCGGCGGTGGC 960

Qy        313 GlySerArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHis 332

Db        961 GGCAGCAGAAACCTCCCCCTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCAC 1020

Qy        333 SerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGlu 352

Db       1021 TCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAA 1080

Qy        353 PheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSer 372

Db       1081 TTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGC 1140

Qy        373 ThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArg 392

Db       1141 ACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGA 1200

Qy        393 GluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThr 412

Db       1201 GAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATG 1260

Qy        413 ThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAla 432

Db       1261 GCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACC 1320

Qy        433 MetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 452

Db       1321 ATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTG 1380

Qy        453 ThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsn 472

Db       1381 GCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAA 1440

Qy        473 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 492

Db       1441 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1500

Qy        493 AlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 511

Db       1501 GCTTTCAGAATTCGGGCAGTGACTATTGACAGAGTGACGAGCTATCTGAATGCTTCC 1557

RESULT 10
US-08-751-767A-9
; Sequence 9, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1623 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1620
US-08-751-767A-9

Alignment Scores:
Pred. No.:                7.64e-249      Length:          1623
Score:                    2320.50        Matches:         441
Percent Similarity:       90.2%          Conservative:    27
Best Local Similarity:    85.0%          Mismatches:      42
Query Match:              86.4%          Indels:          9
DB:                       2              Gaps:            2

US-10-821-670A-44 (1-511) x US-08-751-767A-9 (1-1623)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20

Db         67 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40

Db        127 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60

Db        187 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80

Db        247 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100

Db        307 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120

Db        367 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140

Db        427 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160

Db        487 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 546
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Qy       161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
Db       547 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 603

Qy       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
Db       604 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAA 663

Qy       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
Db       664 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTG 723

Qy       221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
Db       724 CAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACC 783

Qy       241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
Db       784 TGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGC 843

Qy       261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
Db       844 AAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGC 903

Qy       281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
Db       904 AAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAA 963

Qy       301 TrpAlaSerValSerCysSerGlyGly----------GlyGlyGly 312
Db       964 TGGGCATCTGTGCCCTGCAGTGGTGGCGGTGGAAGCGGCGGTGGCGGAAGCGGCGGTGGC 1023

Qy       313 GlySerArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHis 332
Db      1024 GGCAGCAGAAACCTCCCCCTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCAC 1083

Qy       333 SerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGlu 352
Db      1084 TCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAA 1143

Qy       353 PheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSer 372
Db      1144 TTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGC 1203

Qy       373 ThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArg 392
Db      1204 ACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGA 1263

Qy       393 GluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThr 412
Db      1264 GAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATG 1323

Qy       413 ThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAla 432
Db      1324 GCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACC 1383

Qy       433 MetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 452
Db      1384 ATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTG 1443

Qy       453 ThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsn 472
Db      1444 GCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAA 1503

Qy       473 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 492
Db      1504 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 1563

Qy       493 AlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 511
Db      1564 GCTTTCAGAATTCGGGCAGTGACTATTGACAGAGTGACGAGCTATCTGAATGCTTCC 1620

RESULT 11
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US-08-751-767A-7
; Sequence 7, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6139 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3222..4841
US-08-751-767A-7

Alignment Scores:
Pred. No.:                6.89e-248       Length:          6139
Score:                    2320.50         Matches:         441
Percent Similarity:       90.2%           Conservative:    27
Best Local Similarity:    85.0%           Mismatches:      42
Query Match:              86.4%           Indels:          9
DB:                       2               Gaps:            2

US-10-821-670A-44 (1-511) x US-08-751-767A-7 (1-6139)

Qy         1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
Db      3288 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 3347

Qy        21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
Db      3348 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 3407

Qy        41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
Db      3408 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 3467

Qy        61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
Db      3468 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 3527

Qy        81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
Db      3528 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 3587
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Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              |||||||||   ||||||:::|||||||||||||||||||||||||||||||||||||||
Db       3588 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 3647

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||   ||||||||||||||||   |||:::|||||||||||||||||||||
Db       3648 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 3707

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||   ||||||||||||||||||||||||||||||||:::||||||
Db       3708 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 3767

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||:::::|||   :::|||:::|||||||||||||||   ||||||||||||||||
Db       3768 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 3824

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||:::|||||||||:::|||||||||||||||||||
Db       3825 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAA 3884

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3885 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTG 3944

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db       3945 CAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACC 4004

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||:::
Db       4005 TGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGC 4064

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||:::      ||||||||||||||   |||:::|||
Db       4065 AAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGC 4124

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              |||:::|||   |||   |||:::|||:::|||||||||||||||||||||||||||||
Db       4125 AAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAA 4184

Qy        301 TrpAlaSerValSerCysSerGlyGly------------------------GlyGlyGly 312
              ||||||||||||   ||||||||||||                        |||||||||
Db       4185 TGGGCATCTGTGCCCTGCAGTGGTGGCGGTGGAAGCGGCGGTGGCGGAAGCGGCGGTGGC 4244

Qy        313 GlySerArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHis 332
              ||||||||||||||||||||      ||||||   ||||||||||||   ||||||:::|||
Db       4245 GGCAGCAGAAACCTCCCCCTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCAC 4304

Qy        333 SerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGlu 352
              ||||||   ||||||||||||:::||||||   ||||||||||||||||||||||||||||
Db       4305 TCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAA 4364

Qy        353 PheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSer 372
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4365 TTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGC 4424

Qy        373 ThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArg 392
              ||||||||||||||||||||||||||||||   ||||||||||||||   ||||||
Db       4425 ACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGA 4484

Qy        393 GluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThr 412
              |||   |||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db       4485 GAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATG 4544

Qy        413 ThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAla 432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4545 GCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACC 4604

Qy        433 MetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 452
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4605 ATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTG 4664

Qy        453 ThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsn 472
              ||||||||||||:::|||||||||||||   ||||||   ||||||||||||
Db       4665 GCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAA 4724

Qy        473 SerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4725 TCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 4784

Qy        493 AlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 511
              ||||||||||||||||||||||||:::|||:::   ||||||||||||||||||
Db       4785 GCTTTCAGAATTCGGGCAGTGACTATTGACAGAGTGACGAGCTATCTGAATGCTTCC 4841
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RESULT 12
US-09-917-265A-26
; Sequence 26, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(921)
US-09-917-265A-26

Alignment Scores:

Pred. No.:	7.12e-174	Length:	921
Score:	1646.00	Matches:	307
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	61.3%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-44 (1-511) x US-09-917-265A-26 (1-921)

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Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 13
US-09-917-265A-28/c
; Sequence 28, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-28

Alignment Scores:
Pred. No.:              7.12e-174       Length:         921
Score:                  1646.00         Matches:        307
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            61.3%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-44 (1-511) x US-09-917-265A-28 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCAGT 1

RESULT 14
US-09-011-143-6
; Sequence 6, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
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```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  921 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-6

Alignment Scores:
Pred. No.:              4.31e-173       Length:         921
Score:                  1639.00         Matches:        306
Percent Similarity:     99.7%           Conservative:   0
Best Local Similarity:  99.7%           Mismatches:     1
Query Match:            61.0%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-44 (1-511) x US-09-011-143-6 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 15
US-09-011-143-7
; Sequence 7, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  921 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-7

Alignment Scores:
Pred. No.:              4.31e-173      Length:         921
Score:                  1639.00        Matches:        306
Percent Similarity:     99.7%          Conservative:   0
Best Local Similarity:  99.7%          Mismatches:     1
Query Match:            61.0%          Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-44 (1-511) x US-09-011-143-7 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
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Search completed: June 10, 2006, 01:42:41
Job time : 289.906 secs
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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 10, 2006, 01:18:38 ; Search time 1999.43 Seconds
(without alignments)
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Perfect score: 2687
Sequence: 1 IWELEKNVYVVELDWHPDAP.....HAFRIRAVTINRMMSYLNAS 511

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Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	2	2687	100.0	1533	3	US-09-917-265-45	Sequence 45, Appl
	3	2687	100.0	1533	9	US-10-821-670-43	Sequence 43, Appl
c	4	2687	100.0	1533	9	US-10-821-670-45	Sequence 45, Appl
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	18	2330.5	86.7	11453	10	US-10-511-237-3	Sequence 3, Appli
	19	2314	86.1	8608	3	US-09-828-825-7	Sequence 7, Appli
	20	2314	86.1	8629	3	US-09-828-825-15	Sequence 15, Appl
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	23	2309	85.9	8638	3	US-09-828-825-9	Sequence 9, Appli
	24	2309	85.9	8659	3	US-09-828-825-11	Sequence 11, Appl
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	34	1639	61.0	921	6	US-10-079-616-6	Sequence 6, Appli
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ALIGNMENTS

RESULT 1
US-09-917-265-43
; Sequence 43, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)
; OTHER INFORMATION:
US-09-917-265-43

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Score:                  2687.00         Matches:        511
Percent Similarity:     100.0%          Conservative:   0
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Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

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Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
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RESULT 2
US-09-917-265-45/c
; Sequence 45, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE(
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-45

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Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
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Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

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Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260

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Db        333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440

Db        273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460

Db        213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480

Db        153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500

Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511

Db         33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
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RESULT 3
US-10-821-670-43
; Sequence 43, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)
US-10-821-670-43

Alignment Scores:

Pred. No.:	2.11e-314	Length:	1533
Score:	2687.00	Matches:	511
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	9	Gaps:	0

US-10-821-670A-44 (1-511) x US-10-821-670-43 (1-1533)

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Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20

Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40

Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
```

```
Qy        41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy       101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy       121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy       141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy       161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy       181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy       201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy       221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy       241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy       261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy       281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy       301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy       321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020

Qy       341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080

Qy       361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy       381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200

Qy       401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260

Qy       421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320

Qy       441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380

Qy       461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440

Qy       481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500

Qy       501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
             |||||||||||||||||||||||||||||||||
Db      1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
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RESULT 4
US-10-821-670-45/c
; Sequence 45, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
US-10-821-670-45

Alignment Scores:

Pred. No.:	2.11e-314	Length:	1533
Score:	2687.00	Matches:	511
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	9	Gaps:	0

US-10-821-670A-44 (1-511) x US-10-821-670-45 (1-1533)

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Qy         1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy        21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
              |||||||||||||||||||||||||||||||||
Db         33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
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RESULT 5
US-09-917-265-38
; Sequence 38, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1599)
; OTHER INFORMATION:
US-09-917-265-38

Alignment Scores:

Pred. No.:	2.25e-314	Length:	1599
Score:	2687.00	Matches:	511
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-44 (1-511) x US-09-917-265-38 (1-1599)

```
Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
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Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160

Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180

Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200

Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220

Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240

Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260

Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280

Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300

Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320

Db        967 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340

Db       1027 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1086

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360

Db       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1146

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380

Db       1147 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400

Db       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1266

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420

Db       1267 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1326

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440

Db       1327 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1386

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460

Db       1387 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1446

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480

Db       1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1506

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500

Db       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1566

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511

Db       1567 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599

RESULT 6
US-09-917-265-40/c
; Sequence 40, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-40

Alignment Scores:
Pred. No.:                2.25e-314       Length:          1599
Score:                    2687.00         Matches:         511
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              100.0%          Indels:          0
DB:                       3               Gaps:            0

US-10-821-670A-44 (1-511) x US-09-917-265-40 (1-1599)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20

Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40

Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60

Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80

Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100

Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120

Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140

Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160

Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180

Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994
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Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
              ||||||||||||||||||||||||||||||||
Db         33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 7
US-10-821-670-38
; Sequence 38, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-10-821-670-38

Alignment Scores:
Pred. No.:                2.25e-314       Length:          1599
Score:                    2687.00         Matches:         511
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              100.0%          Indels:          0
DB:                       9               Gaps:            0

US-10-821-670A-44 (1-511) x US-10-821-670-38 (1-1599)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
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Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1086

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1146

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1147 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1266

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1267 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1326

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1327 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1386

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1387 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1446

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1447 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1506

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1566

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
              |||||||||||||||||||||||||||||||||
Db       1567 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599

RESULT 8
US-10-821-670-40/c
; Sequence 40, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-40

Alignment Scores:
Pred. No.:              2.25e-314       Length:         1599
Score:                  2687.00         Matches:        511
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-44 (1-511) x US-10-821-670-40 (1-1599)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy         281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy         301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         633 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy         321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         573 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy         341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy         361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy         381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy         401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy         421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy         441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy         461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy         481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy         501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
                |||||||||||||||||||||||||||||||
Db          33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
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RESULT 9
US-09-917-265-66
; Sequence 66, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)

; OTHER INFORMATION:
US-09-917-265-66

Alignment Scores:

Pred. No.:	2.74e-297	Length:	1533
Score:	2546.00	Matches:	482
Percent Similarity:	96.7%	Conservative:	12
Best Local Similarity:	94.3%	Mismatches:	17
Query Match:	94.8%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-44 (1-511) x US-09-917-265-66 (1-1533)

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Qy           1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
                ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db           1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy          21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
                ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db          61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120

Qy          41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy          61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
                ||||||||||||||||||||||||||||||||:::|||||||||   |||   |||
Db         181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240

Qy          81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
                ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db         241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300

Qy         101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360

Qy         121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
                ||||||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db         361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420

Qy         141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
                ||||||||||   ||||||||||||||   ||||||||||||:::||||||||||
Db         421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480

Qy         161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db         481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540

Qy         181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy         201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660

Qy         221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720

Qy         241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
                ||||||||||||||||||||||||||||||||||||   :::|||   ||||||||||||
Db         721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780

Qy         261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
                ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db         781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy         281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db         841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900
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Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        961 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 1020

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
              ||||||||||||||||||||||||||||||||||    ||||||||||||||||||||||
Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 1080

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1200

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
              ||||||||||||||||    |||    ||||||||||||    ||||||||||||||||||||
Db       1201 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1260

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1320

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 1380

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
              |||||||||    ||||||||||||||||||||    ||||||||||||||||||||||||
Db       1381 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1440

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1500

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
              |||||||||||||||||||||||||:::|||
Db       1501 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1533

RESULT 10
US-09-917-265-68/c
; Sequence 68, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-68

Alignment Scores:
Pred. No.:              2.74e-297      Length:          1533
Score:                  2546.00        Matches:         482
Percent Similarity:     96.7%          Conservative:    12
Best Local Similarity:  94.3%          Mismatches:      17
Query Match:            94.8%          Indels:          0
DB:                     3              Gaps:            0

US-10-821-670A-44 (1-511) x US-09-917-265-68 (1-1533)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||:::|||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
                 ||||||||||||||||||||||||||||||||||:::|||||||||    |||    |||
Db       1353 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||
Db       1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||:::|||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||    ||||||||||||||||||    ||||||||||||:::|||||||||
Db       1113 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||    :::|||   ||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db        753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 634

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        573 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 514

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
              ||||||||||||||||||||||||||||||||||    ||||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 454
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Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 334

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
              |||||||||||||||   |||   ||||||||||||   ||||||||||||||||||||
Db        333 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 274

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db        273 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 214

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 154

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
              |||||||||   ||||||||||||||||||||   ||||||||||||||||||||||||
Db        153 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 94

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 34

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
              |||||||||||||||||||||||:::|||
Db         33 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1

RESULT 11
US-10-821-670-66
; Sequence 66, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-10-821-670-66

Alignment Scores:
Pred. No.:              2.74e-297      Length:         1533
Score:                  2546.00        Matches:        482
Percent Similarity:     96.7%          Conservative:   12
Best Local Similarity:  94.3%          Mismatches:     17
Query Match:            94.8%          Indels:         0
DB:                     9              Gaps:           0

US-10-821-670A-44 (1-511) x US-10-821-670-66 (1-1533)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||:::|||||||||   |||   |||
Db        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||:::||||||||||||||
Db        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||   ||||||||||||||   ||||||||||||||:::|||||||||
Db        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||   :::|||   ||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        961 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 1020

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 1080

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1200

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
              |||||||||||||||||   |||   ||||||||||||   ||||||||||||||||||||
Db       1201 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1260

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db       1261 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1320

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 1380

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
              |||||||||   ||||||||||||||||||||   ||||||||||||||||||||||||||
Db       1381 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1440

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1500

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
              |||||||||||||||||||||||||:::|||
Db       1501 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1533

RESULT 12
US-10-821-670-68/c
; Sequence 68, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-68

Alignment Scores:
Pred. No.:              2.74e-297      Length:         1533
Score:                  2546.00        Matches:        482
Percent Similarity:     96.7%          Conservative:   12
Best Local Similarity:  94.3%          Mismatches:     17
Query Match:            94.8%          Indels:         0
DB:                     9              Gaps:           0

US-10-821-670A-44 (1-511) x US-10-821-670-68 (1-1533)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              |||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
                 ||||||||||||||||||||||||||||||:::|||||||||   |||   |||
Db       1353 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||
Db       1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||:::||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||   ||||||||||||||||   ||||||||||||||:::||||||||||
Db       1113 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||   :::|||   ||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 634

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        573 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 514

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 454

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 334

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
              |||||||||||||||   |||   ||||||||||||   ||||||||||||||||||||
Db        333 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 274

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        273 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 214
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Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
Db        213 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 154

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
Db        153 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 94

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 34

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
Db         33 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1

RESULT 13
US-09-917-265-61
; Sequence 61, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
US-09-917-265-61

Alignment Scores:
Pred. No.:              2.94e-297      Length:          1599
Score:                  2546.00        Matches:         482
Percent Similarity:     96.7%          Conservative:    12
Best Local Similarity:  94.3%          Mismatches:      17
Query Match:            94.8%          Indels:          0
DB:                     3              Gaps:            0

US-10-821-670A-44 (1-511) x US-09-917-265-61 (1-1599)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
Db         67 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
Db        127 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
Db        187 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
Db        247 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
Db        307 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
Db        367 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
Db        427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
Db        487 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 606

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 726

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
Db        727 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 786

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
Db        787 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 846

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
Db        847 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 966

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
Db        967 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
Db       1027 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 1086

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
Db       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 1146

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
Db       1147 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
Db       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1266

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
Db       1267 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1326

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
Db       1327 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1386

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
Db       1387 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 1446

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
Db       1447 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1506
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Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1566

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
              |||||||||||||||||||||||||:::|||
Db       1567 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1599

RESULT 14
US-09-917-265-63/c
; Sequence 63, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-63

Alignment Scores:
Pred. No.:              2.94e-297      Length:          1599
Score:                  2546.00        Matches:         482
Percent Similarity:     96.7%          Conservative:    12
Best Local Similarity:  94.3%          Mismatches:      17
Query Match:            94.8%          Indels:          0
DB:                     3              Gaps:            0

US-10-821-670A-44 (1-511) x US-09-917-265-63 (1-1599)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              |||||||||||||||||||||||||||||||:::|||||||||   |||   |||
Db       1353 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||
Db       1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||   ||||||||||||||   ||||||||||||||:::|||||||||
Db       1113 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||   :::|||   ||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 634

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        573 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 514

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 454

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 334

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
              ||||||||||||||   |||   ||||||||||||   ||||||||||||||||||||
Db        333 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 274

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db        273 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 214

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 154

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
              |||||||||   ||||||||||||||||||||   ||||||||||||||||||||||||
Db        153 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 94

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 34

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
              |||||||||||||||||||||||||:::|||
Db         33 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1

RESULT 15
US-10-821-670-61
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; Sequence 61, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-10-821-670-61

Alignment Scores:
Pred. No.:              2.94e-297       Length:         1599
Score:                  2546.00         Matches:        482
Percent Similarity:     96.7%           Conservative:   12
Best Local Similarity:  94.3%           Mismatches:     17
Query Match:            94.8%           Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-44 (1-511) x US-10-821-670-61 (1-1599)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||:::|||||||||   |||   |||
Db        247 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||:::||||||||||||||
Db        307 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||   ||||||||||||||   ||||||||||||||:::||||||||||
Db        487 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 606

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 726

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 786

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||   :::|||   ||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 846

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        847 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 966

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db       1027 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 1086

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 1146

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1147 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1266

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
              ||||||||||||||   |||   ||||||||||||   ||||||||||||||||||||
Db       1267 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1326

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db       1327 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1386

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1387 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 1446

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
              |||||||||   ||||||||||||||||||||   ||||||||||||||||||||||||
Db       1447 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1506

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1566

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
              ||||||||||||||||||||||||||||:::|||
Db       1567 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1599


Search completed: June 10, 2006, 04:33:22
Job time : 2023.43 secs
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; Sequence 61, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1599)
US-10-821-670-61

Alignment Scores:

Pred. No.:	2.94e-297	Length:	1599
Score:	2546.00	Matches:	482
Percent Similarity:	96.7%	Conservative:	12
Best Local Similarity:	94.3%	Mismatches:	17
Query Match:	94.8%	Indels:	0
DB:	9	Gaps:	0

US-10-821-670A-44 (1-511) x US-10-821-670-61 (1-1599)

```
Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||:::|||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||:::|||||||||   |||   |||
Db        247 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||
Db        307 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||:::|||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||   ||||||||||||||   ||||||||||||||:::|||||||||
Db        487 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 606

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 726

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 786

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||   :::|||   ||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 846

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              |||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        847 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 966

Qy        301 TrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThrPro 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db       1027 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 1086

Qy        341 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 360
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Db       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 1146

Qy        361 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 380
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Db       1147 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206

Qy        381 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1266

Qy        401 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 420
              ||||||||||||||   |||   ||||||||||||   ||||||||||||||||||||
Db       1267 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1326

Qy        421 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 440
              ||||||||||||||||||||:::|||||||||||||||||||||||||||||||||||
Db       1327 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1386

Qy        441 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1387 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 1446

Qy        461 AlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPhe 480
              |||||||||   ||||||||||||||||||||   ||||||||||||||||||||||||
Db       1447 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1506

Qy        481 TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThr 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1566

Qy        501 IleAsnArgMetMetSerTyrLeuAsnAlaSer 511
              ||||||||||||||||||||||||||||:::|||
Db       1567 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1599
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Search completed: June 10, 2006, 04:33:22
Job time : 2023.43 secs

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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 10, 2006, 01:18:36 ; Search time 26.5861 Seconds
(without alignments)
3659.318 Million cell updates/sec

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Perfect score: 2687
Sequence: 1 IWELEKNVYVVELDWHPDAP.....HAFRIRAVTINRMMSYLNAS 511

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
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Searched: 253354 seqs, 63461778 residues

Total number of hits satisfying chosen parameters: 506708

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-Q=/abss/ABSSWEB_spool/US10821670/runat_07062006_110114_26355/app_query.fasta_1
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	189.5	7.1	1363	6	US-10-827-684B-6	Sequence 6, Appli
2	189.5	7.1	1369	6	US-10-827-684B-5	Sequence 5, Appli
3	176	6.6	1923	7	US-11-145-307A-52	Sequence 52, Appl
4	134.5	5.0	1161	7	US-11-297-134-9	Sequence 9, Appli
5	112.5	4.2	3123	7	US-11-217-529-76356	Sequence 76356, A
6	107.5	4.0	3646	6	US-10-511-937-358	Sequence 358, App
7	105.5	3.9	1614	7	US-11-217-529-409	Sequence 409, App
8	105.5	3.9	2534	7	US-11-293-697-1946	Sequence 1946, Ap
9	104.5	3.9	2123	7	US-11-274-375-5	Sequence 5, Appli
10	104	3.9	3117	7	US-11-217-529-774	Sequence 774, App
11	103.5	3.9	3084	6	US-10-511-937-448	Sequence 448, App
12	103	3.8	3510	7	US-11-217-529-191047	Sequence 191047,
13	102.5	3.8	2832	7	US-11-145-307A-22	Sequence 22, Appl
14	99.5	3.7	1416	6	US-10-953-349-864	Sequence 864, App
15	99.5	3.7	1875	7	US-11-217-529-174200	Sequence 174200,
16	99.5	3.7	1910	7	US-11-274-375-9	Sequence 9, Appli
17	99.5	3.7	2341	6	US-10-511-937-349	Sequence 349, App
18	99	3.7	6327	7	US-11-217-529-75787	Sequence 75787, A
19	98.5	3.7	4761	7	US-11-217-529-1821	Sequence 1821, Ap
20	98.5	3.7	5997	7	US-11-313-450-1	Sequence 1, Appli
21	98.5	3.7	8370	7	US-11-263-326-90	Sequence 90, Appl
22	98.5	3.7	8377	7	US-11-263-326-95	Sequence 95, Appl
23	98.5	3.7	8380	7	US-11-263-326-89	Sequence 89, Appl
24	98.5	3.7	8381	7	US-11-263-326-1	Sequence 1, Appli
25	98.5	3.7	8381	7	US-11-263-326-3	Sequence 3, Appli
26	98.5	3.7	8381	7	US-11-263-326-5	Sequence 5, Appli
27	98.5	3.7	8381	7	US-11-263-326-7	Sequence 7, Appli
28	98.5	3.7	8381	7	US-11-263-326-8	Sequence 8, Appli
29	98.5	3.7	8381	7	US-11-263-326-11	Sequence 11, Appl
30	98.5	3.7	8381	7	US-11-263-326-91	Sequence 91, Appl
31	98.5	3.7	8381	7	US-11-263-326-92	Sequence 92, Appl
32	98.5	3.7	8381	7	US-11-263-326-93	Sequence 93, Appl
33	98.5	3.7	8381	7	US-11-263-326-96	Sequence 96, Appl
34	98.5	3.7	8381	7	US-11-263-326-97	Sequence 97, Appl
35	98.5	3.7	8381	7	US-11-263-326-108	Sequence 108, App
36	98.5	3.7	8381	7	US-11-263-326-136	Sequence 136, App
37	98.5	3.7	8381	7	US-11-263-326-137	Sequence 137, App
38	98.5	3.7	8381	7	US-11-263-326-138	Sequence 138, App
39	98.5	3.7	8381	7	US-11-263-326-139	Sequence 139, App
40	98.5	3.7	8381	7	US-11-263-326-140	Sequence 140, App
41	98.5	3.7	8381	7	US-11-263-326-141	Sequence 141, App
42	98.5	3.7	8381	7	US-11-263-326-142	Sequence 142, App
43	98.5	3.7	8381	7	US-11-263-326-143	Sequence 143, App
44	98.5	3.7	8381	7	US-11-263-326-144	Sequence 144, App
45	98.5	3.7	8388	7	US-11-263-326-94	Sequence 94, Appl

ALIGNMENTS

RESULT 1
US-10-827-684B-6
; Sequence 6, Application US/10827684B
; Publication No. US20060115807A1
; GENERAL INFORMATION:
; APPLICANT: Chambers, Ian P
; TITLE OF INVENTION: Improved episomal expression system
; FILE REFERENCE: 78870/00003
; CURRENT APPLICATION NUMBER: US/10/827,684B
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 09/359,672
; PRIOR FILING DATE: 1999-07-23
; PRIOR APPLICATION NUMBER: GB 9701492.2
; PRIOR FILING DATE: 1997-01-24
; PRIOR APPLICATION NUMBER: PCT/GB98/00216
; PRIOR FILING DATE: 1998-01-26
; PRIOR APPLICATION NUMBER: GB 0407043.9
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1363
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-827-684B-6

Alignment Scores:

Pred. No.:	1.9e-09	Length:	1363
Score:	189.50	Matches:	96
Percent Similarity:	37.4%	Conservative:	63
Best Local Similarity:	22.6%	Mismatches:	169

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Query Match:          7.1%        Indels:       98
DB:                   6           Gaps:         18

US-10-821-670A-44 (1-511) x US-10-827-684B-6 (1363)

Qy        15 TrpHisProAsp-Ala---ProGlyGluMetValValLeuThrCysAsnThrProGlu-- 32
Db        76 TGGCACAGTGACAAGCCTGCCAGGGGCCACCGTTACCCTGATTTGCCCCGGGAAGGAAGC 135

Qy        33 -GluAspAspIleThr-----------TrpThrSerAspGlnSerSerGluValLeuGl 48
Db       136 AGCAGGCAATGTTACCATTCACTGGGTGTACTCTGGCTCACAAAACAGAGAATGGACTAC 195

Qy        48 ySerGlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCy 68
Db       196 CACAGGAAACACACTGGTTCTGAGGGACGTGCAGCTCAGCGACACTGGGGACTATTTATG 255

Qy        68 sHisLysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGl 88
Db       256 CTCCCTGAATGATCACCTGGTGGGGACTGTGCCCTTGCTGGTG---------------- 298

Qy        88 yIleTrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLy 108
Db       299 ------------GATGTTCCCCCAGAGGAGCCCAAG-----------------CTCTC 327

Qy       108 sCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerTh 128
Db       328 CTGCTTCCGGAAGAACCCCCTTGTCAACGCCATCTGTGAGTGG---------------- 370

Qy       128 rAspLeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGluValThrCy 148
Db       371 ----------------------------CGTCCGAGCAGCACCCCCTCTCCAACCACG-- 400

Qy       148 sGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTy 168
Db       401 ----AAGGCTGTGCTGTTTGCAAAGAAAATCAACACCACCAAC---GGGAAGAGTGACTT 453

Qy       168 rThrValGluCysGlnGluGlySerAlaCys---------------------------Pr 179
Db       454 CCAGGTGCCCTGCCAGTATTC-TCAGCAGCTGAAAAGCTTCTCCTGCCAGGTGGAGATCC 512

Qy       179 oAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTy 199
Db       513 TGGAGGGTGACAAAGTATACCACATAGTGTCACTGTGCGTTGCAAACAGTGTGGGAAGCA 572

Qy       199 r-GluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysA 219
Db       573 AGTCCAGCCACAACGAAGCGTTTCACAGCTTAAAAATGGTGCAGCCGGATCCACCTGCCA 632

Qy       219 snLeuGlnLeuLysProLeuLys---AsnSerArgHisValGluValSerTrpGluTyrP 238
Db       633 ACCTTGTGGTATCAGCCATACCTGGAAGGCCGCGCTGGCTCAAAGTCAGCTGGCAGCACC 692

Qy       238 roAspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnG 258
Db       693 CTGAGACCTGGGACCCG------AGTTACTACTTGCTGCAGTTCCAGCTTCGATACCGAC 746

Qy       258 lyLysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValV 278
Db       747 CTGTATGGTCAAAGGAG---TTCACGGTGTTGCTGCTCCCGGTGGCCCAGTACCAATGCG 803

Qy       278 alCysHisLysAspAlaLys--------------IleArgValGlnAlaArgAspArgT 293
Db       804 TCATCCATGATGCCTTGCGAGGAGTGAAGCACGTGGTCCAGGTCCGTGGGAAGGAGGAGC 863

Qy       293 yrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlyG 313
Db       864 TTGACCTTGGCCAGTGGAGTGAATGGTCC---------------------------- 892

Qy       313 lySerArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisS 333
Db       893 -------------CCAGAGGTCACGGGCACTCCTTGGATAGCAGAG---------CCCA 929

Qy       333 erGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluP 353
Db       930 GGACCACCCCGGCAGGAATCCTCTGGAACCCCACACAGGTCTCT--------------- 973

Qy       353 heTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerT 373
Db       974 -----------GTTGAAGACTCTGCCAACCACGAGGATCAGTACGAAAGTTCTACAGAAG 1022

Qy       373 hrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgG 393
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Qy       393 luIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrT 413
Db      1071 CCACATTCCTGGTAGCTGGAGGAAGC----------------TTGGCGTTTGGGTTGC 1112

Qy       413 hrLeuCysLeu 416
Db      1113 TTCTCTGTGTC 1123

RESULT 2
US-10-827-684B-5
; Sequence 5, Application US/10827684B
; Publication No. US20060115807A1
; GENERAL INFORMATION:
;  APPLICANT: Chambers, Ian P
;  TITLE OF INVENTION: Improved episomal expression system
;  FILE REFERENCE: 78870/00003
;  CURRENT APPLICATION NUMBER: US/10/827,684B
;  CURRENT FILING DATE:  2004-04-19
;  PRIOR APPLICATION NUMBER: US 09/359,672
;  PRIOR FILING DATE: 1999-07-23
;  PRIOR APPLICATION NUMBER: GB 9701492.2
;  PRIOR FILING DATE: 1997-01-24
;  PRIOR APPLICATION NUMBER: PCT/GB98/00216
;  PRIOR FILING DATE: 1998-01-26
;  PRIOR APPLICATION NUMBER: GB 0407043.9
;  PRIOR FILING DATE: 2004-03-29
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 1369
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-827-684B-5

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Score:                  189.50        Matches:         96
Percent Similarity:     37.4%         Conservative:    63
Best Local Similarity:  22.6%         Mismatches:      169
Query Match:            7.1%          Indels:          98
DB:                     6             Gaps:            18

US-10-821-670A-44 (1-511) x US-10-827-684B-5 (1-1369)

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Qy        33 -GluAspAspIleThr-----------TrpThrSerAspGlnSerSerGluValLeuGl 48
Db       142 AGCAGGCAATGTTACCATTCACTGGGTGTACTCTGGCTCACAAAACAGAGAATGGACTAC 201

Qy        48 ySerGlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCy 68
Db       202 CACAGGAAACACACTGGTTCTGAGGGACGTGCAGCTCAGCGACACTGGGGACTATTTATG 261

Qy        68 sHisLysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGl 88
Db       262 CTCCCTGAATGATCACCTGGTGGGGACTGTGCCCTTGCTGGTG---------------- 304
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Qy        88 yIleTrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLy 108
Db       305 ------------GATGTTCCCCCAGAGGAGCCCAAG-----------------CTCTC 333

Qy       108 sCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerTh 128
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Qy       128 rAspLeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGluValThrCy 148
Db       377 ----------------------------CGTCCGAGCAGCACCCCCTCTCCAACCACG-- 406

Qy       148 sGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTy 168
Db       407 ----AAGGCTGTGCTGTTTGCAAAGAAAATCAACACCACCAAC---GGGAAGAGTGACTT 459

Qy       168 rThrValGluCysGlnGluGlySerAlaCys--------------------------Pr 179
Db       460 CCAGGTGCCCTGCCAGTATTC-TCAGCAGCTGAAAAGCTTCTCCTGCCAGGTGGAGATCC 518

Qy       179 oAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTy 199
Db       519 TGGAGGGTGACAAAGTATACCACATAGTGTCACTGTGCGTTGCAAACAGTGTGGGAAGCA 578

Qy       199 r-GluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysA 219
Db       579 AGTCCAGCCACAACGAAGCGTTTCACAGCTTAAAAATGGTGCAGCCGGATCCACCTGCCA 638

Qy       219 snLeuGlnLeuLysProLeuLys---AsnSerArgHisValGluValSerTrpGluTyrP 238
Db       639 ACCTTGTGGTATCAGCCATACCTGGAAGGCCGCGCTGGCTCAAAGTCAGCTGGCAGCACC 698

Qy       238 roAspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnG 258
Db       699 CTGAGACCTGGGACCCG------AGTTACTACTTGCTGCAGTTCCAGCTTCGATACCGAC 752

Qy       258 lyLysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValV 278
Db       753 CTGTATGGTCAAAGGAG---TTCACGGTGTTGCTGCTCCCGGTGGCCCAGTACCAATGCG 809

Qy       278 alCysHisLysAspAlaLys---------------IleArgValGlnAlaArgAspArgT 293
Db       810 TCATCCATGATGCCTTGCGAGGAGTGAAGCACGTGGTCCAGGTCCGTGGGAAGGAGGAGC 869

Qy       293 yrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlyG 313
Db       870 TTGACCTTGGCCAGTGGAGTGAATGGTCC------------------------------ 898

Qy       313 lySerArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisS 333
Db       899 -------------CCAGAGGTCACGGGCACTCCTTGGATAGCAGAG---------CCCA 935

Qy       333 erGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluP 353
Db       936 GGACCACCCCGGCAGGAATCCTCTGGAACCCCACACAGGTCTCT---------------- 979

Qy       353 heTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerT 373
Db       980 -----------GTTGAAGACTCTGCCAACCACGAGGATCAGTACGAAAGTTCTACAGAAG 1028

Qy       373 hrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgG 393
Db      1029 CAACGAGTGTCCTCGCCCCAGTGCAA-----------GAATCCTCGTCCATGTCCCTGC 1076

Qy       393 luIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrT 413
Db      1077 CCACATTCCTGGTAGCTGGAGGAAGC-----------------TTGGCGTTTGGGTTGC 1118

Qy       413 hrLeuCysLeu 416
Db      1119 TTCTCTGTGTC 1129
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RESULT 3
US-11-145-307A-52
; Sequence 52, Application US/11145307A
; Publication No. US20060094035A1
; GENERAL INFORMATION:
;  APPLICANT: Arcturus Bioscience, Inc.
;  APPLICANT:  Erlander, Mark G.
;  APPLICANT:  Ma, Xiao-Jun
;  TITLE OF INVENTION: Identification of Tumors
;  FILE REFERENCE: 022041-002020US
;  CURRENT APPLICATION NUMBER: US/11/145,307A
;  CURRENT FILING DATE:  2005-06-03
;  PRIOR APPLICATION NUMBER: US 60/577,084
;  PRIOR FILING DATE: 2004-06-04
;  NUMBER OF SEQ ID NOS: 268
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
;   LENGTH: 1923
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-145-307A-52

Alignment Scores:
Pred. No.:              6.64e-08        Length:         1923
Score:                  176.00          Matches:        79
Percent Similarity:     37.8%           Conservative:   40
Best Local Similarity:  25.1%           Mismatches:     105
Query Match:            6.6%            Indels:         93
DB:                     7               Gaps:           17

US-10-821-670A-44 (1-511) x US-11-145-307A-52 (1-1923)

Qy        21 GlyGluMetValValLeuThrCysAsnThrProGluGluAsp---AspIleThrTrpThr 39
Db       264 GGCTCTGACGTGACACTGCCATGTGGGACAGCAAACTGGGATGCTGCGGTGACGTGGCGG 323

Qy        40 ---------SerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGln 56
Db       324 GTAAATGGGACAGACCTGGCCCCTGACCTGCTC---AACGGCTCTCAGCTGGTGCTCCAT 380

Qy        57 ValLysGluPheAlaAspAlaGlyGlnTyrThrCys---HisLysGlyGlyGluValLeu 75
Db       381 GGCCTGGAACTGGGCCACAGTGGCCTCTACGCCTGCTTCCACCGTGACTCCTGGCACCTG 440

Qy        76 SerHisSerPheLeuLeu---------IleHisLysLysGluAspGlyIleTrpSerThr 92
Db       441 CGCCACCAAGTCCTGCTGCATGTGGGCTTGCCGCCGCGGGAGCCT--------------- 485

Qy        93 AspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLys 112
Db       486 ------------------------------------GTGCTCAGCTGCCGCTCCAAC 506

Qy       113 AsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPhe 132
Db       507 ACTTACCCCAAGGGCTTCTACTGCAGCTGGCATCTGCCCACCCCCACCTACATT------ 560

Qy       133 ThrValLysSerSerArgGlySerSerAspProGlnGluValThrCysGlyAlaAlaThr 152
Db       561 ----------------------------CCCAAC------ACCTTCAATGTGACTGTG 584

Qy       153 LeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrValGluCys 172
Db       585 CTGCATGGCTCCAAAATTATGGTC------------------------------TGT 611

Qy       173 GlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValValValAsp 192
Db       612 GA-GAAGGA---------CCCAGCCCTCAAGAACCGCTGCCACATTCGCTACATGCACCT 661

Qy       193 AlaIleHisLysLeuLysTyrGlu--------------------------------Asn 201
Db       662 GTTCTCCACC--ATCAAGTACAAGGTCTCCATAAGTGTCAGCAATGCCCTGGGCCACAAT 719

Qy       202 TyrThrSerSerPhePheIleArg---AspIleIleLysProAspProProLysAsnLeu 220
```

```
Db        720 GCCACAGCTATCACCTTTGACGAGTTCACCATTGTGAAGCCTGATCCTCCAGAAAATGTG 779

Qy        221 GlnLeuLysProLeu---LysAsnSerArgHisValGluValSerTrpGluTyrProAsp 239

Db        780 GTAGCCCGGCCAGTGCCCAGCAACCCTCGCCGGCTGGAGGTGACGTGGCAGACCCCCTCG 839

Qy        240 ThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLys 259

Db        840 ACCTGGCCTGACCCTGAGTCT---TTTCCTCTCAAGTTCTTTCTGCGCTACCGA------ 890

Qy        260 AsnAsnArgGluLysLysAspArgLeuSerValAspLys---------------------- 272

Db        891 ----------------------CCCCTCATCCTGGACCAGTGGCAGCATGTGGAGCTGTCC 929

Qy        273 --------------ThrSerAlaLysValValCysHisLysAspAlaLysIleArgVal 287

Db        930 GACGGCACAGCACACACCATCACAGATGCCTACGCCGGGAAGGAGTACATTATCCAGGTG 989

Qy        288 GlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAla 302

Db        990 GCAGCCAAGGACAATGAGATT---GGGACATGGAGTGACTGGAGC 1031
```

RESULT 4
US-11-297-134-9
; Sequence 9, Application US/11297134
; Publication No. US20060111297A1
; GENERAL INFORMATION:
; APPLICANT: Genzyme Corporation
; APPLICANT: Roberts, Bruce
; TITLE OF INVENTION: BLOOD FACTOR DOMAINS
; FILE REFERENCE: 5270C
; CURRENT APPLICATION NUMBER: US/11/297,134
; CURRENT FILING DATE: 2005-12-08
; PRIOR APPLICATION NUMBER: PCT/US2005/018461
; PRIOR FILING DATE: 2004-06-09
; PRIOR APPLICATION NUMBER: US 60/477,291
; PRIOR FILING DATE: 2003-06-09
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 1161
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-297-134-9

Alignment Scores:

Pred. No.:	0.000353	Length:	1161
Score:	134.50	Matches:	53
Percent Similarity:	39.0%	Conservative:	36
Best Local Similarity:	23.2%	Mismatches:	82
Query Match:	5.0%	Indels:	57
DB:	7	Gaps:	9

US-10-821-670A-44 (1-511) x US-11-297-134-9 (1-1161)

```
Qy        107 LeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIle 126

Db        110 GTGCAATGCCGAGCCTCTCGGTACCCGATCGCCGTGGATTGCTCCTGGACCCTGCCGCCT 169

Qy        127 SerThrAspLeuLysPheThrValLys--------------------------SerSer 137

Db        170 GCTCCAAACTCCACCAGCCCCGTGTCCTTCATTGCCACGTACAGGCTCGGCATGGCTGCC 229

Qy        138 ArgGlySerSerAspPro---------GlnGluValThrCysGlyAlaAlaThrLeuSer 154

Db        230 CGGGGCCACAGCTGGCCCTGCCTGCAGCAGACGCCAACGTCCACCAGCTGCACCATCACG 289

Qy        155 AlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGlu 174

Db        290 --------------------------GATGTCCAGCTGTTCTCCATG------------ 310

Qy        175 GlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIle 194

Db        311 ----------------------------GCTCCCTACGTGCTCAATGTCACCGCCGTC 340

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214

Db        341 CACCCCTGGGGCTCCAGCAGCAGCTTCGTGCCTTTCATAACAGAGCACATCATCAAGCCC 400

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSer 234

Db        401 GACCCTCCAGAAGGCGTGCGCCTAAGCCCCCTCGCT---GAGCGCCACGTACAGGTGCAG 457

Qy        235 TrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyVal 254

Db        458 TGGGAGCCTCCCGGGTCCTGGCCCTTCCCA---GAGATCTTCTCACTGAAGTACTGGATC 514

Qy        255 GlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSer 274

Db        515 CGTTACAAG---CGTCAGGGAGCTGCGCGCTTCCACCGGGTGGGGCCCATTGAAGCCACG 571

Qy        275 AlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyr 294

Db        572 TCCTTCATCCTC-----------------AGGGCTGTGCGGCCCCGAGCCAGGTACTAC 613

Qy        295 ------------------------------------SerSerSerTrpSerAsnTrp 301

Db        614 GTCCAAGTGGCGGCTCAGGACCTCACAGACTACGGGGAACTGAGTGACTGGAGTCTCCCC 673

Qy        302 AlaSerValSerCysSerGlyGly 309

Db        674 GCCACTGCCACAATGAGCCTGGGC 697
```

RESULT 5
US-11-217-529-76356
; Sequence 76356, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76356
; LENGTH: 3123
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76356

Alignment Scores:

Pred. No.:	0.221	Length:	3123
Score:	112.50	Matches:	110
Percent Similarity:	31.6%	Conservative:	63
Best Local Similarity:	20.1%	Mismatches:	168
Query Match:	4.2%	Indels:	206
DB:	7	Gaps:	24

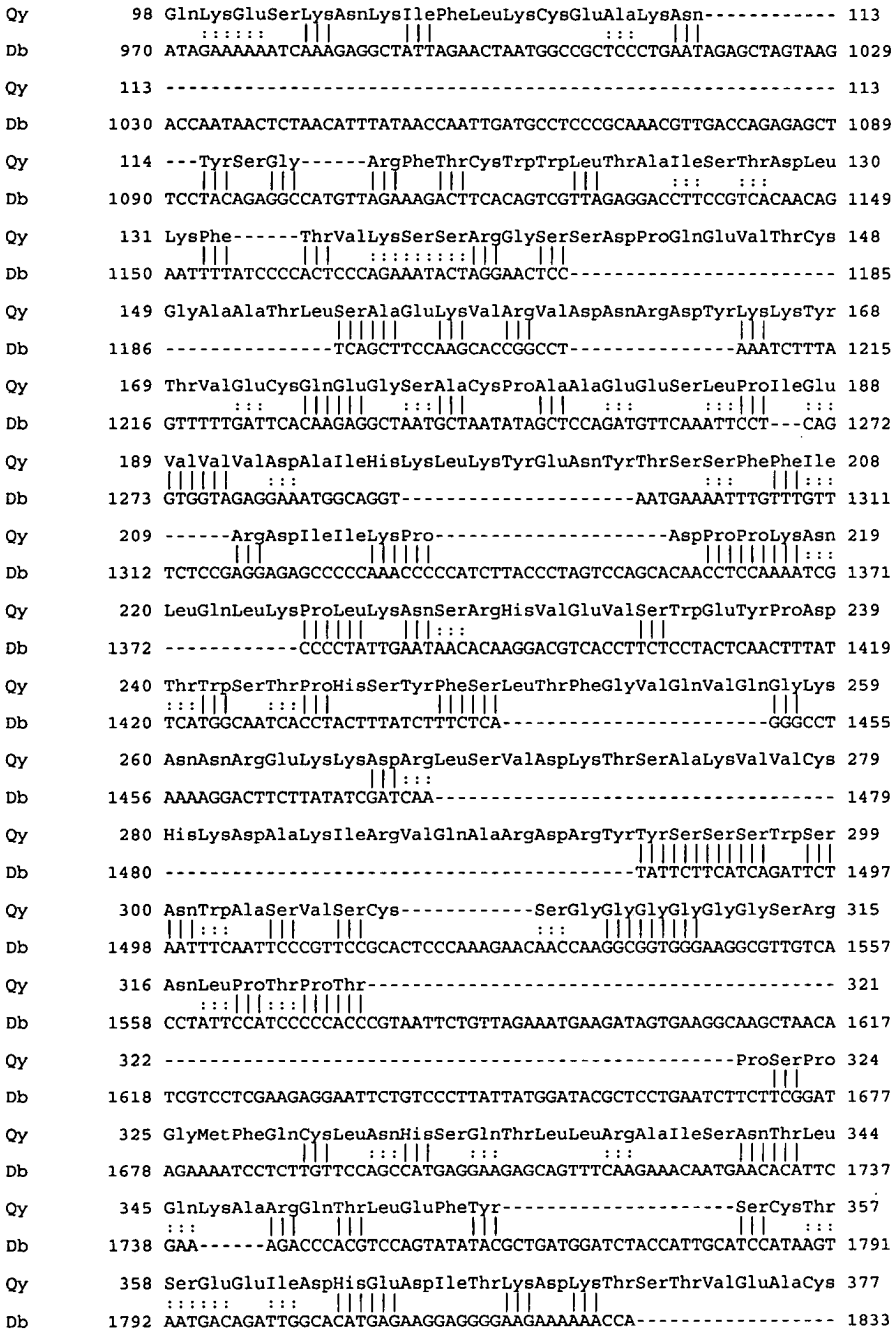
US-10-821-670A-44 (1-511) x US-11-217-529-76356 (1-3123)

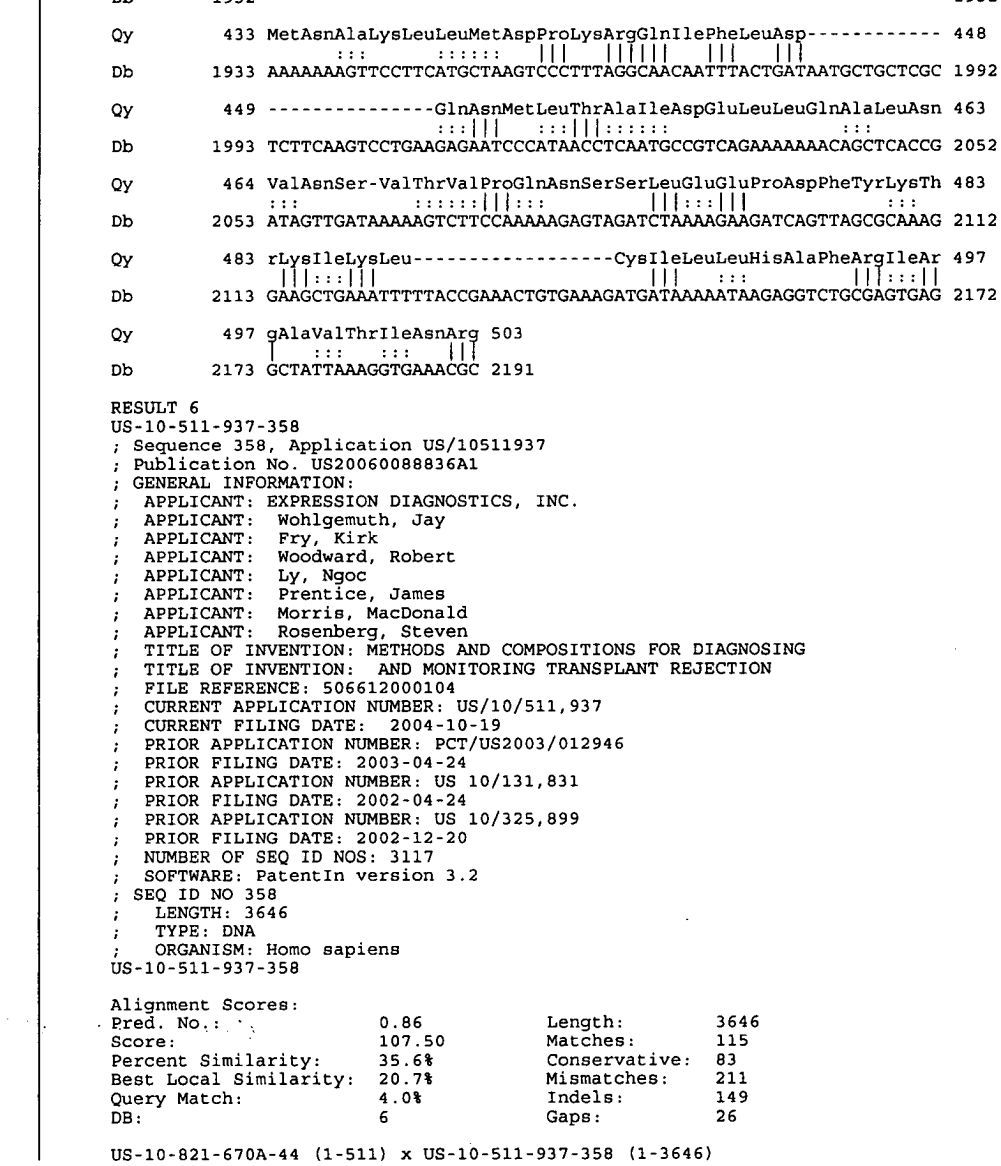
```
Qy         63 AlaGlyGlnTyrThrCysHisLys---GlyGlyGluValLeuSerHisSerPheLeuLeu 81

Db        853 GCCTCTAGATTCCAGAAGCACAAAATATCGGGTAAAATTTTGTTA---GAGTTAGAGCTT 909

Qy         82 IleHisLysLysGluAspGlyIleTrpSer------------ThrAspIleLeuArgGlu 97

Db        910 GTTCATTTAAAAGAGTTGGGCATAAATTCTTTTGGGACAAGATTTGAGATTTTCAAAGAA 969
```





RESULT 6
US-10-511-937-358
; Sequence 358, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 358
; LENGTH: 3646
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-358

Alignment Scores:

Pred. No.:	0.86	Length:	3646
Score:	107.50	Matches:	115
Percent Similarity:	35.6%	Conservative:	83
Best Local Similarity:	20.7%	Mismatches:	211
Query Match:	4.0%	Indels:	149
DB:	6	Gaps:	26

US-10-821-670A-44 (1-511) x US-10-511-937-358 (1-3646)

```
Qy        17 ProAspAlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIle 36
Db       611 CCACAGAAACCTGCTGCCCTGCTCTGCAGAGGCCTCACTCAGCCT-----------CTG 658

Qy        37 ThrTrpThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGln 56
Db       659 CTCTGGACCAGTCTCCATGTGCTCAGCCCACAATGCCCTGGCAAGATGGA-CCAAAGCAG 717

Qy        57 ValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSer 76
Db       718 ACCTCCCCAAGTAGAGAAGCTTCAGCTCTGACAGCAGAGGGTGGAAGCTGCCTCATCTCA 777

Qy        77 ------------------HisSerPheLeuLeuIleHisLysLysGluAspGlyIle--- 89
Db       778 GGACTCCAGCCTGGCAACTCCTACTGGCTGCAGCTGCGCAGCGAACCTGATGGGATCTCC 837

Qy        90 --------------------TrpSerThrAspIleLeuArgGluGlnLysGluSerLys 102
Db       838 CTCGGTGGCTCCTGGGGATCCTGGTCCCTCCCTGTGACTGTGGACCTGCCTGGAGATGCA 897

Qy       103 AsnLysIlePheLeuLysCys---------GluAlaLysAsnTyrSerGlyArgPheThr 119
Db       898 GTGGCACTTGGACTGCAATGCTTTACCTTGGACCTGAAGAAT-----------GTTACC 945

Qy       120 CysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGly 139
Db       946 TGTCAATGGCAGCAACAGGACCATGCTAGCTCCCAAGGCTTCTTCTACCACAGCAGGGCA 1005

Qy       140 -SerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValAr 159
Db      1006 CGGTGCTGCCCCAGAGACAGGTACCCCATCTGGGAGAACT------GCGAAGAGGAAGAG 1059

Qy       159 gValAspAsnArgAspTyrLysLysTyrThr-ValGluCysGlnGluGlySerAlaCysP 179
Db      1060 AAAACAAATCCAGGACTACAGACCCCACAGTTCTC------------------------ 1094

Qy       179 roAlaAlaGluGluSerLeuProIleGluValValVal-AspAlaIleHisLysLeuLys 198
Db      1095 -------------TCGCTGCCACTTCAAGTCACGAAATGACAGCATTATTCACATCCTT 1140

Qy       199 TyrGluAsnTyrThr-----------------------------SerSerPhePheIle 208
Db      1141 GTGGAGGTGACCACAGCCCCGGGTACTGTTCACAGCTACCTGGGCTCCCCTTTCTGGATC 1200

Qy       209 ArgAspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSer 228
Db      1201 CACCAGGCTGTGCGCCTC---CCCACCCCAAACTTGCACTGGAGGGAGATC---TCCAGT 1254

Qy       229 ArgHisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPhe 248
Db      1255 GGGCATCTGGAATTGGAGTGGCAGCACCCATCGTCCTGGGCAGCCCAAGAGACCTGTTAT 1314

Qy       249 SerLeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGlu---LysLysAspArg 267
Db      1315 CAACTCCGATAC------------ACAGGAGAAGGCCATCAGGACTGGAAGGTGCTGGAG 1362

Qy       268 LeuSerValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgVal 287
Db      1363 CCGCCTCTCGGGGCCCGAGGAGGGACCCTGGAGCTGCGCCCGCGATCTCGCTACCGTTTA 1422

Qy       288 GlnAlaArgAspArgTyr------------TyrSerSerSerTrpSerAsnTrpAlaSer 303
Db      1423 CAGCTGCGCGCCAGGCTCAACGGCCCCACCTACCAAGGTCCCTGGAGCTCGTGGTCGGAC 1482

Qy       304 ---------------------------------------------ValSerCysSerGly 308
Db      1483 CCAACTAGGGTGGAGACCGCCACCGAGACCGCCTGGATCTCCTTGGTGACCGC-TCTGCA 1541

Qy       309 GlyGlyGlyGlyGlySerArgAsnLeuProThrProThrProSerProGly-MetPheGl 328
Db      1542 TCTAGTGCTGGGCCTCAGCGCCGT---------CCTGGGCCTGCTGCTGCTGAGGTGGCA 1592

Qy       328 nCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaAr 348
Db      1593 GTTTCCTGCACACTACAGGAGACTGAGGCATGCCCTGTGGCCCTCACTTCCAGACCTGCA 1652

Qy       348 gGlnThrLeuGluPheTyr---------------------------------------- 354
Db      1653 CCGGGTCCTAGGCCAGTACCTTAGGGACACTGCAGCCCTGAGCCCGCCCAAGGCCACAGT 1712

Qy       355 -SerCysThrSerGluGluIleAspHis---------GluAspIleThrLysAspLysTh 371
Db      1713 CTCAGATACCTGTGAAGAAGTGGAACCCAGCCTCCTTGAAATCCTCCCCAAGTCCTCAGA 1772

Qy       371 rSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGlu-------------- 386
Db      1773 GAGGACT--------------CCTTTGCCCCTGTGTTCCTCCCAGGCCCAGATGGACTA 1817

Qy       387 ----------------SerCysLeuAlaSerArgGluIleSer------------LeuIl 397
Db      1818 CCGAAGATTGCAGCCTTCTTGCCTGGGGACCATGCCCCTGTCTGTGTGCCCACCCATGGC 1877

Qy       397 eThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSe 417
Db      1878 TGAGTCAGGGTCCTGC-----------------------TGTACCACCCACATTGCCAA 1913

Qy       417 rSerIleTyrGluAspLeuLysMetTyrGlnValGlu---PheLysAlaMetAsnAlaLy 436
Db      1914 CCATTCCTACCTACCACTAAGCTATTGGCAGCAGCCTTGAGGACAGGCTCCTCACTCCCA 1973

Qy       436 sLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAs 456
Db      1974 GTTC---------CCTGGACAGAGCTAAACTCTCGAGACTTCTCTGTGAACT-------- 2016

Qy       456 pGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGl 476
Db      2017 --------------------------TCCCTACCCTACCCCCACAACACAAGC----- 2043

Qy       476 uGluProAspPheTyrLysThrLysIleLysLeuCysIle 489
Db      2044 -ACCCCAGACCTC------ACCTCCATCCCCCTCTGTCTG 2076
```

RESULT 7
US-11-217-529-409
; Sequence 409, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 409
; LENGTH: 1614
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-409

Alignment Scores:

Pred. No.:	0.395	Length:	1614
Score:	105.50	Matches:	76
Percent Similarity:	36.0%	Conservative:	58
Best Local Similarity:	20.4%	Mismatches:	137
Query Match:	3.9%	Indels:	101
DB:	7	Gaps:	18

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US-10-821-670A-44 (1-511) x US-11-217-529-409 (1-1614)

Qy        113 AsnTyrSerGlyArgPheThrCysTrpTrpLeu-----------ThrAlaIleSerThr 128
Db        553 AATTATAATCCAAAGATGCAA---TGGTCTCTTCAGGACAATAGTGCTGCAATAAATAAT 609

Qy        129 AspLeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGluValThrCys 148
Db        610 GAAGACGCAAGAACTATCTTCAATAACGAATTTGACTCTGATGATGACGATATCAGT--- 666

Qy        149 GlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyr 168
Db        667 --------------GACGATGAAGAAGACGAAATTGAAGACGAAGAT------------ 699

Qy        169 ThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGlu 188
Db        700 CGTTTGCAACAACAAGAG--------------------GAAATCCTTTTGCCATTAGAC 738

Qy        189 Val------------ValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSer 204
Db        739 GTCACCTCAGTATCGATATTTGATGCCGATCATAAAATAAATCAT-------------- 783

Qy        205 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGlnLeuLysPro 224
Db        783 ------------------------------------------------------------ 783

Qy        225 LeuLysAsnSerArgHisValGluValSerTrpGluTyrProAsp-------------- 239
Db        784 TTAAAGAGTGCTGGTCATGTATTTAATGAATACAGTTACGTTGATTCTAATACAGACGAC 843

Qy        240 ---ThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 258
Db        844 ACAACCAACATCACACCCAAAAATACGTTAGAAGAACAGGAAAATGCAAACGCTGAGGAA 903

Qy        259 LysAsnAsnArgGluLysLysAspArgLeuSerValAsp---------------------- 271
Db        904 GGGGGTGAGGAGGAAGATAACGATCTTCTCGACGAAGATGATTTATATGATATTTCTCTT 963

Qy        272 ---------LysThrSerAlaLysValValCysHisLysAsp------------------- 282
Db        964 TTGAAGAACAAAAGGAAGCAAAGTTTTGTACTCAATAAGAATACCGTTGGTTTTGAAAGA 1023

Qy        283 ---------------AlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSer 297
Db       1024 CTATCGTCTCCATCAACTCCGGTAAAGGTACCGTCTAACACTACTACTACTACTAAA 1083

Qy        298 TrpSerAsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlySerArgAsnLeu 317
Db       1084 AGGAAATCTACAAAGTCGTTCAATAATAGTGGTGGCACTAACAGTAATAACGAAAACACC 1143

Qy        318 Pro---------------ThrProThrProSerProGlyMetPheGlnCysLeuAsnHis 332
Db       1144 CCGATGGAAAGAATAAAGAAACCGACTTCGTCC-----------------GTGTCAAAT 1185

Qy        333 SerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLys------AlaArgGlnThr 350
Db       1186 TCTAATAGTAGTAGGCGGAAACTAATTAACTATACCAAAAAACATCTATCATCACATCCT 1245

Qy        351 LeuGluPheTyrSer------------CysThrSerGluGluIleAspHisGluAspIle 366
Db       1246 ACACCATTCAGTTCGAGCCCAAGTCCTACAACCACATCATCTTCGGCACACGCGTCG--- 1302

Qy        367 ThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGlu 386
Db       1303 TCTTCGGACGGTAGCAACGAAATATTTGCGTGCCAAATCATGAATCTTACTAGTAATGAA 1362

Qy        387 SerCysLeuAla------SerArgGluIleSerLeuIleThrAsnGlySerCysLeu--- 403
Db       1363 CCATGTGGTGCACAATTTTCAAGATCATACGACTTGACAAGGCACCAAAATACCATACAT 1422

Qy        404 AlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeu 423
Db       1423 GCCAAGAGAAAGATTGTATTCCGTTGCTCTGAATGTATAAAAATTCTGGGATCAGAA--- 1479

Qy        424 LysMetTyrGlnValGluPheLysAlaMetAsnAla 435
Db       1480 ---GGTTATCAGAAGACATTTTCGAGATTAGACGCT 1512

RESULT 8
US-11-293-697-1946
; Sequence 1946, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1946
;   LENGTH: 2534
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1946

Alignment Scores:
Pred. No.:              0.779          Length:          2534
Score:                  105.50         Matches:         62
Percent Similarity:     35.6%          Conservative:    33
Best Local Similarity:  23.2%          Mismatches:      107
Query Match:            3.9%           Indels:          65
DB:                     7              Gaps:            13

US-10-821-670A-44 (1-511) x US-11-293-697-1946 (1-2534)

Qy         24 ValValLeuThrCysAsnThrProGlu---GluAspAspIleTrpThrSerAsp--- 41
Db        298 CTGGCCCTGCAGTGTGAAGTCTCTGACCCCGAGGCCCATGTGGTGTGGCGCAAAGATGGC 357

Qy         42 ------------------GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIle 55
Db        358 GTGCAGCTGGGCCCCAGTGACAAGTATGACTTCCTGCACACGGCGGGCACGCGGGGGCTC 417

Qy         56 GlnValLysGluPheAla------AspAlaGlyGlnTyrThrCysHisLysGlyGlyGlu 73
Db        418 GTGGTGCATGACGTGAGCCCTGAAGACGCCGGCCTGTACACCTGCCACGTGGGCTCCGAG 477

Qy         74 ValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAsp 93
Db        478 GAG---ACCCGGGCCCGGGTCCGCGTGCACGATCTGCACGTGGGCATC------------ 522

Qy         94 IleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsn 113
Db        523 ------------ACCAAGAGGCTGAAGACAATGGAGGTGCTGGAAGGGGAA--------- 561

Qy        114 TyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThr 133
Db        562 ---AGCTGCAGCTTTGAGTGC---------------------------------------- 579

Qy        134 ValLysSerSerArgGlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeu 153
Db        580 GTCCTGTCCCACGAGAGTGCCAGCGACCCGGCCATGTGGACAGTCGGTGGGAAGACAGTG 639

Qy        154 SerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGln 173
Db        640 GGCAGCTCCAGCCGCTTCCAGGCCACACGTCAGGGCCGAAAATACATCCTGGTGGTCCGG 699

Qy        174 GluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValValValAspAla 193
Db        700 GAGGCTGCACCAAGTGATGCCGGGGAG--------------------GTGGTCTTCTCT 738

Qy        194 IleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLys 213
```

```
Db        739 GTGCGGGGCCTCACCTCCAAG---------GCCTCACTCATTGTCAGA------------ 777

Qy        214 ProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluVal 233
                 :::   |||       :::   :::||||||||:::
Db        778 ---GAGAGGCCGGCCACCATC---ATCAAGCCCCTGGAA--------------------- 810

Qy        234 SerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGly 253
                          |||   |||       |||                 |||
Db        811 --------------GACCAGTGGGTGGCGCCAGGGGAGGACGTGGAGCTGCGCTGTGAG 855

Qy        254 ValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThr 273
                 :::       |||              ||||||||   ::::::   |||:::
Db        856 CTGTCACGGGCGGGAACGCCCGTGCACTGGCTGAAGGACAGGAAGGCCATCCGCAAGAGC 915

Qy        274 SerAla---LysValValCys 279
                       |||||||||
Db        916 CAGAAGTATGATGTGGTCTGC 936

RESULT 9
US-11-274-375-5
; Sequence 5, Application US/11274375
; Publication No. US20060106201A1
; GENERAL INFORMATION:
;  APPLICANT: Maeda, Masatsugu
;  APPLICANT:  Yaguchi, Noriko
;  TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
;  FILE REFERENCE: 06501-105US1
;  CURRENT APPLICATION NUMBER: US/11/274,375
;  CURRENT FILING DATE:  2005-11-14
;  PRIOR APPLICATION NUMBER: US/10/105,930
;  PRIOR FILING DATE: 2002-03-25
;  PRIOR APPLICATION NUMBER: PCT/JP00/06654
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: JP 2000-240397
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: JP 11-273358
;  PRIOR FILING DATE: 1999-09-27
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 2123
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (98)...(1984)
US-11-274-375-5

Alignment Scores:
Pred. No.:              0.748          Length:         2123
Score:                  104.50         Matches:        94
Percent Similarity:     33.1%          Conservative:   47
Best Local Similarity:  22.1%          Mismatches:     181
Query Match:            3.9%           Indels:         104
DB:                     7              Gaps:           18

US-10-821-670A-44 (1-511) x US-11-274-375-5 (1-2123)

Qy        109 CysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrp-----------LeuThr 124
              |||          |||||||||      ||||||   |||           ||||||
Db        494 TGTGTCATTTATGAATATTCAGGCAACATGACTTGCACCTGGAATGCTGGGAGGCTCACC 553

Qy        125 AlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSerAspProGln 144
                 |||   |||                |||||||||                :::   |||
Db        554 TACATAGACACAAAATACGTGGTACATGTGAAGAGTTTAGAGACAGAAGAAGAGCAACAG 613

Qy        145 GluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAsp 164
                 :::|||              :::|||   :::   :::             :::
Db        614 TATCTCACCTCAAGCTATATTAACATCTCCACTGATTCATTA-----------CAAGGT 661

Qy        165 TyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSer 184
                 |||||||||   |||       |||   :::|||                |||||||||
Db        662 GGCAAGAAGTACTTGGTTTGGGTCCAAGCAGCAAACGCACTA---GGCATGGAAGAGTCA 718

Qy        185 LeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSer 204
                       :::::::::   :::|||   |||       |||                :::
Db        719 AAACAACTGCAAATTCACCTGGATGATATAGTGATACTTTCTGCAGCCGTCATTTCCAGG 778

Qy        205 SerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu------------ 220
                 :::            :::   |||             ||||||   :::
Db        779 GCT------------GAGACTATAAATGCTACAGTGCCCAAGACCATAATTTATTGGGAT 826

Qy        221 ---GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAsp 239
                    |||             |||   |||       :::
Db        827 AGTCAAACAACAATTGAAAAGGTTTCCTGTGAAATGAGATACAAGGCTACAACAAACCAA 886

Qy        240 ThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLys 259
                 ||||||:::          |||       |||             |||   :::
Db        887 ACTTGGAATGTTAAAGAA------TTTGACACCAATTTTACATATGTGCAACAGTCAGAA 940

Qy        260 AsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCys 279
                       |||                       |||          :::|||   |||
Db        941 TTCTACTTGGAGCCAAAC--------------ATTAAGTACGTATTTCAAGTGAGATGT 985

Qy        280 HisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSer 299
                    :::      |||                 ||||||                 |||
Db        986 CAAGAAACAGGCAAA--------------------AGGTAC------------TGGCAG 1012

Qy        300 AsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuProThr 319
                    |||:::|||:::                                      |||
Db       1013 CCTTGGAGTTCACTGTTTTTTCAT-----------------------------AAAACA 1042

Qy        320 ProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAla 339
                 |||         |||                              |||         ::|||
Db       1043 CCTGAAACAGTTCCC-------------------------CAGGTCACATCAAAAGCA 1075

Qy        340 IleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGlu 359
                       :::          :::      |||:::         |||
Db       1076 TTCCAACATGACACATGGAATTCTGGGCTAACAGTTGCTTCCATCTCT------------ 1123

Qy        360 GluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuPro 379
                             |||          ||||||          :::
Db       1124 --------------------ACAGGGCACCTTACTTCTGACAACAGAGGAGACATTGGA 1162

Qy        380 LeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsn 399
                 |||   |||   |||          :::          :::||||||||||
Db       1163 CTTTTATTGGGAATGATCGTCTTTGCTGTTATGTTGTCAATTCTTTCTTTGATT------ 1216

Qy        400 GlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeu--------- 416
                 |||:::          |||   :::|||               :::   |||
Db       1217 GGGACATTTAACAGATCATTCCGAACTGGGATTAAAAGAAGGATCTTATTGTTAATACCA 1276

Qy        417 SerSerIleTyrGluAspLeu--------------------------LysMetTyrGln 427
                    :::|||||||||:::                                ||||||   |||
Db       1277 AAGTGGCTTTATGAAGATATTCCTAATATGAAAAACAGCAATGTTGTGAAAATGCTACAG 1336

Qy        428 ValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeu 447
                       :::   ||||||               :::         |||:::
Db       1337 GAAAATAGTGAACTTATGAAT------------AATAATTCCAGTGAGCAGGTCCTATAT 1384

Qy        448 AspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerVal 467
                       |||:::|||   |||   |||:::
Db       1385 GTTGATCCCATGATTACAGAGATAAAAGAAATCTTC------------------------ 1420

Qy        468 ThrValProGlnAsn----------------------------SerSerLeuGluGlu 477
                    :::|||::::::                                  ||||||
Db       1421 ---ATCCCAGAACACAAGCCTACAGACTACAAGAAGGAGAATACAGGACCCCTGGAGACA 1477

Qy        478 ProAspPhe-TyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleAr 497
                    |||:::    ||||||:::            :::   |||:::   |||   |||
Db       1478 AGAGACTACCCGCAAAACTCGCTATTCGACAATACTACAGTTGTATATATTCCTGATCTC 1537

Qy        497 gAlaValThrIleAsn 502
                    :::   ||||||
Db       1538 AACACTGGATATAAAC 1553
```

```
RESULT 10
US-11-217-529-774
; Sequence 774, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 774
;   LENGTH: 3117
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-774

Alignment Scores:
Pred. No.:                1.49          Length:          3117
Score:                    104.00        Matches:         110
Percent Similarity:       33.1%         Conservative:    68
Best Local Similarity:    20.4%         Mismatches:      167
Query Match:              3.9%          Indels:          193
DB:                       7             Gaps:            25

US-10-821-670A-44 (1-511) x US-11-217-529-774 (1-3117)

Qy         31 ProGluGluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGly 50
Db        778 CCTGTTGAAGCGGAAATG---TGGACACCTGAAGAAATAACAGCATAT------------ 822

Qy         51 LysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLys 70
Db        823 ------TTTATCATGGAAGGATATGATGTCCAATCCGCCTCTAGGTTTCAAAAACATAAG 876

Qy         71 ---GlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIle 89
Db        877 ATATCAGGTAGAATTTTATTA---GAACTAGAACTAGTCCATTTAAAAGAGCTAGATATA 933

Qy         90 TrpSer------------ThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIle 105
Db        934 AATTCCTTTGGTACAAGATTTGAGATTTTCAAAGAAATTGAAAAAATCAAAGAGGCAATT 993

Qy        106 ------------------PheLeuLysCysGluAlaLysAsn------------------ 113
Db        994 AGGACAAATGGTCACTCATTTAACAGAGTTAGCAAGGCTAATAATAACACTAACAGTTAC 1053

Qy        114 ----------------------------------------TyrSerGly------Arg 117
Db       1054 AACCAATTGATGCCTCCTGCGAACGTCGACCAGAGGGTATCCTACAGGGGCCATGTCAGA 1113

Qy        118 PheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrVal--------- 134
Db       1114 AAAACTTCACAGTCGTTAGATGACCTTCCATCACAACAGAATTTTACTGCTACCCCTCAA 1173

Qy        135 ---------LysSerSerArgGlySerSerAspProGlnGluValThrCysGlyAlaAla 151
Db       1174 GGTAACAGAAATTCTTCAACAGGTAAACATAGACCG---------------------- 1209

Qy        152 ThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrValGlu 171
Db       1210 ----------------------------------------AAATCTTTAACTCTTGAT 1227

Qy        172 CysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValValVal 191
Db       1228 ACTCAAGAAGGCGATTCC------AGTGCTACTCCAAAAATTCAGATTCCTCAAGTTGTA 1281

Qy        192 AspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIle------Arg 209
Db       1282 GAAGAAATTGCTAGTAATGAATAT-----------------TTGTTTGTTTCCCCAAGA 1323

Qy        210 AspIleIleLysPro--------------------AspProProLysAsnLeuGlnLeu 222
Db       1324 AGGGCACCCAAACCTCCATCTTATCCAAGCCCTGCACAACCTCCCAAGTCA--------- 1374

Qy        223 LysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThrTrpSer 242
Db       1375 ---CCCCTCCTAAGTAATAGAAAGGCCTCACCGTCTCCCACCCAATTACATTCATGGCAA 1431

Qy        243 ThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsnAsnArg 262
Db       1432 TCACCAAGTTCATCTTACTCG---------------------------------------- 1452

Qy        263 GluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHisLysAsp 282
Db       1453 GACTCAAAAAAAAATTTGTATACCGACCAATCTTCATCGAAT----------------- 1494

Qy        283 AlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAla 302
Db       1495 ------------------------------------TCTAATTCAAATTCCCGTTTGCA 1518

Qy        303 SerValSerCysSerGlyGlyGlyGlyGlySerArgAsnLeuProThrProThrPro 322
Db       1519 CTTTCAAAAAACAACCAAGGGAACGGGAGGCCATTGTCTCCTATTCCTCCCCCCACT--- 1575

Qy        323 SerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsn 342
Db       1576 ----------------------------------------CTTAAAGCAATTTCAAAT 1593

Qy        343 ThrLeuGlnLysAlaArgGlnThr---------------------------------- 350
Db       1594 TCTGCAGACAAAACGAAAGACACAAATACAGTATCTGCAAATAGAAATTCCGTTCTTTAT 1653

Qy        351 ----------------------------LeuGluPheTyrSerCysThrSerGluGlu 360
Db       1654 TCAGGATATGCTGTTGACTCTTTCAACAGAAAATCTTCTTATTCCAGTGGTGAGGAAGAG 1713

Qy        361 IleAspHisGlu------AspIleThrLysAspLysThrSerThrValGluAla------ 376
Db       1714 CACTTCCAAGAAACGTTGGATACACTCGAAAGACCCACATCCAGCATATACGCCGATGGG 1773

Qy        377 ------------------------CysLeuProLeuGlu---------------------- 381
Db       1774 TCTACAATCGCATCAATGAGTAATGCTAGGCCAATACAAGACAATGAAAAGAAGAAAAAA 1833

Qy        382 LeuThrMetAsnGluSerCysLeuAlaSer----------------------ArgGluIle 394
Db       1834 CCGACGAGACATTCTTCCTTGTTATCTTCAAAATCCAAAGGTGATCCCAAAAGGAACTCT 1893

Qy        395 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 414
Db       1894 TCTTTAAAGAGAAGCAGTAGC------GCATCAAGAACCAGTTCATTCAGAAAAAGCACT 1947

Qy        415 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 434
Db       1948 TTTATG-----------------CTAAGTCCCTTTAGACAACAGTTCACTGAAAATGCG 1989

Qy        435 AlaLysLeuLeuMetAspPro-LysArgGlnIlePheLeuAspGlnAsnMetLeuThrAl 454
Db       1990 GCTCGTTCTTCACCAAGTCCTGAAAAAAATTCTATGGCTTCAACGCCACTATCCCCAACC 2049

Qy        454 aIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGln 471
Db       2050 GATAACAAATCTTCCAAGGACAAATCAAAAGCAAGATCTGTCAGCGCCAAAG 2101

RESULT 11
US-10-511-937-448
; Sequence 448, Application US/10511937
```

```
; Publication No. US20060088836A1
; GENERAL INFORMATION:
;  APPLICANT: EXPRESSION DIAGNOSTICS, INC.
;  APPLICANT:  Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  APPLICANT:  Prentice, James
;  APPLICANT:  Morris, MacDonald
;  APPLICANT:  Rosenberg, Steven
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
;  TITLE OF INVENTION:  AND MONITORING TRANSPLANT REJECTION
;  FILE REFERENCE: 506612000104
;  CURRENT APPLICATION NUMBER: US/10/511,937
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: PCT/US2003/012946
;  PRIOR FILING DATE: 2003-04-24
;  PRIOR APPLICATION NUMBER: US 10/131,831
;  PRIOR FILING DATE: 2002-04-24
;  PRIOR APPLICATION NUMBER: US 10/325,899
;  PRIOR FILING DATE: 2002-12-20
;  NUMBER OF SEQ ID NOS: 3117
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 448
;   LENGTH: 3084
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-511-937-448

Alignment Scores:
Pred. No.:                1.64          Length:          3084
Score:                    103.50        Matches:         94
Percent Similarity:       31.2%         Conservative:    47
Best Local Similarity:    20.8%         Mismatches:      137
Query Match:              3.9%          Indels:          174
DB:                       6             Gaps:            24

US-10-821-670A-44 (1-511) x US-10-511-937-448 (1-3084)

Qy         16 HisProAspAla-ProGlyGluMetValValLeuThrCysAsnThrPro------GluGl 33
Db        542 CACCCACCTGCTTCAGGGGCAGAGCCTGACCCTGACCTTGGAGAGCCCCCCTGGTAGTAG 601

Qy         33 uAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLe 53
Db        602 CCCCTCAGTGCAATGTAGGAGTCCAAGGGGTAAAAACATACAGGGG---GGGAAGACCCT 658

Qy         53 uThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCys-------------- 68
Db        659 CTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGCACCTGGACATGCACTGTCTTGCAGAA 718

Qy         69 -HisLysGlyGlyGlu-----------------------ValLeuSerHisSerPheLe 80
Db        719 CCAGAAGAAGGTGGAGTTCAAAATAGACATCGTGGTGCTAGCTTTCCAGAAGGCCTCCAG 778

Qy         80 uLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGl 100
Db        779 CATAGTCTATAAGAAAGAGGGG-------------------------GAACAGGTGGA 811

Qy        100 uSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCy 120
Db        812 GTTCTCCTTCCCACTCGCCTTTACAGTTGAAAAGCTGACGGGCAGTGGCGAGCTG----- 866

Qy        120 sTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySe 140
Db        867 -TGGTGG-----------------------------------CAGGCGGAGAGGGCTTC 889

Qy        140 rSerAspProGlnGluValThrCysGlyAlaAlaThr------LeuSerAlaGluLysVa 158
Db        890 CTCCTCCAAGTCTTGGATCACCTTTGACCTGAAGAACAAGGAAGTGTCTGTAAAACGGGT 949

Qy        158 lArgValAspAsnArgAspTyr------LysLysTyrThrValGluCysGlnGluGlySe 176

Db        950 TACCCAGGACCCTAAGCTCCAGATGGGCAAGAAGCTCCCGCTCCACCTCACCCTGCCCCA 1009

Qy        176 rAlaCysPro------------AlaAlaGluGluSerLeuProIleGluValValValAs 192
Db       1010 GGCCTTGCCTCAGTATGCTGGCTCTGGAAACCTCACCCTGGCCCTTGAAGCGAAAACAGG 1069

Qy        192 pAlaIleHisLys-----------------------------LeuLysTyrGluAsnTy 202
Db       1070 AAAGTTGCATCAGGAAGTGAACCTGGTGGTGATGAGAGCCACTCAGCTCCAGAAAAATTT 1129

Qy        202 rThrSerSerPhePheIleArgAspIleIleLysProAspProProLys---------- 218
Db       1130 GACCTGT--------------GAGGTGTGGGGACCCACCTCCCCTAAGCTGATGCTGAG 1174

Qy        219 ----AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrp----- 235
Db       1175 CTTGAAACTGGAGAACAAGGAGGCAAAGGTCTCGAAGCGGGAGAAGGCGGTGTGGGTGCT 1234

Qy        235 ------------------------------------------------------------ 235
Db       1235 GAACCCTGAGGCGGGGATGTGGCAGTGTCTGCTGAGTGACTCGGGACAGGTCCTGCTGGA 1294

Qy        236 ----------GluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeuThrPh 252
Db       1295 ATCCAACATCAAGGTTCTGCCCACATGGTCCACCCCGGTGCAGCCAATGGCCCTGATTGT 1354

Qy        252 e------GlyValGln-----------------------------------------ValGl 257
Db       1355 GCTGGGGGGCGTCGCCGGCCTCCTGCTTTTCATTGGGCTAGGCATCTTCTTCTGTGTCAG 1414

Qy        257 nGlyLysAsnAsnArgGluLysLysAspArgLeuSerValAspLys------ThrSerAl 275
Db       1415 GTGCCGGCACCGAAGGCGCCAAGCAGAGCGGATGTCTCAGATCAAGAGACTCCTCAGTGA 1474

Qy        275 aLysValValCysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSe 295
Db       1475 GAAGAAGACCTGC----------------------CAGTGCCCTCACCGGTTTCAGAA 1510

Qy        295 rSerSerTrpSerAsnTrpAlaSerValSerCysSer---------GlyGlyGlyGlyGl 312
Db       1511 G--------------------------ACATGTAGCCCCATTTGAGGCACGAGGCCAGG 1543

Qy        312 yGlySerArg---------------------------------------------------- 315
Db       1544 CAGATCCCACTTGCAGCCTCCCCAGGTGTCTGCCCCGCGTTTCCTGCCTGCGGACCAGAT 1603

Qy        316 -AsnLeuProThrProThrPro---------------------------------------- 322
Db       1604 GAATGTAGCAGATCCCAGGCCTCTGGCCTCCTGTTCGCCTCCTCTACAATTTGCCATTGT 1663

Qy        323 -SerProGlyMet-------------------------------------PheGlnCysLe 330
Db       1664 TTCTCCTGGGTTAGGCCCCGGCTTCACTGGTTGAGTGTTGCTCTCTAGTTTCCAGAGGCT 1723

Qy        330 uAsnHisSerGlnThrLeuLeuArgAlaIleSer 341
Db       1724 TAATCAC------ACCGTCCTCCACGCCATTTCC 1751

RESULT 12
US-11-217-529-191047
; Sequence 191047, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
```

```
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 191047
;   LENGTH: 3510
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-191047

Alignment Scores:
Pred. No.:                2.24          Length:          3510
Score:                    103.00        Matches:         105
Percent Similarity:       32.7%         Conservative:    69
Best Local Similarity:    19.7%         Mismatches:      214
Query Match:              3.8%          Indels:          144
DB:                       7             Gaps:            20

US-10-821-670A-44 (1-511) x US-11-217-529-191047 (1-3510)

Qy          9 TyrValValGluLeuAspTrpHisProAspAlaProGlyGluMetValValLeuThrCys 28
              ||||||          |||                     |||         |||
Db        976 TATGTCACTAGCTCTTCCTGG------------TCGTCCAGTGAAGTCTGTACAGAGTGC 1023

Qy         29 AsnThrProGluGluAspAsp--------------IleThrTrpThrSerAspGlnSer 43
                  |||                          :::|||   :::|||      |||
Db       1024 ACCGAGACCGAGTCTACTAGCACCTCTACTCCATATGTCACCAGCTCTTCCTCGTCGTCC 1083

Qy         44 SerGluVal------------------LeuGlySerGlyLysThrLeuThrIleGlnVal 57
              |||||||||                        |||         :::|||      |||
Db       1084 AGTGAAGTCTGTACGGAGTGCACCGAAACTGAGTCTACCAGTTATGTGACACCATATGTC 1143

Qy         58 LysGluPheAlaAspAlaGlyGlnTyrThr---------------------------Cys 68
                     |||      ||||||                                   |||
Db       1144 AGCTCGTCTACTGCTGCCGCAAACTACACTAGCTCATTCTCATCGTCCAGTGAAGTCTGT 1203

Qy         69 HisLysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGly 88
                 :::      |||      |||   |||           :::
Db       1204 ACAGAGTGCACCGAAACTGAGTCTACTAGCACCTCTACTCCATATGTCACTAGCTCTTCC 1263

Qy         89 IleTrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeu--- 107
                 |||:::::::::      |||      |||:::::::::      ::::::
Db       1264 TGGTCGTCCAGTGAAGTCTGTACAGAGTGCACCGAGACCGAGTCTACCAGTTATGTGACA 1323

Qy        108 ---------------LysCysGluAlaLysAsnTyrSerGlyArgPheThr--------- 119
                           |||   ||||||:::     |||:::
Db       1324 CCATATGTCAGCTCGTCTACTGCTGCCGCAAACTACACTAGCTCATTCTCATCGTCCAGT 1383

Qy        120 ---------------CysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrVal 134
                           |||           :::   ||||||          :::
Db       1384 GAAGTCTGTACAGAGTGCACCGAAACTGAGTCTACTAGCACCTCTACTCCATATGTCACT 1443

Qy        135 LysSerSerArgGlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSer 154
                 ||||||      ||||||:::                                 :::
Db       1444 AGCTCTTCCTCGTCGTCCAGTGAA----------------------------GTCTGT 1473

Qy        155 AlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGlu 174
                 |||           ::::::      |||           |||
Db       1474 ACAGAGTGCACCGAGACCGAGTCTACCAGTTATGTGACACCATATGTCAGCTCGTCTACT 1533

Qy        175 GlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIle 194
                 :::|||
Db       1534 GCTGCCGCA------------------------------------------------- 1542

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
                           ||||||||||||||||||
Db       1543 -----------------AACTACACTAGCTCTTTC----------------------- 1560

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSer 234
                                                 |||       ||||||
Db       1561 ------------------------------------TCATCGTCCAGTGAAGTCTGT 1581

Qy        235 TrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyVal 254
                    |||      :::|||   ||||||       |||         :::|||
Db       1582 ACAGAGTGCACCGAAACCGAGTCTACTAGCACCTCTACTCCATATGTCACC--------- 1632

Qy        255 GlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSer 274
                          ::::::                    :::      :::   |||
Db       1633 --------------AGCTCTTCCTGGTCGTCCAGTGAAGTCTGTACAGAGTGCACCGAG 1677

Qy        275 AlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyr 294
                 :::         :::         :::                          |||
Db       1678 ACCGAGTCTACCAGTTATGTGACACCATATGTCAGCTCGTCTACTGCTGCCGCAAACTAC 1737

Qy        295 SerSerSerTrpSerAsnTrpAlaSerValSerCysSerGlyGlyGlyGlyGlyGlySer 314
                 :::||||||:::|||:::   :::   |||   |||:::                |||
Db       1738 ACTAGCTCATTCTCATCGTCCAGTGAAGTC---TGTACAGAGTGCACCGAAACCGAGTCT 1794

Qy        315 ArgAsnLeuProThrPro------ThrProSerProGlyMetPheGlnCysLeuAsnHis 332
                 :::      ||||||      |||   |||   |||
Db       1795 ACAAGCACATCCACTCCATATGCAACCTCATCTACTGGCACA------------------ 1836

Qy        333 SerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln------Thr 350
                 :::   :::         :::   |||||||||:::                |||      |||
Db       1837 GCTACTTCATTTACCGCTTCAACTTCCAATACCATGACGTCTTTGGTCCAAACAGACACA 1896

Qy        351 LeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLys 370
                       :::|||   :::|||         :::|||         |||
Db       1897 ACCGTTTCTTTCAGCCTATCTTCAACTGTAAGCGAGCAT---------ACCAACGCTCCA 1947

Qy        371 ThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAla 390
                 ||||||:::||||||:::                ::::::   |||:::      :::
Db       1948 ACTTCATCTGTAGAGTCAAATGCTAGTACTTTCATATCGTCAAATAAAGGCAGCGTTAAA 2007

Qy        391 SerArgGluIleSer---------------------------------------LeuIle 397
                 |||         |||                                      :::
Db       2008 AGTTATGTTACGTCATCCATACATAGCATTACGCCCATGTATCCTAGTAACCAAACCGTA 2067

Qy        398 ThrAsnGlySerCysLeuAla------------------SerArgLysThrSerPheMet 411
                 |||:::   |||   ::::::               |||   ::::::|||
Db       2068 ACATCTAGCTCTGTTGTCTCCACACCAATTACTTCCGAATCTTCTGAATCCTCGGCCTCA 2127

Qy        412 ThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLys 431
                 |||:::      |||:::|||      :::   |||         ::::::   |||
Db       2128 GTTACCATTCTACCCTCAACTATCACTTCTGAATTCAAACCATCTACAATGAAAACGAAG 2187

Qy        432 AlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMet 451
                 ::::::      :::         |||                        |||:::
Db       2188 GTCGTTAGT------ATCTCCTCATCACCA--------------------ACTAATTTG 2220

Qy        452 LeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThr------Val 469
                 :::|||:::   |||      :::         |||   |||   |||      |||
Db       2221 ATTACCAGCTATGACACTACATCTAAGGATTCAACTGTTGGTTCATCCACATCGTCTGTA 2280

Qy        470 ProGlnAsnSerSerLeuGluGluProAspPheTyr 481
                       ||||||:::      |||      |||
Db       2281 AGCCTGATCTCTAGTATTTCTCTACCAAGTAGTTAT 2316

RESULT 13
US-11-145-307A-22
; Sequence 22, Application US/11145307A
; Publication No. US20060094035A1
; GENERAL INFORMATION:
;  APPLICANT: Arcturus Bioscience, Inc.
;  APPLICANT:  Erlander, Mark G.
;  APPLICANT:  Ma, Xiao-Jun
;  TITLE OF INVENTION: Identification of Tumors
;  FILE REFERENCE: 022041-002020US
;  CURRENT APPLICATION NUMBER: US/11/145,307A
;  CURRENT FILING DATE:  2005-06-03
;  PRIOR APPLICATION NUMBER: US 60/577,084
;  PRIOR FILING DATE: 2004-06-04
;  NUMBER OF SEQ ID NOS: 268
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
;   LENGTH: 2832
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```
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-145-307A-22

Alignment Scores:
Pred. No.:              1.81          Length:        2832
Score:                  102.50        Matches:       91
Percent Similarity:     36.3%         Conservative:  87
Best Local Similarity:  18.5%         Mismatches:    151
Query Match:            3.8%          Indels:        164
DB:                     7             Gaps:          22

US-10-821-670A-44 (1-511) x US-11-145-307A-22 (1-2832)

Qy         60 PheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeu------------ 75
              |||:::     |||:::     |||||||||||||   :::   |||
Db        186 TTCAGTGGAATGGGCAGAAGGAGGTGCCACAAAGGGCA-AAGAGATTGATTTTGATGATG 244

Qy         76 --------------------SerHisSerPheLeuLeuIleHisLysLysGluAspGly 88
                                 |||:::||||||      :::|||   |||   |||
Db        245 TGGCTGCAATAAACCCAGAACTCTTACAGCTTCTTCCC-TTACATCCGAAG---GACAAT 300

Qy         89 IleTrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLys 108
              :::       :::   :::      ||||||:::   :::       :::       |||
Db        301 CTGCCCTTGCAGGAAAATGTAACAATCCAGAAACAAAAACGGAGATCCGTCAACTCCAAA 360

Qy        109 CysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThr 128
                 |||          |||   |||                 ::::::   :::|||
Db        361 ATTCCTGCTCCAAAAGAAAGTCTTCGAAGCCGCTCCACTCGCATGTCCACTGTCTCA--- 417

Qy        129 AspLeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGluValThrCys 148
              :::|||:::   |||   :::                 :::       ||||||
Db        418 GAGCTTCGCATCACGGCTCAG--------------GAGAATGACATGGAGGTGGAGCTG 462

Qy        149 GlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyr 168
                 ||||||      |||   ::::::      |||                   :::
Db        463 CCTGCAGCTGCAAACTCCCGCAAGCAGTTTTCAGTTCCTCCTGCCCCCACTAGG------ 516

Qy        169 ThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGlu 188
                                    :::|||||||||       |||   :::|||:::
Db        517 --------------------CCTTCCTGCCCTGCAGTGGCTGAA---ATACCATTGAGG 552

Qy        189 ValValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIle 208
              :::|||   :::   :::   :::      :::                       |||
Db        553 ATGGTCAGCGAGGAGATGGAAGAGCAAGTCCATTCC--------------------ATC 591

Qy        209 ArgAspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSer 228
              |||          :::|||      :::::::::   |||
Db        592 CGAGGCAGCTCTTCTGCAAACCCTGTGAACTCAGTTCGGAGGAAATCATGTCTT---GTG 648

Qy        229 ArgHisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPhe 248
              :::   ||||||
Db        649 AAGGAAGTGGAA---------------------------------------------- 660

Qy        249 SerLeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeu 268
                                    :::   ||||||   ||||||:::|||
Db        661 ----------------------AAAATGAAGAACAAGCGAGAAGAGAAGAAGGCC--- 693

Qy        269 SerValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGln 288
                                           ::::::::::::::|||::::::
Db        694 ---------------------------------CAGAACTCTGAAATGAGAATGAAG 717

Qy        289 AlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrp--------------------- 301
                 |||   :::   |||   ||||||:::   ||||||
Db        718 ---AGAGCTCAGGAGTATGACAGTAGTTTTCCAAACTGGGAATTTGCCCGAATGATTAAA 774

Qy        302 ---------AlaSerValSerCysSerGlyGlyGlyGlyGlyGlySerArgAsnLeuPro 318
                        |||::::::   |||                       :::
Db        775 GAATTTCGGGCTACTTTGGAATGTCAT-----------------CCACTTACTATGACT 816

Qy        319 ThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArg 338
              |||                 :::      |||:::                     :::
Db        817 GATCCTATCGAAGAGCACAGAATATGTGTCTGTGTTAGG-----------------AAA 858
```

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Qy        339 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 358
                    |||      :::   |||::::::   ::::::      |||      |||
Db        859 CGCCCACTGAATAAGCAAGAATTGGCCAAGAAAGAAATTGATGTGATTTCCATTCCTAGC 918

Qy        359 Glu------GluIleAspHisGlu--------------AspIleThrLys--------- 368
              :::         :::   ||||||               |||:::||||||
Db        919 AAGTGTCTCCTCTTGGTACATGAACCCAAGTTGAAAGTGGACTTAACAAAGTATCTGGAG 978

Qy        369 ----------------------------AspLysThrSerThrValGlu--------- 375
                                          |||:::|||::::::   |||
Db        979 AACCAAGCATTCTGCTTTGACTTTGCATTTGATGAAACAGCTTCGAATGAAGTTGTCTAC 1038

Qy        376 ------AlaCysLeuProLeuGluLeuThrMetAsnGluSer------------------ 387
                     ||||||      |||:::   |||
Db       1039 AGGTTCACAGCAAGGCCACTGGTACAGACAATCTTTGAAGGTGGAAAAGCAACTTGTTTT 1098

Qy        387 ------------------------------------------------------------ 387

Db       1099 GCATATGGCCAGACAGGAAGTGGCAAGACACATACTATGGGCGGAGACCTCTCTGGGAAA 1158

Qy        388 --------------------------CysLeuAlaSerArgGluIleSerLeuIleThr 398
                                         :::|||||||||::::::   |||:::
Db       1159 GCCCAGAATGCATCCAAAGGGATCTATGCCATGGCCTCCCGGGACGTCTTCCTCCTGAAG 1218

Qy        399 AsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSer 418
              |||       |||       ||||||            :::
Db       1219 AATCAACCCTGCTAC------CGGAAGTTGGGCCTGGAAGTCTATGTGACATTCTTCGAG 1272

Qy        419 IleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeu 438
              ||||||         |||::::::   :::       |||             ::::::|||
Db       1273 ATCTACAATGGG---AAGCTGTTTGACCTGCTCAACAAGAAGGCCAAGCTGCGCGTGCTG 1329

Qy        439 MetAspProLysArgGln---------IlePheLeuAspGlnAsnMetLeuThrAlaIle 455
                 |||   |||:::|||         :::   |||   ::::::::::::   :::
Db       1330 GAGGACGGCAAGCAACAGGTGCAAGTGGTGGGGCTGCAGGAGCATCTGGTTAACTCTGCT 1389

Qy        456 AspGluLeuLeuGlnAlaLeuAsnValAsnSer 466
              |||::::::::::::   :::::::::   |||
Db       1390 GATGATGTCATCAAGATGATCGACATGGGCAGC 1422

RESULT 14
US-10-953-349-864
; Sequence 864, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 864
;   LENGTH: 1416
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-864

Alignment Scores:
Pred. No.:              1.25          Length:        1416
Score:                  99.50         Matches:       82
Percent Similarity:     37.6%         Conservative:  50
Best Local Similarity:  23.4%         Mismatches:    137
Query Match:            3.7%          Indels:        85
DB:                     6             Gaps:          14

US-10-821-670A-44 (1-511) x US-10-953-349-864 (1-1416)

Qy        193 AlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArg--------- 209
              |||:::   ||||||   |||   :::   |||   :::       :::|||
Db        321 GCTCTGATGAAACTCCACTACGCCGATCTCACCGACGCTTCCTCTCTCCGTCGTTGGATC 380
```

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Qy        210 AspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
              |||:::|||||||||||||         ||||||      :::
Db        381 GATGTGATCAAGCCTGACGAAGTTTATAACCTAGCTGCTCAA--------------TCT 425

Qy        230 HisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSer 249
              ||||||   ||||||:::|||   ||||||
Db        426 CACGTCGCTGTCTCCTTCGAGATCCCTGATTA-------------------------- 457

Qy        250 LeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSer 269
                                          ::::::|||     ::::::|||   |||
Db        458 ----------------------------CACAGCCGATGTAGTCGCAACCGGTGCTCT 487

Qy        270 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 289
                      |||   ::::::      |||:::           |||
Db        488 CCGTCTCCTTGAAGCCGTCAGATCTCACACCATCGACAGTGGCCGTACCGTCAAGTATTA 547

Qy        290 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSerGlyGly 309
                 |||  :::          |||   |||  :::|||
Db        548 CCAAGCCGGATCTTCGGAGATGTTTGGATCAACTCCTCCTCCACAATC------------ 595

Qy        310 GlyGlyGlyGlySerArgAsnLeuProThrProThrProSerProGlyMetPheGln--- 328
                          :::      :::|||      |||          ||||||
Db        596 ------------GGAGACGACGCCGTTTCACCCCAGATCTCCTTACGCAGCTTCCAAATG 643

Qy        329 ------CysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsn------------ 342
                  |||   ||||||:::   |||   |||   :::   :::
Db        644 CGCTGCTCATTGGTACACAGTGAA---TTACAGAGAGGCGTACGGTCTCTTCGCTTGTAA 700

Qy        343 ---ThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIle 361
                 |||   :::::::|||   |||      :::                 ||||||
Db        701 CGGAATCTTGTTCAATCACGAGTCACCTCGCCGTGGTGAGAATTTCGTGACGAGGAA--- 757

Qy        362 AspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGlu 381
              ||||||:::   |||   ||||||:::           :::      :::|||   |||
Db        758 GATCACAAGAGCATTGGGAAGGATCAAGGTTGGTTTGCAGACGAAGCTATTCCTTGGGAA 817

Qy        382 LeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySer 401
                      :::                 :::||||||                 |||
Db        818 TTTGCAAG-CGTCAAGAGATTGGGGATTTGCAGGAGATTATGTGGAAGCAATGTGGTTGA 876

Qy        402 CysLeuAlaSerArgLysThrSerPheMetThrThrLeu-------------------- 414
              |||   :::   |||      |||   |||   ||||||
Db        877 TGTTGCAGCAAGAGA------AGCCAGATGATTACGTTGTGGCAACAGAGGAAGGACACA 930

Qy        415 --------------------CysLeuSerSerIleTyrGluAspLeuLysMetTyrGln 427
                               |||         |||::::::   :::
Db        931 CAGTGGAAGAGTTTCTTGATGTGTCATTTGGGTATTTGGGACTCAATTGGAAAGAT-TAT 989

Qy        428 ValGluPhe---------------------------------------------LysAla 432
              ||||||                                                 |||
Db        990 GTTGAGATTGACCAGAGGTACTTTAGGCCTGCTGAAGTAGATAACCTTCAAGGAGATGCA 1049

Qy        433 MetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu 452
                  ||||||   ::::::      |||   |||:::     ::::::   :::
Db       1050 AGCAAGGCAAAGGAAGTGTTGGGGTGGAAACCACAAGTAGGGTTTGAGAAGCTTGTGAAG 1109

Qy        453 ThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsn 472
                 :::||||||   |||:::                  |||   |||
Db       1110 ATGATGGTTGATGAAGATCTTGAGCTTGCTAAGAGGGAGAAAGTGCTTGTTGATGCTGGA 1169

Qy        473 ------SerSerLeuGluGluProAspPhe---------TyrLysThrLysIleLys--- 486
                    :::   ::::::|||   |||         ||||||      :::
Db       1170 TACATGGATGCTAAGCAGCAACCTTGATTTGATCAATTATACAAAGATGGAGTTTCTTAC 1229

Qy        487 LeuCysIleLeuLeuHisAlaPheArgIleArg 497
              :::   :::||||||   :::|||:::   |||
Db       1230 ATTTATCTGCTTTTATAGAGTTTTAAATTTCGT 1262

RESULT 15
US-11-217-529-174200
; Sequence 174200, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174200
;   LENGTH: 1875
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-174200

Alignment Scores:
Pred. No.:              1.91          Length:          1875
Score:                  99.50         Matches:         48
Percent Similarity:     40.7%         Conservative:    35
Best Local Similarity:  23.5%         Mismatches:      69
Query Match:            3.7%          Indels:          52
DB:                     7             Gaps:            10

US-10-821-670A-44 (1-511) x US-11-217-529-174200 (1-1875)

Qy        304 ValSerCysSerGlyGly---------GlyGlyGlyGlySerArgAsnLeuProThrPro 320
              ::::::   |||||||||            |||   |||   |||   :::   ||||||
Db        136 TTAACAGTTTCTGGCGGTGTAGAAATCGATGGGTCTGGTTTAAGATTTATCATGACACCT 195

Qy        321 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 340
                  |||   |||      :::      ||||||      |||::::::::::|||
Db        196 TTATATTCCAGTGGCTCACAGGAACTT------CACTCAGATTTTTTGGTTAAAAGCATC 249

Qy        341 ---------SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThr 357
                       :::|||::::::   :::                 |||      |||:::
Db        250 CAAGATCTTACGAATTCGATGTTACAATTTAGTGATCCATTGACCACATATAATAGGTAC 309

Qy        358 SerGlu---GluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAla 376
                 |||   :::|||          |||   :::   |||      |||   :::||||||
Db        310 AAAGAAGATGACATTAGCTCTTCAGACAGTAGTAGTGATCTCAACTCTAATATAGAAGCT 369

Qy        377 CysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeu 396
                    |||
Db        370 TCAAAACCA---------------------------------------------------- 378

Qy        397 IleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeu 416
                  |||||||||                        :::                :::   |||
Db        379 GCCGCAAATGGTTCTTATACTCTTCAAAATATGCGGAACAAGGCCCTTAATGTAGCCTTA 438

Qy        417 SerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLys 436
              :::   :::                        ::::::      |||   :::      :::
Db        439 GCGAAATTG--------------------AAAATAGCATTAAAGGACGTTACCATACGT 477

Qy        437 LeuLeuMet---------AspProLysArg---------GlnIlePheLeuAspGlnAsn 450
              |||::::::         ||||||                ::::::   |||:::
Db        478 TTAATAGTAAATGATAGAGATCCTTCCGATAACATCGTGGAGGTTCATCTAGAAAGCATA 537

Qy        451 MetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal-Pr 470
                 |||          |||      |||:::   :::|||:::   ::::::|||::: ||
Db        538 CAACTTATTACTACAGACGCAAATTTACGACATATAAACATTGAAAATATCACCATTTCC 597

Qy        470 oGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIle---------LysLe 487
              ||||                          ||||||   |||:::           ||
Db        598 TCAA--------------------------TACAAAAACAAGCTGTACCCGACTCTCCT 630

Qy        487 uCysIleLeu 490
              |||||||||
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Db 631 GTGCATCCTT 640

Search completed: June 10, 2006, 01:21:38
Job time : 49.5861 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 10, 2006, 03:13:25 ; Search time 2434.29 Seconds
(without alignments)
15525.205 Million cell updates/sec

Title: US-10-821-670A-35
Perfect score: 591
Sequence: 1 aggaacctccccacacccac.....tgagctatctgaatgcttcc 591

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	591	100.0	591	2	AR595954	AR595954 Sequence
c 2	591	100.0	591	2	AR595955	AR595955 Sequence
3	591	100.0	669	14	FCIL12P35	Y07761 Felis catus
4	589.4	99.7	666	2	AR595952	AR595952 Sequence
c 5	589.4	99.7	666	2	AR595953	AR595953 Sequence
6	587.8	99.5	669	14	FCU83185	U83185 Felis catus
7	584.6	98.9	591	2	AR242439	AR242439 Sequence
8	584.6	98.9	591	2	AR280207	AR280207 Sequence
9	584.6	98.9	591	2	AR322422	AR322422 Sequence
10	584.6	98.9	1441	2	AR242438	AR242438 Sequence
11	584.6	98.9	1441	2	AR280206	AR280206 Sequence
12	584.6	98.9	1441	2	AR322421	AR322421 Sequence
13	575	97.3	669	2	AX076201	AX076201 Sequence
14	575	97.3	669	2	AX076483	AX076483 Sequence
15	575	97.3	689	2	AR242451	AR242451 Sequence
16	575	97.3	689	2	AR280219	AR280219 Sequence
17	575	97.3	689	2	AR322434	AR322434 Sequence
18	575	97.3	4201	2	AX076477	AX076477 Sequence
19	573.4	97.0	1533	2	AR595959	AR595959 Sequence
c 20	573.4	97.0	1533	2	AR595960	AR595960 Sequence
21	573.4	97.0	1599	2	AR595956	AR595956 Sequence
c 22	573.4	97.0	1599	2	AR595957	AR595957 Sequence
23	557.8	94.4	561	2	AR596007	AR596007 Sequence
c 24	557.8	94.4	561	2	AR596008	AR596008 Sequence
25	536.6	90.8	669	2	AR151072	AR151072 Sequence
26	536.6	90.8	669	2	E15018	E15018 Canine mRNA
27	536.6	90.8	669	2	AR316471	AR316471 Sequence
28	535	90.5	591	2	BD171284	BD171284 Novel can
29	535	90.5	591	2	AR595963	AR595963 Sequence
c 30	535	90.5	591	2	AR595964	AR595964 Sequence
31	535	90.5	666	2	AR595961	AR595961 Sequence
c 32	535	90.5	666	2	AR595962	AR595962 Sequence
33	535	90.5	669	2	BD014664	BD014664 Process f
34	535	90.5	1282	2	BD171283	BD171283 Novel can
35	535	90.5	1455	2	AR596009	AR596009 Sequence
c 36	535	90.5	1455	2	AR596010	AR596010 Sequence
37	533.4	90.3	669	2	AR151062	AR151062 Sequence
38	533.4	90.3	669	2	BD014654	BD014654 Process f
39	533.4	90.3	669	2	AR316461	AR316461 Sequence
40	530.2	89.7	657	8	AY191828	AY191828 Synthetic
41	530.2	89.7	660	2	AX154617	AX154617 Sequence
42	530.2	89.7	660	2	AX154619	AX154619 Sequence
43	528.6	89.4	660	2	AX154615	AX154615 Sequence
44	527	89.2	669	14	CFU49085	U49085 Canis famil
45	525.4	88.9	660	2	AX154616	AX154616 Sequence

ALIGNMENTS

RESULT 1
AR595954
LOCUS AR595954 591 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 35 from patent US 6818444.
ACCESSION AR595954
VERSION AR595954.1 GI:56646935
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 591)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 35 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .591
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 100.0%; Score 591; DB 2; Length 591;
Best Local Similarity 100.0%; Pred. No. 5.8e-174;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
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Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
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Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591


RESULT 2
AR595955/c
LOCUS       AR595955                591 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 37 from patent US 6818444.
ACCESSION   AR595955
VERSION     AR595955.1  GI:56646936
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 37 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           100.0%;  Score 591;  DB 2;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-174;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
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Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1


RESULT 3
FCIL12P35
LOCUS       FCIL12P35               669 bp    mRNA    linear   MAM 18-APR-2005
DEFINITION  Felis catus mRNA for interleukin-12 p35 chain.
ACCESSION   Y07761
VERSION     Y07761.1  GI:2102662
KEYWORDS    interleukin-12 subunit p35.
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1
  AUTHORS   Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
  TITLE     Molecular cloning of cat interleukin-12
  JOURNAL   Immunogenetics 45 (6), 462-463 (1997)
   PUBMED   9089110
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Schijns,V.E.C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
            Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
            Utrecht, NETHERLANDS
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Felis catus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
                     /cell_type="lymphocyte"
                     /tissue_type="peripheral blood"
     gene            1. .669
                     /gene="IL-12.p35"
     CDS             1. .669
                     /gene="IL-12.p35"
                     /function="heterodimer with IL-12 p40 chain"
                     /codon_start=1
                     /product="interleukin-12 p35 chain"
                     /protein_id="CAA69067.1"
                     /db_xref="GI:2102663"
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                     /db_xref="InterPro:IPR004281"
                     /db_xref="InterPro:IPR009079"
                     /db_xref="UniProtKB/Swiss-Prot:O02743"
                     /translation="MCPPRGLLLVTILVLLNHLDHLSLARNLPTPTPSPGMFQCLNHS
                     QTLLRAISNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
                     REISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAMNAKLLMDPKRQIFLDQ
                     NMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSY
                     LNAS"
ORIGIN

  Query Match           100.0%;  Score 591;  DB 14;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 5.9e-174;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
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Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666
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RESULT 4
AR595952
LOCUS       AR595952                 666 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 32 from patent US 6818444.
ACCESSION   AR595952
VERSION     AR595952.1  GI:56646933
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 32 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             99.7%;  Score 589.4;  DB 2;  Length 666;
  Best Local Similarity   99.8%;  Pred. No. 1.9e-173;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195
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Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
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Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
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Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666
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RESULT 5
AR595953/c
LOCUS       AR595953                 666 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 34 from patent US 6818444.
ACCESSION   AR595953
VERSION     AR595953.1  GI:56646934
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 34 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             99.7%;  Score 589.4;  DB 2;  Length 666;
  Best Local Similarity   99.8%;  Pred. No. 1.9e-173;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352
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Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
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Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
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Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1


RESULT 6
FCU83185
LOCUS       FCU83185                669 bp    mRNA    linear   MAM 16-JUL-1999
DEFINITION  Felis catus interleukin-12 p35 subunit (IL-12) mRNA, complete cds.
ACCESSION   U83185
VERSION     U83185.1  GI:2735052
KEYWORDS    .
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Nucleotide and predicted peptide sequence of feline interleukin-12
            (IL-12)
  JOURNAL   DNA Seq. 8 (1-2), 77-82 (1997)
   PUBMED   9522125
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal
            Veterinary Medicine, University of Zurich, Winterthurerstrasse 260,
            Zurich, ZH 8057, Switzerland
FEATURES             Location/Qualifiers
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                     /organism="Felis catus"
                     /mol_type="mRNA"
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     CDS             1. .669
                     /note="cytokine"
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                     /db_xref="GI:2735053"
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                     LNSS"
ORIGIN

  Query Match             99.5%;  Score 587.8;  DB 14;  Length 669;
  Best Local Similarity   99.7%;  Pred. No. 6e-173;
  Matches  589;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
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Db        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
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Db        556 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATTCTTCC 666


RESULT 7
AR242439
LOCUS       AR242439                591 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 9 from patent US 6472509.
ACCESSION   AR242439
VERSION     AR242439.1  GI:27288856
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 9 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             98.9%;  Score 584.6;  DB 2;  Length 591;
  Best Local Similarity   99.3%;  Pred. No. 6e-172;
  Matches  587;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
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Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
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Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 591


RESULT 8
AR280207
LOCUS       AR280207                591 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 9 from patent US 6518045.
ACCESSION   AR280207
VERSION     AR280207.1  GI:29715597
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 9 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match            98.9%;  Score 584.6;  DB 2;  Length 591;
  Best Local Similarity  99.3%;  Pred. No. 6e-172;
  Matches  587;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
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Db        481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
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Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 591


RESULT 9
AR322422
LOCUS       AR322422                591 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 9 from patent US 6566097.
ACCESSION   AR322422
VERSION     AR322422.1  GI:33708175
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 9 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match            98.9%;  Score 584.6;  DB 2;  Length 591;
  Best Local Similarity  99.3%;  Pred. No. 6e-172;
  Matches  587;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||| |||||| |||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 591


RESULT 10
AR242438
LOCUS       AR242438               1441 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 8 from patent US 6472509.
ACCESSION   AR242438
VERSION     AR242438.1  GI:27288855
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1441)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 8 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .1441
                     /organism="unknown"
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ORIGIN

  Query Match             98.9%;  Score 584.6;  DB 2;  Length 1441;
  Best Local Similarity   99.3%;  Pred. No. 6.5e-172;
  Matches  587;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 277

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 337

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 397

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 457

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 517

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 577

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        578 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 637

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        638 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 697

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        698 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 757

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||| |||||| |||||
Db        758 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 808


RESULT 11
AR280206
LOCUS       AR280206               1441 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 8 from patent US 6518045.
ACCESSION   AR280206
VERSION     AR280206.1  GI:29715596
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1441)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 8 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .1441
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             98.9%;  Score 584.6;  DB 2;  Length 1441;
  Best Local Similarity   99.3%;  Pred. No. 6.5e-172;
  Matches  587;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 277

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 337

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 397

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 457

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 517

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 577
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Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        578 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 637

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        638 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 697

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        698 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 757

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              ||||||||||||||||||||||||||||||||||||| |||||| |||||
Db        758 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 808


RESULT 12
AR322421
LOCUS       AR322421               1441 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 8 from patent US 6566097.
ACCESSION   AR322421
VERSION     AR322421.1  GI:33708174
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1441)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 8 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .1441
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             98.9%;  Score 584.6;  DB 2;  Length 1441;
  Best Local Similarity   99.3%;  Pred. No. 6.5e-172;
  Matches  587;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
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Db        218 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 277

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 337

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
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Db        338 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 397

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
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Db        398 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 457

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
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Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
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Db        518 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 577

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
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Db        578 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 637

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
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Db        638 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 697

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
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Db        698 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 757

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
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Db        758 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 808


RESULT 13
AX076201
LOCUS       AX076201               669 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 2 from Patent WO0104155.
ACCESSION   AX076201
VERSION     AX076201.1  GI:12710826
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 2 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="feline IL-12 p35"
ORIGIN

  Query Match             97.3%;  Score 575;  DB 2;  Length 669;
  Best Local Similarity   98.3%;  Pred. No. 6.3e-169;
  Matches  581;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
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Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
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Db        256 GAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
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Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
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Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
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Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
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Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
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Db        556 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
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Db        616 AGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666


RESULT 14
AX076483
LOCUS       AX076483                669 bp    DNA     linear   PAT 07-FEB-2001
DEFINITION  Sequence 9 from Patent WO0104280.
ACCESSION   AX076483
VERSION     AX076483.1  GI:12711035
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 9 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .669
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ORIGIN

  Query Match             97.3%;  Score 575;  DB 2;  Length 669;
  Best Local Similarity   98.3%;  Pred. No. 6.3e-169;
  Matches  581;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
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Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
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Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
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Db        196 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
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Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
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Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
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Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
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Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
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Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
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Db        616 AGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666


RESULT 15
AR242451
LOCUS       AR242451                689 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 26 from patent US 6472509.
ACCESSION   AR242451
VERSION     AR242451.1  GI:27288868
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 26 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             97.3%;  Score 575;  DB 2;  Length 689;
  Best Local Similarity   98.3%;  Pred. No. 6.3e-169;
  Matches  581;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
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Db         82 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 141

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
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Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
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Db        262 GAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 321

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
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Db        322 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 381

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 441

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||| | |||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 GCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 501

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
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Db        502 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 561

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
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	1	591	100.0	591	6	ABK98948	Abk98948 Feline in
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	3	591	100.0	591	14	ADV34688	Adv34688 Feline si
c	4	591	100.0	591	14	ADV34690	Adv34690 Feline si
c	5	589.4	99.7	666	6	ABK98947	Abk98947 Feline in
	6	589.4	99.7	666	6	ABK98946	Abk98946 Feline in
	7	589.4	99.7	666	14	ADV34685	Adv34685 Feline si
c	8	589.4	99.7	666	14	ADV34687	Adv34687 Feline si
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	10	584.6	98.9	1441	2	AAV56628	Aav56628 Feline FL
	11	579.8	98.1	679	4	AAF26097	Aaf26097 Feline fi
	12	575	97.3	669	4	AAF26083	Aaf26083 Feline IL
	13	575	97.3	669	4	AAF26086	Aaf26086 Feline IL
	14	575	97.3	689	2	AAV56641	Aav56641 Feline FL
	15	575	97.3	4201	4	AAF26077	Aaf26077 Feline IL
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c	17	573.4	97.0	1533	6	ABK98954	Abk98954 Feline in
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c	19	573.4	97.0	1533	14	ADV34697	Adv34697 Feline si
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c	22	573.4	97.0	1599	6	ABK98951	Abk98951 Feline in
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	27	557.8	94.4	561	14	ADV34751	Adv34751 Feline N-
c	28	557.8	94.4	561	14	ADV34753	Adv34753 Feline N-
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	39	535	90.5	669	2	AAX03163	Aax03163 Nucleic a
	40	535	90.5	669	2	AAX35626	Aax35626 Nucleic a
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	42	535	90.5	1282	2	AAX18178	Aax18178 Canine fu
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c	45	535	90.5	1455	14	ADV34756	Adv34756 Canine si

ALIGNMENTS

RESULT 1
ABK98948
ID ABK98948 standard; cDNA; 591 BP.
XX
AC ABK98948;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p35-591 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69305.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 1; Page 56-57; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain

```
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 591 BP; 178 A; 149 C; 122 G; 142 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 591;  DB 6;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-172;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
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Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
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Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591


RESULT 2
ABK98949/c
ID   ABK98949 standard; cDNA; 591 BP.
XX
AC   ABK98949;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p35-591 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Disclosure; Page 58; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 591 BP; 142 A; 122 C; 149 G; 178 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 591;  DB 6;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-172;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112
```

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Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
```

RESULT 3
ADV34688
ID ADV34688 standard; cDNA; 591 BP.
XX
AC ADV34688;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain mature IL-12p35 protein cDNA, nFeIL-12p35 591.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; gene; ss.
XX
OS Felis catus.
XX
FH Key Location/Qualifiers
FT CDS 1. .591
FT /*tag= a
FT /product= "PFeIL-12p35 197 protein"
FT /partial
FT /note= "No start and stop codon"
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
DR P-PSDB; ADV34689.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Claim 23; SEQ ID NO 35; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain mature IL-12p35 subunit
CC protein encoding cDNA.
XX
SQ Sequence 591 BP; 178 A; 149 C; 122 G; 142 T; 0 U; 0 Other;

Query Match 100.0%; Score 591; DB 14; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.6e-172;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
```

RESULT 4
ADV34690/c
ID ADV34690 standard; DNA; 591 BP.
XX
AC ADV34690;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain mature IL-12p35 complementary DNA, nFeIL-12p35 591.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Felis catus.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX

PS Example 3; SEQ ID NO 37; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain mature IL-12p35 subunit
CC complementary DNA.
XX
SQ Sequence 591 BP; 142 A; 122 C; 149 G; 178 T; 0 U; 0 Other;

Query Match 100.0%; Score 591; DB 14; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.6e-172;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
```

RESULT 5
ABK98947/c
ID ABK98947 standard; cDNA; 666 BP.
XX
AC ABK98947;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p35-666 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Example 3; Page 56; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 666 BP; 160 A; 138 C; 179 G; 189 T; 0 U; 0 Other;

Query Match 99.7%; Score 589.4; DB 6; Length 666;
Best Local Similarity 99.8%; Pred. No. 8.5e-172;
Matches 590; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112
```

```
Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1


RESULT 6
ABK98946
ID   ABK98946 standard; cDNA; 666 BP.
XX
AC   ABK98946;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p35-666 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69304.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 54-55; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 666 BP; 189 A; 179 C; 138 G; 160 T; 0 U; 0 Other;

  Query Match             99.7%;  Score 589.4;  DB 6;  Length 666;
  Best Local Similarity   99.8%;  Pred. No. 8.5e-172;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666


RESULT 7
ADV34685
ID   ADV34685 standard; cDNA; 666 BP.
XX
AC   ADV34685;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12p35 full-length cDNA, nFeIL-12p35 666.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .666
FT                   /*tag=  a
FT                   /product= "PFeIL-12p35 222 protein "
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
```

DR P-PSDB; ADV34686.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Claim 23; SEQ ID NO 32; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain IL-12p35 subunit protein
CC encoding full-length cDNA.
XX
SQ Sequence 666 BP; 189 A; 179 C; 138 G; 160 T; 0 U; 0 Other;

Query Match 99.7%; Score 589.4; DB 14; Length 666;
Best Local Similarity 99.8%; Pred. No. 8.5e-172;
Matches 590; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666
```

RESULT 8
ADV34687/c
ID ADV34687 standard; DNA; 666 BP.
XX
AC ADV34687;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain IL-12p35 complementary DNA, nFeIL-12p35 666.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Felis catus.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-0091726S.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 3; SEQ ID NO 34; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain IL-12p35 subunit full-length
CC complementary DNA.
XX
SQ Sequence 666 BP; 160 A; 138 C; 179 G; 189 T; 0 U; 0 Other;

Query Match 99.7%; Score 589.4; DB 14; Length 666;
Best Local Similarity 99.8%; Pred. No. 8.5e-172;
Matches 590; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1


RESULT 9
AAV56629
ID   AAV56629 standard; cDNA; 591 BP.
XX
AC   AAV56629;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp35 cDNA mature transcript.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP001824.
XX
PR   04-JUN-1996;   96JP-00165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76176.
XX
PT   Novel feline cytokine protein - useful for treating feline auto:immune
PT   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS   Claim 23; Page 59; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine mature protein, FLAFp35.
CC   This protein can be used in the production of a FLAFp35/FLAFp40
CC   heterodimer which can potentiate the cytotoxic activity of feline
CC   cytotoxic T lymphocyte cells. Such proteins are used for treatment of
CC   feline autoimmune diseases e.g. as caused by feline herpes virus or
CC   feline calcivirus
XX
SQ   Sequence 591 BP; 179 A; 151 C; 120 G; 141 T; 0 U; 0 Other;

  Query Match             98.9%;  Score 584.6;  DB 2;  Length 591;
  Best Local Similarity   99.3%;  Pred. No. 2.5e-170;
  Matches  587;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||||| |||||| |||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 591


RESULT 10
AAV56628
ID   AAV56628 standard; cDNA; 1441 BP.
XX
AC   AAV56628;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp35 cDNA.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             133. .811
FT                   /*tag=  a
FT   sig_peptide     133. .217
FT                   /*tag=  b
FT   mat_peptide     218. .808
FT                   /*tag=  c
FT                   /product= "FLAFp35"
FT                   /note= "feline cytokine"
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP001824.
XX
PR   04-JUN-1996;   96JP-00165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76175.
XX
PT   Novel feline cytokine protein - useful for treating feline auto:immune
PT   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS   Claim 22; Page 57-58; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine protein, FLAFp35. This
```

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CC   protein can be used in the production of a FLAFp35/FLAFp40 heterodimer
CC   which can potentiate the cytotoxic activity of feline cytotoxic T
CC   lymphocyte cells. Such proteins are used for treatment of feline
CC   autoimmune diseases e.g. as caused by feline herpes virus or feline
CC   calcivirus
XX
SQ   Sequence 1441 BP; 451 A; 325 C; 258 G; 407 T; 0 U; 0 Other;

  Query Match             98.9%;  Score 584.6;  DB 2;  Length 1441;
  Best Local Similarity   99.3%;  Pred. No. 3.8e-170;
  Matches  587;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 277

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 337

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 397

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 457

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 517

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 577

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        578 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 637

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        638 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 697

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        698 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 757

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              ||||||||||||||||||||||||||||||||||||| |||||| |||||
Db        758 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 808


RESULT 11
AAF26097
ID   AAF26097 standard; DNA; 679 BP.
XX
AC   AAF26097;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline fil12p35a DNA.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS   Felis sp.
XX
PN   WO200104155-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002263.
XX
PR   08-JUL-1999;   99CH-00001259.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Lutz H,  Leutenegger C,  Pedersen N,  Schroff M,  Wittig B;
XX
DR   WPI; 2001-147178/15.
XX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs.
XX
PS   Disclosure; Fig 2; 35pp; German.
XX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
CC   following: (i) as immunostimulant, for preventative or therapeutic use;
CC   and (ii) treating tumors and autoimmune diseases, or diseases associated
CC   with a Th1 defect, especially pre-existing infections by feline immune
CC   deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ   Sequence 679 BP; 196 A; 180 C; 140 G; 163 T; 0 U; 0 Other;

  Query Match             98.1%;  Score 579.8;  DB 4;  Length 679;
  Best Local Similarity   98.8%;  Pred. No. 8.1e-169;
  Matches  584;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        316 TCTCTGATAACTAATGGGAGTTGGCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495
```

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Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||||
Db        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAAACCCTCC 555

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              ||||||||||||||||||||||| | ||||||||||||||||| |||||
Db        616 AGAATTCGTGCAGTGACCATCAATAAAGTGATGAGCTATCTGAATTCTTCC 666
```

RESULT 12
AAF26083
ID AAF26083 standard; DNA; 669 BP.
XX
AC AAF26083;
XX
DT 24-APR-2001 (first entry)
XX
DE Feline IL-12p35 encoding DNA SEQ ID 4.
XX
KW Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS Felis sp.
XX
PN WO200104280-A2.
XX
PD 18-JAN-2001.
XX
PF 08-JUL-2000; 2000WO-DE002262.
XX
PR 08-JUL-1999; 99CH-00001258.
XX
PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA (UYZU-) UNIV ZUERICH.
XX
PI Leutenegger C, Schroff M, Wittig B, Lutz H;
XX
DR WPI; 2001-147190/15.
XX
PT Vaccine for treating or preventing lentivirus infection in cats, contains
PT nucleic acid sequence encoding viral protein under control of eukaryotic
PT promoter.
XX
PS Claim 14; Page 37; 37pp; German.
XX
CC This invention describes a novel vaccine (A) for prevention or treatment
CC of lentivirus infection in felines which comprises an immunizing nucleic
CC acid sequence (I) that contains, or comprises, at least part of a gene
CC encoding a protein (II) of the virus, under control of a eukaryotic
CC promoter functional in the relevant animal. (II) is especially the
CC envelope (env) protein. The invention also describes (1) vaccine (A)
CC containing an immunizing protein, or fragment, from a lentivirus plus at
CC least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC lentivirus protein, or fragment, especially derived from feline immune
CC deficiency virus (FIV), by expressing the corresponding nucleic acid
CC sequence in a host cell. The products of the invention have antiviral
CC activity. The vaccine (A) and related protein-based vaccines, are
CC particularly used to treat or prevent lentivirus infections in domestic
CC cats, especially feline immune deficiency virus (FIV). Vaccination with
CC (A) allows differentiation between vaccinated and infected animals, from
CC the antibody status. The vaccines may be formulated with an adjuvant
CC (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC immune response, particularly a Th1 response
XX
SQ Sequence 669 BP; 189 A; 179 C; 140 G; 161 T; 0 U; 0 Other;

Query Match 97.3%; Score 575; DB 4; Length 669;
Best Local Similarity 98.3%; Pred. No. 2.5e-167;

Matches 581; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              |||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              |||||||||||| | |||||||||||| ||||||||||||||||||||||||||||||||
Db        496 ATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              ||||| |||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666
```

RESULT 13
AAF26086
ID AAF26086 standard; DNA; 669 BP.
XX
AC AAF26086;
XX
DT 24-APR-2001 (first entry)
XX
DE Feline IL-12p35 encoding DNA.
XX
KW Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS Felis sp.
XX
PN WO200104155-A2.
XX
PD 18-JAN-2001.
XX
PF 08-JUL-2000; 2000WO-DE002263.
XX
PR 08-JUL-1999; 99CH-00001259.
XX
PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA (UYZU-) UNIV ZUERICH.
PA (REGC) UNIV CALIFORNIA.
XX
PI Lutz H, Leutenegger C, Pedersen N, Schroff M, Wittig B;
XX

```
DR   WPI; 2001-147178/15.
XX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs.
XX
PS   Claim 3; Page 31; 35pp; German.
XX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
CC   following: (i) as immunostimulant, for preventative or therapeutic use;
CC   and (ii) treating tumors and autoimmune diseases, or diseases associated
CC   with a Th1 defect, especially pre-existing infections by feline immune
CC   deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ   Sequence 669 BP; 189 A; 179 C; 140 G; 161 T; 0 U; 0 Other;

  Query Match            97.3%;  Score 575;  DB 4;  Length 669;
  Best Local Similarity  98.3%;  Pred. No. 2.5e-167;
  Matches  581;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              |||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              |||||||||||| | |||||||||||| ||||||||||||||||||||||||||||||
Db        496 ATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666


RESULT 14
AAV56641
ID   AAV56641 standard; DNA; 689 BP.
XX
AC   AAV56641;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp35 DNA fragment.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ss.
XX
OS   Felis catus.
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP001824.
XX
PR   04-JUN-1996;   96JP-00165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
XX
PT   Novel feline cytokine protein - useful for treating feline auto:immune
PT   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS   Claim 24; Page 67; 94pp; Japanese.
XX
CC   This sequence encodes a fragment of a novel feline cytokine protein,
CC   FLAFp35. This protein can be used in the production of a FLAFp35/FLAFp40
CC   heterodimer which can potentiate the cytotoxic activity of feline
CC   cytotoxic T lymphocyte cells. Such proteins are used for treatment of
CC   feline autoimmune diseases e.g. as caused by feline herpes virus or
CC   feline calcivirus
XX
SQ   Sequence 689 BP; 192 A; 193 C; 145 G; 159 T; 0 U; 0 Other;

  Query Match            97.3%;  Score 575;  DB 2;  Length 689;
  Best Local Similarity  98.3%;  Pred. No. 2.5e-167;
  Matches  581;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 141

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 201

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 261

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||| | ||||||||| | ||||||||||||||||||||||||||||||||||||
Db        262 GAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 321

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 381

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        382 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 441

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||| | ||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 GCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 501

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        502 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 561

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        562 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 621

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||| |||||| |||||
Db        622 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 672


RESULT 15
AAF26077
ID   AAF26077 standard; DNA; 4201 BP.
XX
AC   AAF26077;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p35 encoding DNA SEQ ID 3.
XX
KW   Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW   interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS   Felis sp.
XX
PN   WO200104280-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002262.
XX
PR   08-JUL-1999;   99CH-00001258.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
XX
PI   Leutenegger C,  Schroff M,  Wittig B,  Lutz H;
XX
DR   WPI; 2001-147190/15.
XX
PT   Vaccine for treating or preventing lentivirus infection in cats, contains
PT   nucleic acid sequence encoding viral protein under control of eukaryotic
PT   promoter.
XX
PS   Disclosure; Page 31-33; 37pp; German.
XX
CC   This invention describes a novel vaccine (A) for prevention or treatment
CC   of lentivirus infection in felines which comprises an immunizing nucleic
CC   acid sequence (I) that contains, or comprises, at least part of a gene
CC   encoding a protein (II) of the virus, under control of a eukaryotic
CC   promoter functional in the relevant animal. (II) is especially the
CC   envelope (env) protein. The invention also describes (1) vaccine (A)
CC   containing an immunizing protein, or fragment, from a lentivirus plus at
CC   least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC   lentivirus protein, or fragment, especially derived from feline immune
CC   deficiency virus (FIV), by expressing the corresponding nucleic acid
CC   sequence in a host cell. The products of the invention have antiviral
CC   activity. The vaccine (A) and related protein-based vaccines, are
CC   particularly used to treat or prevent lentivirus infections in domestic
CC   cats, especially feline immune deficiency virus (FIV). Vaccination with
CC   (A) allows differentiation between vaccinated and infected animals, from
CC   the antibody status. The vaccines may be formulated with an adjuvant
CC   (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC   immune response, particularly a Th1 response
XX
SQ   Sequence 4201 BP; 1086 A; 1055 C; 999 G; 1061 T; 0 U; 0 Other;

  Query Match             97.3%;  Score 575;  DB 4;  Length 4201;
  Best Local Similarity   98.3%;  Pred. No. 6.1e-167;
  Matches  581;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3122 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 3181

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3182 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 3241

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3242 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 3301

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       3302 GAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 3361

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              |||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db       3362 TCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCTTTTATGACGACCCTG 3421

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3422 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 3481

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3482 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 3541

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
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Db       3602 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 3661

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
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Db       3662 AGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 3712


Search completed: June 10, 2006, 04:50:52
Job time : 436.576 secs
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 10, 2006, 03:16:38 ; Search time 3451.4 Seconds
(without alignments)
9575.336 Million cell updates/sec

Title: US-10-821-670A-35
Perfect score: 591
Sequence: 1 aggaacctccccacacccac.....tgagctatctgaatgcttcc 591

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	501.4	84.8	762	14	DQ033872	DQ033872 Homo sapi
	2	498.2	84.3	762	14	DQ033873	DQ033873 Pan trogl
	3	415.4	70.3	935	4	CD013914	CD013914 90138124
	4	414.8	70.2	1136	4	CD013915	CD013915 90138132
	5	331.2	56.0	863	4	CD013916	CD013916 90138296
	6	258	43.7	1938	6	BC035571	BC035571 Homo sapi
	7	233.4	39.5	812	2	BG702253	BG702253 602683459
	8	218	36.9	589	1	AI050362	AI050362 ub30a07.r
	9	215.8	36.5	563	3	BU698113	BU698113 LL2in1206
c	10	215	36.4	1099	2	BI523344	BI523344 603175938
c	11	207.6	35.1	778	1	AJ820622	AJ820622 AJ820622
	12	200	33.8	373	7	BF552757	BF552757 UI-R-C0-i
	13	190	32.1	561	3	BU699383	BU699383 LL2in1157
	14	175.2	29.6	412	4	CB801533	CB801533 AMGNNUC:S
c	15	173.8	29.4	777	4	CB168830	CB168830 CWI602769
	16	173	29.3	427	10	DT930939	DT930939 S13.1784
	17	170.6	28.9	832	2	BI523569	BI523569 603175938
	18	166.8	28.2	456	10	DT913216	DT913216 S13.1426
	19	165	27.9	371	3	BU699957	BU699957 B4-79 Hem
	20	160.2	27.1	581	3	BP260963	BP260963 BP260963
	21	157.8	26.7	354	4	BY230958	BY230958 BY230958
	22	154	26.1	1299	6	AK153729	AK153729 Mus muscu
	23	131.6	22.3	571	3	BP261459	BP261459 BP261459
	24	129.4	21.9	777	14	CT080894	CT080894 Sus scrof
	25	117.8	19.9	551	10	DT919655	DT919655 PCRS30821
	26	111.2	18.8	373	3	BU695376	BU695376 B1-30 Hem
	27	101	17.1	692	5	CJ137697	CJ137697 CJ137697
	28	95.8	16.2	342	2	BM257856	BM257856 521721 MA
	29	86.2	14.6	592	12	CE159257	CE159257 tigr-gss-
	30	77.6	13.1	840	11	BZ261813	BZ261813 CH230-420
	31	76	12.9	447	2	BI824638	BI824638 603033580
c	32	74.6	12.6	940	14	BX963061	BX963061 Forward s
	33	69.6	11.8	382	4	CB809298	CB809298 AMGNNUC:T
	34	69.4	11.7	508	9	DA505380	DA505380 DA505380
	35	69	11.7	558	9	CX570753	CX570753 RVL1941 W
	36	64.2	10.9	463	9	DR007201	DR007201 TC124111
	37	62.2	10.5	361	3	BU694675	BU694675 B2-56 Hem
	38	61.6	10.4	344	14	BX537236	BX537236 INRA porc
c	39	59.4	10.1	528	1	AI332701	AI332701 qq19a07.x
	40	44.6	7.5	477	4	BX258839	BX258839 BX258839
	41	44.6	7.5	840	8	CN228296	CN228296 RJB052F11
	42	43	7.3	532	2	BI065861	BI065861 pgf1n.pk0
	43	43	7.3	627	3	BU123439	BU123439 603149370
	44	43	7.3	789	3	BU446520	BU446520 603765726
c	45	39.6	6.7	812	9	CX916558	CX916558 JGI_CAAN5

ALIGNMENTS

RESULT 1
DQ033872
LOCUS DQ033872 762 bp DNA linear GSS 02-JUN-2005
DEFINITION Homo sapiens IL12A gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION DQ033872
VERSION DQ033872.1 GI:66885081
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 762)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 762)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.
FEATURES Location/Qualifiers
source 1. .762
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="3"
gene <1. .>762
/gene="IL12A"
/locus_tag="HC3464"
ORIGIN

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  Best Local Similarity   90.5%;  Pred. No. 1.8e-136;
  Matches  535;  Conservative    0;  Mismatches   56;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              || |||||||||    |||| |||  ||||||||||||||  |||||  ||||||||||
Db        169 AGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 228

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              | ||||||| | ||| ||||||||| ||| ||||||||||||||||||||||||||||
Db        229 AACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTTTAC 288

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              | ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db        289 CCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 348

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              |||||||| |||||| |||||||||||| ||||||||||||||   |||||||||| |
Db        349 GAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGAGAGACC 408

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||| | ||||||||||||||||||||||||||||||||||||||||||| |||||
Db        409 TCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATGGCCCTG 468

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              |||||||| ||||| ||||| ||||||||||||||||||||||||||||| ||||||||
Db        469 TGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAAT 528

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||  | |||||||||| |||||||||||| |||||||||||||| ||| |
Db        529 GCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCAGTT 588

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              |||||||||||| | |||||||||||| ||||||||| |||||||||||| || ||||||
Db        589 ATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCC 648

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        649 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 708

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
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Db        709 AGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTCC 759
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RESULT 2
DQ033873

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LOCUS       DQ033873                762 bp    DNA     linear   GSS 02-JUN-2005
DEFINITION  Pan troglodytes IL12A gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   DQ033873
VERSION     DQ033873.1  GI:66885082
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     A Scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
  JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
   PUBMED   15869325
REFERENCE   2  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.  Translation starts at the beginning of
            alignment.
FEATURES             Location/Qualifiers
     source          1. .762
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     gene            <1. .>762
                     /gene="IL12A"
                     /locus_tag="HC3464"
ORIGIN
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  Query Match            84.3%;  Score 498.2;  DB 14;  Length 762;
  Best Local Similarity   90.2%;  Pred. No. 1.6e-135;
  Matches  533;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
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Db        169 AGAAACCTCCCCGTGGCCACCCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 228

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              | ||||||| | ||| ||||||||| ||| ||||||||||||||||||||||||||||
Db        229 AACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTTTAC 288

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              | ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db        289 CCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 348

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              |||||||| |||||| |||||||||||| ||||||||||||||   |||||||||| |
Db        349 GAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGAGAGACC 408

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||| | ||||||||||||||||||||||||||||||||||||||||||| |||||
Db        409 TCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATGGCCCTG 468

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
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Db        469 TGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAAT 528

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||  | |||||||||| |||||||||||| |||||||||||||| ||| |
Db        529 GCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCAGTT 588

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
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Db        589 ATTGACGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCC 648

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
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Db        649 CTTGAAGAACTGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 708

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
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Db        709 AGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTCC 759
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RESULT 3
CD013914

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LOCUS       CD013914                935 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION  90138124 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD013914
VERSION     CD013914.1  GI:37777444
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 935)
  AUTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
            Au-Young,J. and Stuve,L.L.
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  TITLE     PCR isolation and cloning of novel splice variant mRNAs from known
            drug target genes
  JOURNAL   Genomics 83 (4), 566-571 (2004)
   PUBMED   15028279
COMMENT     Contact: Jin, P.
            Incyte Corporation
            3160 Porter Drive, Palo Alto, CA 94304, USA
            Tel: 650 621 8639
            Fax: 650 621 8965
            Email: pjin@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .935
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Single gene library"
                     /note="Vector: pDrive Cloning Vector; RT-PCR was performed
                     using gene-specific primers flanking the open-reading
                     frame. PCR products were subcloned into pDrive Cloning
                     Vector and sequenced completely using M13 forward and
                     reverse primers. Sequencing gaps were closed by
                     re-sequencig using primers flanking the gapped areas."
ORIGIN

  Query Match             70.3%;  Score 415.4;  DB 4;  Length 935;
  Best Local Similarity   84.3%;  Pred. No. 5e-111;
  Matches  498;  Conservative    0;  Mismatches   51;  Indels   42;  Gaps    1;

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Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
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Db        332 AACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTTTAC 391

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
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Db        392 CCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 451

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
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Db        452 GAGGCCTGTTTACCATTGGAATTAACCAAG------------------------------ 481

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
                          ||||||||||||||||||||||||||||||||||||||||  | |||||
Db        482 ------------AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATGGCCCTG 529

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||  |||||  |||||  ||||||||||||||||||||||||||||||  ||||||||
Db        530 TGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAAT 589

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||  | ||||||||||| ||||||||||||| ||||||||||||||  ||| |
Db        590 GCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCAGTT 649

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||| | ||||||||||| |||||||| |||||||||| || ||||||
Db        650 ATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCC 709

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
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Db        710 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 769

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||| |||||||| ||  ||||| |||||||||||||||||||||
Db        770 AGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTCC 820


RESULT 4
CD013915
LOCUS       CD013915               1136 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION  90138132 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD013915
VERSION     CD013915.1  GI:37777445
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1136)
  AUTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
            Au-Young,J. and Stuve,L.L.
  TITLE     PCR isolation and cloning of novel splice variant mRNAs from known
            drug target genes
  JOURNAL   Genomics 83 (4), 566-571 (2004)
   PUBMED   15028279
COMMENT     Contact: Jin, P.
            Incyte Corporation
            3160 Porter Drive, Palo Alto, CA 94304, USA
            Tel: 650 621 8639
            Fax: 650 621 8965
            Email: pjin@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .1136
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Single gene library"
                     /note="Vector: pDrive Cloning Vector; RT-PCR was performed
                     using gene-specific primers flanking the open-reading
                     frame. PCR products were subcloned into pDrive Cloning
                     Vector and sequenced completely using M13 forward and
                     reverse primers. Sequencing gaps were closed by
                     re-sequencig using primers flanking the gapped areas."
ORIGIN

  Query Match             70.2%;  Score 414.8;  DB 4;  Length 1136;
  Best Local Similarity   80.2%;  Pred. No. 8.1e-111;
  Matches  534;  Conservative    0;  Mismatches   57;  Indels   75;  Gaps    1;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
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Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              | |||||||  | |||  |||||||||  |||  ||||||||||||||||||||||||||||||
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Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              | ||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        476 CCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 535

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||  ||||||  ||||||||||||  |||||||||||||||  ||||||||||| |
Db        536 GAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGAGAGACC 595

Qy        241 TCTCTGATAACT---------------------------------------------- 252
              |||  |  ||||||
Db        596 TCTTTCATAACTGTAAGTCAAAAAATGAAAAGTTTCAGCCTGTATGATGAATTCATATCA 655

Qy        253 --------------------------AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 285
                                         |||||||||||||||||||||||||||||||||
Db        656 CTGATGTCTGATTATTTTTTCCTCTAGAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 715

Qy        286 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 345
              |||||||  |  ||||||||||||  |||||  |||||  ||||||||||||||||||||||
Db        716 TTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAG 775

Qy        346 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 405
              ||||||  ||||||||||||||||  | ||||||||||  |||||||||||||  ||||||
Db        776 TTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAA 835

Qy        406 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 465
              |||||||||  |||  ||||||||||||| |  ||||||||||||  |||||||||  |||||||
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```
Db        836 AACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTG 895

Qy        466 CCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 525
              ||||| || |||||| | ||||||||||||||||||||||||||||||||||||||||||
Db        896 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 955

Qy        526 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 585
              |||||||||||||||||||||||| |||||||| ||  ||||| ||||||||||||||||
Db        956 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAAT 1015

Qy        586 GCTTCC 591
              ||||||
Db       1016 GCTTCC 1021


RESULT 5
CD013916
LOCUS       CD013916                 863 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION  90138296 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD013916
VERSION     CD013916.1  GI:37777446
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 863)
  AUTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
            Au-Young,J. and Stuve,L.L.
  TITLE     PCR isolation and cloning of novel splice variant mRNAs from known
            drug target genes
  JOURNAL   Genomics 83 (4), 566-571 (2004)
   PUBMED   15028279
COMMENT     Contact: Jin, P.
            Incyte Corporation
            3160 Porter Drive, Palo Alto, CA 94304, USA
            Tel: 650 621 8639
            Fax: 650 621 8965
            Email: pjin@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .863
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Single gene library"
                     /note="Vector: pDrive Cloning Vector; RT-PCR was performed
                     using gene-specific primers flanking the open-reading
                     frame. PCR products were subcloned into pDrive Cloning
                     Vector and sequenced completely using M13 forward and
                     reverse primers. Sequencing gaps were closed by
                     re-sequencig using primers flanking the gapped areas."
ORIGIN

  Query Match           56.0%;  Score 331.2;  DB 4;  Length 863;
  Best Local Similarity   91.4%;  Pred. No. 3.7e-86;
  Matches  351;  Conservative    0;  Mismatches   33;  Indels    0;  Gaps    0;

Qy        208 ATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTG 267
              | |||||||||||||||   |||||||||||| |||| | ||||||||||||||||||||
Db        365 AAGAATGAGAGTTGCCTAAATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTG 424

Qy        268 GCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTG 327
              |||||||||||||||||||||||| | |||||||||||||| ||||| ||||| ||||||
Db        425 GCCTCCAGAAAGACCTCTTTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTG 484

Qy        328 AAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGG 387
              |||||||||||||||||||||||| ||||||||||||||   | |||||||||| |||
Db        485 AAGATGTACCAGGTGGAGTTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGG 544

Qy        388 CAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAAT 447
              |||||||||||| |||||||||||||| ||| |||||||||||| | ||||||||||||
Db        545 CAGATCTTTCTAGATCAAAACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAAT 604

Qy        448 GTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACT 507
              |||||||| |||||||||||| || |||||| | |||||||||||||||||||||||||
Db        605 TTCAACAGTGAGACTGTGCCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACT 664

Qy        508 AAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGA 567
              |||||||||||||||||||||||||||||||||||||||||||| |||||||| ||  |||||
Db        665 AAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGA 724

Qy        568 ATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||
Db        725 GTGATGAGCTATCTGAATGCTTCC 748


RESULT 6
BC035571
LOCUS       BC035571                 1938 bp    mRNA    linear   HTC 04-MAR-2003
DEFINITION  Homo sapiens, clone IMAGE:5240216, mRNA.
ACCESSION   BC035571
VERSION     BC035571.1  GI:23958681
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1938)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 69 Row: b Column: 15
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 4504638
            This clone has the following problem: retained intron.
FEATURES             Location/Qualifiers
     source          1. .1938
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240216"
                     /tissue_type="Brain, fetal, whole pooled"
                     /clone_lib="NIH_MGC_121"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
ORIGIN

  Query Match           43.7%;  Score 258;  DB 6;  Length 1938;
  Best Local Similarity   91.6%;  Pred. No. 2.1e-64;
```

```
  Matches  273;  Conservative    0;  Mismatches   25;  Indels    0;  Gaps    0;

Qy        294 GACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGC 353
              | |||||||||||||| ||||| ||||| |||||||||||||||||||||||||||||| |
Db       1145 GGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGAC 1204

Qy        354 CATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCT 413
              ||||||||||||||   | |||||||||| |||||||||||||| ||||||||||||||
Db       1205 CATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCT 1264

Qy        414 GACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAA 473
              | ||| |||||||||||||| | |||||||||||| ||||||||| |||||||||||| ||
Db       1265 GGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAA 1324

Qy        474 CTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCA 533
              |||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1325 ATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCA 1384

Qy        534 TGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||| |||||||| ||  ||||| ||||||||||||||||||||||
Db       1385 TGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTCC 1442


RESULT 7
BG702253
LOCUS       BG702253                812 bp    mRNA    linear   EST 07-MAY-2001
DEFINITION  602683459F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4816118 5',
            mRNA sequence.
ACCESSION   BG702253
VERSION     BG702253.1  GI:13973409
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 812)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10714  row: e  column: 15
            High quality sequence stop: 804.
FEATURES             Location/Qualifiers
     source          1. .812
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4816118"
                     /tissue_type="hippocampus"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_95"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
                     (gtcgag); Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTTTTVN-3', size-selected for  average
                     insert size 2.5 kb and normalized to ROT 5. This is a
                     primary library enriched for  full-length clones and
                     constructed using the Cap-trapper method (Carninci, in
                     preparation).  Library constructed by M. Brownstein
                     (NIMH/NHGRI, National Institutes of Health).  Note: this
                     is a NIH_MGC Library."
ORIGIN
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  Query Match           39.5%;  Score 233.4;  DB 2;  Length 812;
  Best Local Similarity   85.3%;  Pred. No. 2.9e-57;
  Matches  284;  Conservative    0;  Mismatches   46;  Indels    3;  Gaps    2;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              || |||||||||     |||| |||  |||||||||||||||  |||||  ||||||||||
Db        483 AGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 542

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              | ||||||| | ||| ||||||||| ||| ||||||||||||||||||||||||||||||
Db        543 AACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTTTAC 602

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              | |||||||| |||||||| ||||||||||||||||||||||||||||||||||||||||
Db        603 CCTTGCACTTCTGAAGAGATCGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 662

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              |||||||| |||||| |||||||||||| ||||||||||||       |||||||||| |
Db        663 GAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGC--TAAATCCAGAGAGACC 720

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||| | ||||||||||||||||||||| ||||||||||||||||||||||| |   ||||
Db        721 TCTTTCATAACTAATGGGAGTTGCCTGG-CTCCAGAAAGACCTCTTTTATGATGTGCCTG 779

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
              |||||||| |||||     ||    |  ||||||
Db        780 TGCCTTAGTAGTATTATGAAGACTTGAAAGATG 812


RESULT 8
AI050362
LOCUS       AI050362                589 bp    mRNA    linear   EST 09-JUL-1998
DEFINITION  ub30a07.r1 Soares_thymus_2NbMT Mus musculus cDNA clone
            IMAGE:1379220 5' similar to gb:M65291 INTERLEUKIN-12 ALPHA CHAIN
            PRECURSOR (HUMAN); gb:M86672 Mus musculus interleukin 12 p35
            subunit, complete cds (MOUSE);, mRNA sequence.
ACCESSION   AI050362
VERSION     AI050362.1  GI:3299479
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 589)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:901688
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 60.
FEATURES             Location/Qualifiers
     source          1. .589
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1379220"
                     /sex="male"
                     /tissue_type="Thymus"
```

/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares_thymus_2NbMT"
/note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCGTTTTTTTTTTTTTTTTTTTTTTTT 3'}; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 36.9%; Score 218; DB 1; Length 589;
Best Local Similarity 72.1%; Pred. No. 9.4e-53;
Matches 284; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

```
Qy         95 AGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATA 154
              |||||||| |||  ||  ||  ||| ||||||||| | ||||| || ||||||||||| |
Db        109 AGGCCAGAGAAAAACTGAAACATTATTCCTGCACTGCTGAAGACATCGATCATGAAGACA 168

Qy        155 TCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATG 214
              |||||   ||  |||||||||||| || || |||| |||||||||||| ||  || ||| |
Db        169 TCACACGGGACCAAACCAGCACATTGAAGACCTGTTTACCACTGGAACTACACAAGAACG 228

Qy        215 AGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCA 274
              ||||||||||||| | |||||||  |||   | ||| |  ||||| |||||| || |
Db        229 AGAGTTGCCTGGCTACTAGAGAGACTTCTTCCACAACAAGAGGGAGCTGCCTGCCCCCAC 288

Qy        275 GAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGT 334
                |||||  ||||| |||| |||||||||||| | || ||||||||||||||||||||||
Db        289 AGAAGACGTCTTTGATGATGACCCTGTGCCTTGGTAGCATCTATGAGGACTTGAAGATGT 348

Qy        335 ACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCT 394
              |||||   |||||| ||||||| || |||   ||    |   |     |   |||||||
Db        349 ACCAGACAGAGTTCCAGGCCATCAACGCAGCACTTCAGAATCACAACCATCAGCAGATCA 408

Qy        395 TTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACA 454
              |||| ||  |   |||||||   |  || |||||||| | ||| | ||||||   ||
Db        409 TTCTAGACAAGGGCATGCTGGGTGGCATCGATGAGCTGATGCAGTCTCTGAATCATAATG 468

Qy        455 GTGTGACTGTGCCACAGAACTCCTCCTTGGAAGA 488
              | | |||| |||  |||||  |  |||  |  ||
Db        469 GCGAGACTCTGCGCCAGAAACCTCCCTGTGGGGA 502
```

RESULT 9
BU698113
LOCUS BU698113 563 bp mRNA linear EST 09-OCT-2002
DEFINITION LL2in12067T7 Hematopoietic Stem Cell Subtracted Library Mus musculus cDNA 5' similar to interleukin 12 p35 subunit, mRNA sequence.
ACCESSION BU698113
VERSION BU698113.1 GI:23610620
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 563)
AUTHORS Phillips,R.L., Ernst,R.E., Brunk,B.P., Ivanova,N., Mahan,M.A., Deanehan,J.K., Moore,K.A., Overton,G.C. and Lemischka,I.R.
TITLE The genetic program of hematopoietic stem cells
JOURNAL Science 288 (5471), 1635-1640 (2000)
PUBMED 10834841
COMMENT Contact: Lemischka, Ihor R.
Department of Molecular Biology
Princeton University
Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544, USA
Tel: 609 258 2838
Fax: 609 258 2759
Email: ilemischka@molbio.princeton.edu
These ESTs are derived from a subtracted cDNA library enriched for gene products expressed in day 14-14.5 fetal liver hematopoietic stem cells defined as Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E (Sca-1)pos
Seq primer: M13Reverse or T7.
FEATURES Location/Qualifiers
source 1. .563
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/tissue_type="Hematopoietic"
/cell_type="Stem Cells; Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E (Sca-1)pos"
/dev_stage="Embryonic day 14-14.5"
/lab_host="DH10B"
/clone_lib="Hematopoietic Stem Cell Subtracted Library"
/note="Organ: Fetal Liver; Vector: Sport 1; Site_1: Sal I; Site_2: Not I; Two directionally cloned cDNA libraries were made from fetal liver hematopoietic stem cells enriched to be Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E (Sca-1)pos called Scapos and from AA4.1neg fetal liver cells. Subtractive hybridization was performed by hybridization of the target, Scapos, single stranded cDNA library in pSport1 to biotinylated RNA transcribed from the driver, AA4.1neg cDNA library in pSport2 with inserts cloned in the complementary orientation. For detailed protocols and additional information please see our website at http://stemcell.princeton.edu."

ORIGIN

Query Match 36.5%; Score 215.8; DB 3; Length 563;
Best Local Similarity 69.9%; Pred. No. 4.1e-52;
Matches 306; Conservative 0; Mismatches 128; Indels 4; Gaps 1;

```
Qy         95 AGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATA 154
              |||||||| |||  ||  ||  ||| ||||||||| | ||||| || ||||||||||| |
Db        100 AGGCCAGAGAAAAACTGAAACATTATTCCTGCACTGCTGAAGACATCGATCATGAAGACA 159

Qy        155 TCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATG 214
              |||||   ||  |||||||||||| || || |||| |||||||||||| ||  || ||| |
Db        160 TCACACGGGACCAAACCAGCACATTGAAGACCTGTTTACCACTGGAACTACACAAGAACG 219

Qy        215 AGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCA 274
              ||||||||||||| | |||||||  |||   | ||| |  ||||| |||||| || |
Db        220 AGAGTTGCCTGGCTACTAGAGAGACTTCTTCCACAACAAGAGGGAGCTGCCTGCCCCCAC 279

Qy        275 GAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGT 334
                |||||  ||||| |||| |||||||||||| | || ||||||||||||||||||||||
Db        280 AGAAGACGTCTTTGATGATGACCCTGTGCCTTGGTAGCATCTATGAGGACTTGAAGATGT 339

Qy        335 ACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCT 394
              |||||   |||||| ||||||| || |||   ||    |   |     |   |||||||
Db        340 ACCAGACAGAGTTCCAGGCCATCAACGCAGCACTTCAGAATCACAACCATCAGCAGATCA 399

Qy        395 TTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACA 454
              |||| ||  |   |||||||   |  || |||||||| | ||| | ||||||   ||
Db        400 TTCTAGACAAGGGCATGCTGGTGGCCATCGATGAGCTGATGCAGTCTCTGAATCATAATG 459

Qy        455 GTG----TGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAA 510
              |      || |||| | | || |   | |||  | | |||   ||| | |   |||
Db        460 GGNGAGACTCTTGCGCCAGAAACCTTCCTGTGGGAGAAGCAGGACCCTTACAGAGTGAAA 519

Qy        511 ATCAAGCTCTGCATACTT 528
              || |||||||  || | |
Db        520 ATGAAGCTCTTGATTCCT 537
```

RESULT 10
BI523344/c
LOCUS BI523344 1099 bp mRNA linear EST 29-AUG-2001

```
DEFINITION  603175938T1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 3',
            mRNA sequence.
ACCESSION   BI523344
VERSION     BI523344.1  GI:15348136
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1099)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11605  row: l  column: 09
            High quality sequence start: 40
            High quality sequence stop: 727.
FEATURES             Location/Qualifiers
     source          1. .1099
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240216"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_121"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 017. Note:
                     this is a NIH_MGC Library."
ORIGIN

  Query Match             36.4%;  Score 215;  DB 2;  Length 1099;
  Best Local Similarity   88.7%;  Pred. No. 8.8e-52;
  Matches  267;  Conservative    0;  Mismatches   30;  Indels    4;  Gaps    3;

Qy        294 GACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGC 353
              | |||||||| |||| ||||| ||||| ||| |||||||||||||||||||||||||| |
Db        741 GGCCCTGTGCTTTAGTAGTATTTATGAAGAC-TGAAGATGTACCAGGTGGAGTTCAAGAC 683

Qy        354 CATGAATGCAAAGC-TGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGC 412
              ||||||||||||| |  | |||||||||| ||||||||||||| ||||||||||||
Db        682 CATGAATGCAAAGCTTCCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGC 623

Qy        413 TGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGA 472
              || ||| |||||||||||||| | |||||||||||| ||||||||| |||||||||||| |
Db        622 TGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAA 563

Qy        473 ACTCCTCCTTGGAAGAACCGGAT--TTTTATAAAACTAAAATCAAGCTCTGCATACTTCT 530
              | |||||| | |||||||||||  |||   |||||| ||||||||||||||||||||||
Db        562 AATCCTCCCTTGAAGAACCGGATTGTTTATCAAAACTGAAATCAAGCTCTGCATACTTCT 503

Qy        531 TCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTC 590
              |||||||||||||||||| ||||||| ||  ||||| ||||||||||||||||||||||
Db        502 TCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTC 443

Qy        591 C 591
              |
Db        442 C 442
```

```
RESULT 11
AJ820622/c
LOCUS       AJ820622                778 bp    mRNA    linear   EST 12-MAY-2005
DEFINITION  AJ820622 KN206 Bos sp. cDNA clone C0006020h12, mRNA sequence.
ACCESSION   AJ820622
VERSION     AJ820622.1  GI:51888098
KEYWORDS    EST.
SOURCE      Bos sp.
  ORGANISM  Bos sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 778)
  AUTHORS   McGuire,K. and Glass,E.J.
  TITLE     The expanding role of microarrays in the investigation of
            macrophage responses to pathogens
  JOURNAL   Vet. Immunol. Immunopathol. 105 (3-4), 259-275 (2005)
COMMENT     Contact: McGuire K
            Genomics and Genetics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
            Single pass sequencing. Bases called and trimmed with phred
            v0.020425.c. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options. Vector:pBluescriptII(SK+) R. Site
            1:EcoRV(lost) R. Site 2:NotI Seq Primer: T7 Normalised library
            constructed from pooled monocytes from Bos taurus (Holstein) and
            Bos indicus (Sahiwals) cattle subjected to various stimuli,
            including infection with the protozoan parasite Theileria annulata.
FEATURES             Location/Qualifiers
     source          1. .778
                     /organism="Bos sp."
                     /mol_type="mRNA"
                     /db_xref="taxon:29061"
                     /clone="C0006020h12"
                     /tissue_type="blood"
                     /cell_type="bovine monocyte"
                     /clone_lib="KN206"
                     /note="Vector: pBluescriptII(SK+); Site_1: EcoRV(lost);
                     Site_2: NotI; Normalised library constructed from pooled
                     monocytes from Bos taurus (Holstein) and Bos indicus
                     (Sahiwals) cattle subjected to various stimuli, including
                     infection with the protozoan parasite Theileria annulata"
ORIGIN

  Query Match             35.1%;  Score 207.6;  DB 1;  Length 778;
  Best Local Similarity   87.0%;  Pred. No. 1.2e-49;
  Matches  228;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy        330 GATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCA 389
              |||||||| |||||||| ||||||||||||||||||  | |||||||||| |||||
Db        778 GATGTACCACGTGGAGTTCCAGGCCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCA 719

Qy        390 GATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGT 449
              |||||||| || || ||||||||| |||||||| ||||||| | ||||||||||||| |
Db        718 AATCTTTCTAGACCAGAACATGCTGGCAGCTATTGCTGAGCTGATGCAGGCCCTGAATTT 659

Qy        450 CAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAA 509
              | |||||| ||||||||||||||  ||||| || |||||| ||||||||| || || ||
Db        658 CGACAGTGAGACTGTGCCACAGAAACCCTCCCTGAAAGAACTGGATTTTTACAAGACAAA 599

Qy        510 AATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAAT 569
              | |||||||||||| |||||||| || |||||||||||||| ||||||||| | |||||
Db        598 AGTCAAGCTCTGCATCCTTCTTCACGCCTTCAGAATTCGTGCGGTGACCATCGACAGAAT 539

Qy        570 GATGAGCTATCTGAATGCTTCC 591
              |||||||||||||| | |||||
Db        538 GATGAGCTATCTGAGTTCTTCC 517


RESULT 12
BF552757
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LOCUS       BF552757                373 bp    mRNA    linear   EST 12-DEC-2000
DEFINITION  UI-R-C0-iz-d-02-0-UI.r1 UI-R-C0 Rattus norvegicus cDNA clone
            UI-R-C0-iz-d-02-0-UI 5', mRNA sequence.
ACCESSION   BF552757
VERSION     BF552757.1  GI:11662487
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 373)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
   PUBMED   8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156  MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            cDNA Library Preparation: M.B. Soares Lab Clone distribution:
            clones will be available through Research Genetics (www.resgen.com)
            This clone is also available through the I.M.A.G.E. Consortium at
            LLNL (info@image.llnl.gov). IMAGE ID= 1782759
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .373
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="UI-R-C0-iz-d-02-0-UI"
                     /dev_stage="adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="UI-R-C0"
                     /note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI;
                     The UI-R-C0 library is a subtracted library derived from
                     the UI-R-A1 and UI-R-E1 libraries. The UI-R-A1 library
                     consisted of a mixture of individually tagged normalized
                     libraries constructed from rat  placenta, adult lung,
                     brain, liver, kidney, heart, spleen, ovary,  and muscle.
                     The UI-R-E1 library  consisted of a mixture of
                     individually tagged normalized libraries constructed from
                     8, 12 and 18-day embryo. The tag is a string of 3-5
                     nucleotides present between the Not I  site and the
                     oligo-dT track which allows identification of the library
                     of origin of a clone within the mixture. The subtracted
                     library (UI-R-C0) was constructed as follows: PCR
                     amplified cDNA inserts from a pool of UI-R-A1 and UI-R-E1
                     clones from which 3' ESTs had been derived was used as a
                     driver in a hybridization with the pooled UI-R-A1 and
                     UI-R-E1 library in the form of single-stranded circles.
                     The remaining single-stranded circles (subtracted library)
                     was purified by hydroxyapatite column chromatography,
                     converted to double-stranded circles and electroporated
                     into DH10B bacteria (Life Technologies) to generate the
                     UI-R-C0 library. This procedure has been previously
                     described (Bonaldo, Lennon and Soares, Genome Research 6:
                     791-806, 1996)"
ORIGIN

  Query Match             33.8%;  Score 200;  DB 7;  Length 373;
  Best Local Similarity   71.5%;  Pred. No. 1.7e-47;
  Matches  263;  Conservative    0;  Mismatches  105;  Indels    0;  Gaps    0;

Qy        216 GAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAG 275
              ||| |||||||||| | | |||||  |||   ||||  |  ||||| ||||||  |  |
Db          4 GAGGTGCCTGGCTACTAAAGAGACTTCTTCCATAATAAGAGGGAGCTGCCTGCCTCCACA 63

Qy        276 AAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTA 335
              |||||| ||||| |||| ||||||||||||| | || ||||||||||||||||||||||
Db         64 AAAGACTTCTTTGATGATGACCCTGTGCCTTGGTAGCATCTATGAGGACTTGAAGATGTA 123

Qy        336 CCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTT 395
              ||||   |||||| ||||||| ||||||   ||    |   |  |  |||||||
Db        124 CCAGTCAGAGTTCCAGGCCATAAATGCAGCACTTCAGAGCCACAATCATCAGCAGATCAC 183

Qy        396 TCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAG 455
              ||||||   ||||||||||||  ||||||||||||||  | | | | ||||||  || | |
Db        184 TCTGGACAGAAACATGCTGATGGCTATTGATGAGCTAATGCGGTCTCTGAATCACAGCGG 243

Qy        456 TGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAA 515
              | || | |||  |||||  |  || ||| |||| | |||  ||| | |   || || ||
Db        244 CGAGATTCTGCACCAGAAAGCTCCCATGGGAGAAGCAGATCCTTACAGAGTGAAGATGAA 303

Qy        516 GCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAG 575
              |||||| || || || ||||| ||||| |  || |   |||| ||||| ||  ||||||
Db        304 GCTCTGTATCCTGCTCCATGCCTTCAGCACACGCGTCATGACTATCAACAGGGTGATGAA 363

Qy        576 CTATCTGA 583
              ||||||||
Db        364 CTATCTGA 371


RESULT 13
BU699383
LOCUS       BU699383                561 bp    mRNA    linear   EST 09-OCT-2002
DEFINITION  LL2in11573T7 Hematopoietic Stem Cell Subtracted Library Mus
            musculus cDNA 5' similar to interleukin 12 p35 subunit, mRNA
            sequence.
ACCESSION   BU699383
VERSION     BU699383.1  GI:23615967
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 561)
  AUTHORS   Phillips,R.L., Ernst,R.E., Brunk,B.P., Ivanova,N., Mahan,M.A.,
            Deanehan,J.K., Moore,K.A., Overton,G.C. and Lemischka,I.R.
  TITLE     The genetic program of hematopoietic stem cells
  JOURNAL   Science 288 (5471), 1635-1640 (2000)
   PUBMED   10834841
COMMENT     Contact: Lemischka, Ihor R.
            Department of Molecular Biology
            Princeton University
            Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544, USA
            Tel: 609 258 2838
            Fax: 609 258 2759
            Email: ilemischka@molbio.princeton.edu
            These ESTs are derived from a subtracted cDNA library enriched for
            gene products expressed in day 14-14.5 fetal liver hematopoietic
            stem cells defined as Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E
            (Sca-1)pos
            Seq primer: M13Reverse or T7.
FEATURES             Location/Qualifiers
     source          1. .561
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /tissue_type="Hematopoietic"
                     /cell_type="Stem Cells; Lineageneg/lo, AA4.1pos, cKitpos,
                     Ly6A/E (Sca-1)pos"
                     /dev_stage="Embryonic day 14-14.5"
                     /lab_host="DH10B"
                     /clone_lib="Hematopoietic Stem Cell Subtracted Library"
                     /note="Organ: Fetal Liver; Vector: Sport 1; Site_1: Sal I;
                     Site_2: Not I; Two directionally cloned cDNA libraries
                     were made from fetal liver  hematopoietic stem cells
                     enriched to be Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E
```

(Sca-1)pos called Scapos and from AA4.1neg fetal liver cells. Subtractive hybridization was performed by hybridization of the target, Scapos, single stranded cDNA library in pSport1 to biotinylated RNA transcribed from the driver, AA4.1neg cDNA library in pSport2 with inserts cloned in the complementary orientation. For detailed protocols and additional information please see our website at http://stemcell.princeton.edu."

ORIGIN

Query Match 32.1%; Score 190; DB 3; Length 561;
Best Local Similarity 68.2%; Pred. No. 1.7e-44;
Matches 275; Conservative 0; Mismatches 125; Indels 3; Gaps 1;

```
Qy        140 TTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGG 199
              | |||||||||||| ||||||   ||  |||||||||||| || || |||| ||||||||||
Db        129 TCGATCATGAAGACATCACACGGGACCAAACCAGCACATTGAAGACCTGTTTACCACTGG 188

Qy        200 AATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGA 259
              || ||  || ||| |||||||||||||| | |||||||  |||   | ||| |  ||||
Db        189 AACTACACAAGAACGAGAGTTGCCTGGCTACTAGAGAGACTTCTTCCACAACAAGAGGGA 248

Qy        260 GTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATG 319
              | |||||| || |    ||||| ||||| |||| |||||||||||||| | || |||||||
Db        249 GCTGCCTGCCCCCACAGAAGACGTCTTTGATGATGACCCTGTGCCTTGGTAGCATCTATG 308

Qy        320 AGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATC 379
              ||||||||||||||||||||   |||||| ||||||| || |||   ||    |   |
Db        309 AGGACTTGAAGATGTACCAGACAGAGTTCCAGGCCATCAACGCAGCACTTCAGAATCACA 368

Qy        380 CTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGG 439
                  |   ||||||| |||| ||  |   |||||||   |  || |||||||| | |||
Db        369 ACCATCAGCAGATCATTCTAGACAAGGGCATGCTGGTGGGCATCGATGAGCTGATGCAGT 428

Qy        440 CCCTGAATGTCAA---CAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATT 496
              | ||| ||   ||     | |   ||| | || | | |||||    ||   | | |
Db        429 CTCTGGATCATAATGGGCGAGACTCTGCGGCAAAAANCTCCTGTNGGGNGAAGCAGANCC 488

Qy        497 TTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTT 539
              |||| | |    |||| |||||||| ||     ||   |||||
Db        489 TTTACAGAGTGGAAATGAAGCTCTGNATCTGCTTTACGGCTTT 531
```

RESULT 14
CB801533
LOCUS CB801533 412 bp mRNA linear EST 16-MAY-2003
DEFINITION AMGNNUC:SRPB2-00244-H1-A srpb2 (10220) Rattus norvegicus cDNA clone srpb2-00244-h1 5', mRNA sequence.
ACCESSION CB801533
VERSION CB801533.1 GI:29914888
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 412)
AUTHORS Amgen EST Program.
TITLE Amgen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00244 row: h column: 1.
FEATURES Location/Qualifiers
source 1. .412
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="srpb2-00244-h1"
/tissue_type="prostate tissue"
/clone_lib="srpb2 (10220)"
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; rat prostate normalized double selected poly(A+) mRNA size fraction > 1 kb"
ORIGIN

Query Match 29.6%; Score 175.2; DB 4; Length 412;
Best Local Similarity 69.5%; Pred. No. 3.7e-40;
Matches 248; Conservative 0; Mismatches 108; Indels 1; Gaps 1;

```
Qy        235 GAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACG 294
              | |  |  | |  ||    |  ||||| ||||||  |   |   |||||| ||||| |||| |
Db          5 GCGTCCGNTNTCCTATANAGAGGGAGCTGCCTGCCTCCACAAAAGACTTCTTTGATGATG 64

Qy        295 ACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCC 354
              |||||||||||| | || |||||||||||| |||||||| ||||    |||||| |||||
Db         65 ACCCTGTGCCTTGGTAGCATCTATGAGGACTNGAAGATGTNCCAGTCAGAGTTCCAGGCC 124

Qy        355 ATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 414
              || ||||||   ||    |   |  | |   |||||||  ||||||   ||||||||||
Db        125 ATAAATGCAGCACTTCAGAGCCACAATCATCAGCAGATCACTCTGGACAGAAACATGCTG 184

Qy        415 ACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAAC 474
              |  |||||||||||||||   | | ||| ||||||  || | | | |||| |||  |||||
Db        185 ATGGCTATTGATGAGCTAATGC-GGCTCTGAATCACAGCGGCGAGACTCTGCACCAGAAA 243

Qy        475 TCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 534
              |  || ||| |||| | |||  ||| | |   || || |||||||| || || || |||
Db        244 GCTCCCATGGGAGAAGCAGATCCTTACAGAGTGAAGATGAAGCTCTGTATCCTGCTCCAT 303

Qy        535 GCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              || ||||| |  || |   |||| ||||| ||  |||||| ||||||||   | |||
Db        304 GCCTTCAGCACCCGCGTCATGACTATCAACAGGGTGATGAACTATCTGAGCTCCTCC 360
```

RESULT 15
CB168830/c
LOCUS CB168830 777 bp mRNA linear EST 30-JAN-2003
DEFINITION CWI602769160.R1 CSEQFXL41 testes Bos taurus cDNA, mRNA sequence.
ACCESSION CB168830
VERSION CB168830.1 GI:28154956
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 777)
AUTHORS Adelson,D.L. and Gill,C.A.
TITLE Bovine ESTs (Adelson and Gill)
JOURNAL Unpublished (2003)
COMMENT Contact: David L. Adelson
Animal Breeding and Genetics
Texas A&M University
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471, USA
Tel: 9798452616
Fax: 9798456970
Email: david.adelson@tamu.edu.
FEATURES Location/Qualifiers
source 1. .777
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="testes"
/clone_lib="CSEQFXL41 testes"
/note="Organ: testes; Vector: pBluescript SK+; Site_1: NotI; Site_2: EcoRI; sequence 5' of the insert (5'-NNN. . .NNNinsert) GCGAATTGGAGCTCCACCGCGGTGGCGGCCGCGGCTCGAG. Sequence 3' of the inserts (AAGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG. non-normalized library, sequenced 3' with M13R primer."
ORIGIN

Query Match 29.4%; Score 173.8; DB 4; Length 777;
Best Local Similarity 86.1%; Pred. No. 1.2e-39;
Matches 204; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

```
Qy        355 ATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 414
              ||||||||||||||  | |||||||||||| | ||| |||||||| || || |||||||||
Db        777 ATGAATGCAAAGCTTCTGATGGATCCTAAGA-GCAAATCTTTCTAGACCAGAACATGCTG 719

Qy        415 ACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAAC 474
              |||||||||  |||||||  | |||||||||||||  || ||||||  ||||||||||||||||
Db        718 GCAGCTATTGCTGAGCTGATGCAGGCCCTGAATTTCGACAGTGAGACTGTGCCACAGAAA 659

Qy        475 TCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCAT 534
              |||||  ||  ||||||  |||||||||  ||  ||  |||  ||||||||||||||  ||||||||
Db        658 CCCTCCCTGAAAGAACTGGATTTTTACAAGACAAAAGTCAAGCTCTGCATCCTTCTTCAC 599

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Db        598 GCCTTCAGAATTCGTGCGGTGACCATCGACAGAATGATGAGCTATCTGAGTTCTTCC 542
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Search completed: June 10, 2006, 17:40:16
Job time : 3452.4 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 10, 2006, 04:51:14 ; Search time 127.578 Seconds
(without alignments)
8667.862 Million cell updates/sec

Title: US-10-821-670A-35
Perfect score: 591
Sequence: 1 aggaacctccccacacccac.....tgagctatctgaatgcttcc 591

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
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5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
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10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	591	100.0	591	3	US-09-917-265A-35	Sequence 35, Appl
c	2	591	100.0	591	3	US-09-917-265A-37	Sequence 37, Appl
	3	589.4	99.7	666	3	US-09-917-265A-32	Sequence 32, Appl
c	4	589.4	99.7	666	3	US-09-917-265A-34	Sequence 34, Appl
	5	584.6	98.9	591	3	US-09-011-143-9	Sequence 9, Appli
	6	584.6	98.9	591	3	US-09-302-495-9	Sequence 9, Appli
	7	584.6	98.9	591	3	US-10-079-616-9	Sequence 9, Appli
	8	584.6	98.9	1441	3	US-09-011-143-8	Sequence 8, Appli
	9	584.6	98.9	1441	3	US-09-302-495-8	Sequence 8, Appli
	10	584.6	98.9	1441	3	US-10-079-616-8	Sequence 8, Appli
	11	575	97.3	689	3	US-09-011-143-26	Sequence 26, Appl
	12	575	97.3	689	3	US-09-302-495-26	Sequence 26, Appl
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	14	573.4	97.0	1533	3	US-09-917-265A-43	Sequence 43, Appl
c	15	573.4	97.0	1533	3	US-09-917-265A-45	Sequence 45, Appl
	16	573.4	97.0	1599	3	US-09-917-265A-38	Sequence 38, Appl
c	17	573.4	97.0	1599	3	US-09-917-265A-40	Sequence 40, Appl
	18	557.8	94.4	561	3	US-09-917-265A-101	Sequence 101, App
c	19	557.8	94.4	561	3	US-09-917-265A-103	Sequence 103, App
	20	536.6	90.8	669	3	US-09-079-984A-12	Sequence 12, Appl
	21	536.6	90.8	669	3	US-09-390-729-12	Sequence 12, Appl
	22	535	90.5	591	3	US-09-917-265A-49	Sequence 49, Appl
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	24	535	90.5	666	3	US-09-917-265A-46	Sequence 46, Appl
c	25	535	90.5	666	3	US-09-917-265A-48	Sequence 48, Appl
	26	535	90.5	1455	3	US-09-917-265A-104	Sequence 104, App
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	35	501.4	84.8	660	2	US-08-640-386A-3	Sequence 3, Appli
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	42	501.4	84.8	1364	2	US-08-265-087-3	Sequence 3, Appli
	43	501.4	84.8	1364	2	US-08-621-493-3	Sequence 3, Appli
	44	501.4	84.8	1364	2	US-08-965-688-3	Sequence 3, Appli
	45	501.4	84.8	1364	3	US-09-260-173-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-917-265A-35
; Sequence 35, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(591)
US-09-917-265A-35

Query Match 100.0%; Score 591; DB 3; Length 591;
Best Local Similarity 100.0%; Pred. No. 4.6e-187;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
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Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
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Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
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Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
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Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591


RESULT 2
US-09-917-265A-37/c
; Sequence 37, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-37

  Query Match            100.0%;  Score 591;  DB 3;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-187;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
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Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
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Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
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Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
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Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
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Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
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Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1


RESULT 3
US-09-917-265A-32
; Sequence 32, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
US-09-917-265A-32

  Query Match            99.7%;  Score 589.4;  DB 3;  Length 666;
  Best Local Similarity   99.8%;  Pred. No. 1.7e-186;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
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Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
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Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
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Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
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Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
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Db        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
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Db        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666


RESULT 4
US-09-917-265A-34/c
; Sequence 34, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-34

  Query Match             99.7%;  Score 589.4;  DB 3;  Length 666;
  Best Local Similarity   99.8%;  Pred. No. 1.7e-186;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
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Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1


RESULT 5
US-09-011-143-9
; Sequence 9, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  591 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-9

  Query Match             98.9%;  Score 584.6;  DB 3;  Length 591;
  Best Local Similarity   99.3%;  Pred. No. 6.4e-185;
  Matches  587;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
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Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
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Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
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Db        481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||| |||||| |||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 591


RESULT 6
US-09-302-495-9
; Sequence 9, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 591 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-302-495-9

  Query Match             98.9%;  Score 584.6;  DB 3;  Length 591;
  Best Local Similarity   99.3%;  Pred. No. 6.4e-185;
  Matches  587;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
               |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||| |||||| |||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 591


RESULT 7
US-10-079-616-9
; Sequence 9, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
```

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;           ZIP: 20004
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/10/079,616
;           FILING DATE: 22-Feb-2002
;           CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: 09/011,143
;           FILING DATE: 04-FEB-1998
;           APPLICATION NUMBER: PCT/JP97/01824
;           FILING DATE: 29-MAY-1997
;           APPLICATION NUMBER: JP 165249/1996
;           FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;           NAME: BROWDY, Roger L.
;           REGISTRATION NUMBER: 25,618
;           REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: 202-628-5197
;           TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 591 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-079-616-9

  Query Match            98.9%;  Score 584.6;  DB 3;  Length 591;
  Best Local Similarity  99.3%;  Pred. No. 6.4e-185;
  Matches  587;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
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Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
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Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
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Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
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Db        481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
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Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 591


RESULT 8
US-09-011-143-8
; Sequence 8, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1441 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-8

  Query Match            98.9%;  Score 584.6;  DB 3;  Length 1441;
  Best Local Similarity  99.3%;  Pred. No. 1.1e-184;
  Matches  587;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
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Db        218 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 277

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
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Db        278 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 337

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 397

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
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Db        398 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 457

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
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Db        458 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 517

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 577

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
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Db        578 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 637

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
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Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
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Db        698 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 757

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Db        758 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 808


RESULT 9
US-09-302-495-8
; Sequence 8, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1441 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-302-495-8

  Query Match             98.9%;  Score 584.6;  DB 3;  Length 1441;
  Best Local Similarity   99.3%;  Pred. No. 1.1e-184;
  Matches  587;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
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Db        218 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 277

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 337

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 397

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 457

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 517

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 577

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        578 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 637

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        638 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 697

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
                 |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        698 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 757

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
                ||||||||||||||||||||||||||||||||||| |||||| |||||
Db        758 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 808


RESULT 10
US-10-079-616-8
; Sequence 8, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
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;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 1441 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-079-616-8

  Query Match             98.9%;  Score 584.6;  DB 3;  Length 1441;
  Best Local Similarity   99.3%;  Pred. No. 1.1e-184;
  Matches  587;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 277

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 337

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 397

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 457

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 517

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 577

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        578 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 637

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        638 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 697

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        698 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 757

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||| |||||| |||||

Db        758 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 808


RESULT 11
US-09-011-143-26
; Sequence 26, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  26:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  689 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-26

  Query Match             97.3%;  Score 575;  DB 3;  Length 689;
  Best Local Similarity   98.3%;  Pred. No. 1.1e-181;
  Matches  581;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 141

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 201

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 261

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||| |||||||||| |||||||||||||||||||||||||||||||||||||||
Db        262 GAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 321
```

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Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 381

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 441

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 GCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 501

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        502 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 561

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        562 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 621

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||| |||||| |||||
Db        622 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 672


RESULT 12
US-09-302-495-26
; Sequence 26, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 26:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 689 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-302-495-26

  Query Match            97.3%;  Score 575;  DB 3;  Length 689;
  Best Local Similarity  98.3%;  Pred. No. 1.1e-181;
  Matches  581;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 141

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 201

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 261

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||| | ||||||||| | ||||||||||||||||||||||||||||||||||||||
Db        262 GAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 321

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 381

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 441

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 GCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 501

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        502 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 561

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        562 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 621

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||| |||||| |||||
Db        622 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 672


RESULT 13
US-10-079-616-26
; Sequence 26, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
```

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;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 26:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 689 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-079-616-26

  Query Match             97.3%;  Score 575;  DB 3;  Length 689;
  Best Local Similarity   98.3%;  Pred. No. 1.1e-181;
  Matches  581;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 141

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 201

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 261

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||| | |||||||||| | ||||||||||||||||||||||||||||||||||||
Db        262 GAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 321

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 381

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 441

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||| | |||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 GCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 501

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        502 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 561

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        562 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 621

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||| |||||| |||||
Db        622 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 672
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RESULT 14
US-09-917-265A-43
; Sequence 43, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-09-917-265A-43

  Query Match             97.0%;  Score 573.4;  DB 3;  Length 1533;
  Best Local Similarity   98.1%;  Pred. No. 6.3e-181;
  Matches  580;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              || ||| | || || || || ||| ||| || ||||||||||||||||||||||||||||
Db        943 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1002

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1003 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1062

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1122

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1123 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1182

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RESULT 15
US-09-917-265A-45/c
; Sequence 45, Application US/09917265A
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; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-45

  Query Match             97.0%;  Score 573.4;  DB 3;  Length 1533;
  Best Local Similarity   98.1%;  Pred. No. 6.3e-181;
  Matches  580;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

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Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
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Job time : 127.578 secs
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

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Perfect score: 591
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	2	591	100.0	591	3	US-09-917-265-37	Sequence 37, Appl
	3	591	100.0	591	9	US-10-821-670-35	Sequence 35, Appl
c	4	591	100.0	591	9	US-10-821-670-37	Sequence 37, Appl
	5	589.4	99.7	666	3	US-09-917-265-32	Sequence 32, Appl
c	6	589.4	99.7	666	3	US-09-917-265-34	Sequence 34, Appl
	7	589.4	99.7	666	9	US-10-821-670-32	Sequence 32, Appl
c	8	589.4	99.7	666	9	US-10-821-670-34	Sequence 34, Appl
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	10	584.6	98.9	1441	6	US-10-079-616-8	Sequence 8, Appli
	11	575	97.3	669	7	US-10-041-672C-2	Sequence 2, Appli
	12	575	97.3	689	6	US-10-079-616-26	Sequence 26, Appl
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	27	535	90.5	591	9	US-10-821-670-49	Sequence 49, Appl
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c	42	512.6	86.7	1599	3	US-09-917-265-63	Sequence 63, Appl
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c	44	512.6	86.7	1599	9	US-10-821-670-63	Sequence 63, Appl
	45	501.4	84.8	762	3	US-09-826-025-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-09-917-265-35
; Sequence 35, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(591)
; OTHER INFORMATION:
US-09-917-265-35

Query Match 100.0%; Score 591; DB 3; Length 591;
Best Local Similarity 100.0%; Pred. No. 6e-178;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
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Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
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Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
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Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

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; Sequence 37, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265-37

Query Match 100.0%; Score 591; DB 3; Length 591;
Best Local Similarity 100.0%; Pred. No. 6e-178;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
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RESULT 3
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; Sequence 35, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(591)
US-10-821-670-35

Query Match 100.0%; Score 591; DB 9; Length 591;
Best Local Similarity 100.0%; Pred. No. 6e-178;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
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Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591


RESULT 4
US-10-821-670-37/c
; Sequence 37, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-37

  Query Match            100.0%;  Score 591;  DB 9;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 6e-178;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1


RESULT 5
US-09-917-265-32
; Sequence 32, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
;   OTHER INFORMATION:
US-09-917-265-32

  Query Match            99.7%;  Score 589.4;  DB 3;  Length 666;
  Best Local Similarity   99.8%;  Pred. No. 2.1e-177;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666


RESULT 6
US-09-917-265-34/c
; Sequence 34, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-34

  Query Match             99.7%;  Score 589.4;  DB 3;  Length 666;
  Best Local Similarity   99.8%;  Pred. No. 2.1e-177;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1


RESULT 7
US-10-821-670-32
; Sequence 32, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
US-10-821-670-32

  Query Match             99.7%;  Score 589.4;  DB 9;  Length 666;
  Best Local Similarity   99.8%;  Pred. No. 2.1e-177;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666
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RESULT 8
US-10-821-670-34/c
; Sequence 34, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-34

  Query Match             99.7%;  Score 589.4;  DB 9;  Length 666;
  Best Local Similarity   99.8%;  Pred. No. 2.1e-177;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1


RESULT 9
US-10-079-616-9
; Sequence 9, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;    INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 591 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-079-616-9

  Query Match             98.9%;  Score 584.6;  DB 6;  Length 591;
  Best Local Similarity   99.3%;  Pred. No. 6.8e-176;
  Matches  587;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||| |||||| |||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 591


RESULT 10
US-10-079-616-8
; Sequence 8, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;    INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1441 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-079-616-8

  Query Match            98.9%;  Score 584.6;  DB 6;  Length 1441;
  Best Local Similarity  99.3%;  Pred. No. 1.1e-175;
  Matches  587;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 277

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 337

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 397

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 457

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 517

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 577

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        578 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 637

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        638 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 697

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        698 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 757

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||| |||||| |||||
Db        758 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 808


RESULT 11
US-10-041-672C-2
; Sequence 2, Application US/10041672C
; Publication No. US20030157059A1
; GENERAL INFORMATION:
;  APPLICANT: Mologen Forschungs-, Entwicklungs- und Vetriebs GmbH
;  APPLICANT:  Universitat Zurich
;  TITLE OF INVENTION: FELINE INTERLEUKIN-12 AS IMMUNOSTIMULANT
;  FILE REFERENCE: NHL-NP-36
;  CURRENT APPLICATION NUMBER: US/10/041,672C
;  CURRENT FILING DATE:  2002-01-08
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 669
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: feline IL-12 p35
US-10-041-672C-2

  Query Match            97.3%;  Score 575;  DB 7;  Length 669;
  Best Local Similarity  98.3%;  Pred. No. 8.6e-173;
  Matches  581;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
                |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
                |||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
                |||||||||||  | ||||||||||| ||||||||||||||||||||||||||||||||
Db        496 ATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
                | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
                ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666
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RESULT 12
US-10-079-616-26
; Sequence 26, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 26:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 689 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-079-616-26

  Query Match             97.3%;  Score 575;  DB 6;  Length 689;
  Best Local Similarity   98.3%;  Pred. No. 8.7e-173;
  Matches  581;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 141

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 201

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 261

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||| | ||||||||| | ||||||||||||||||||||||||||||||||||||
Db        262 GAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 321

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 381

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 441

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||| | ||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 GCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 501

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        502 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 561

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        562 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 621

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||| |||||| |||||
Db        622 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 672
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RESULT 13
US-09-917-265-43
; Sequence 43, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
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;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
;   OTHER INFORMATION:
US-09-917-265-43

  Query Match             97.0%;  Score 573.4;  DB 3;  Length 1533;
  Best Local Similarity   98.1%;  Pred. No. 4.4e-172;
  Matches  580;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              || ||| | || || || || |||  ||| || ||||||||||||||||||||||||||||
Db        943 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1002

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1003 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1062

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1122

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1123 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1182

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1183 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1242

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1243 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1302

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1303 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1362

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1363 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1422

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1423 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1482

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1483 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533


RESULT 14
US-09-917-265-45/c
; Sequence 45, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-45

  Query Match             97.0%;  Score 573.4;  DB 3;  Length 1533;
  Best Local Similarity   98.1%;  Pred. No. 4.4e-172;
  Matches  580;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              || ||| | || || || || |||  ||| || ||||||||||||||||||||||||||||
Db        591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
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Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
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Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1


RESULT 15
US-10-821-670-43
; Sequence 43, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
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US-10-821-670-43

Query Match 97.0%; Score 573.4; DB 9; Length 1533;
Best Local Similarity 98.1%; Pred. No. 4.4e-172;
Matches 580; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
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Db        943 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1002

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1003 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1062

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1122

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1123 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1182

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1183 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1242

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1243 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1302

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1303 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1362

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1363 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1422

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1423 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1482

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1483 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
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Search completed: June 10, 2006, 18:16:33
Job time : 674.783 secs

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OM nucleic - nucleic search, using sw model

Run on: June 10, 2006, 15:46:40 ; Search time 10.2451 Seconds
(without alignments)
7321.729 Million cell updates/sec

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Perfect score: 591
Sequence: 1 aggaacctccccacacccac.....tgagctatctgaatgcttcc 591

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 253354 seqs, 63461778 residues

Total number of hits satisfying chosen parameters: 506708

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	35	5.9	2487	6	US-10-471-571A-3681	Sequence 3681, Ap
	2	33.8	5.7	1287	7	US-11-217-529-80999	Sequence 80999, A
	3	33.2	5.6	1710	7	US-11-217-529-79541	Sequence 79541, A
	4	32.4	5.5	2338	7	US-11-293-697-1600	Sequence 1600, Ap
c	5	31.4	5.3	654	6	US-10-488-619-2605	Sequence 2605, Ap
c	6	31.2	5.3	1532	6	US-10-196-749-121	Sequence 121, App
	7	30.8	5.2	588	6	US-10-953-349-2851	Sequence 2851, Ap
	8	30.8	5.2	1212	6	US-10-471-571A-4253	Sequence 4253, Ap
c	9	30.8	5.2	2920	7	US-11-293-697-683	Sequence 683, App
c	10	30.2	5.1	1422	6	US-10-953-349-31587	Sequence 31587, A
	11	30.2	5.1	1491	6	US-10-953-349-10993	Sequence 10993, A
	12	29.8	5.0	1846	7	US-11-293-697-2144	Sequence 2144, Ap
c	13	29.8	5.0	2267	7	US-11-293-697-2354	Sequence 2354, Ap
c	14	29.6	5.0	1336	6	US-10-953-349-23670	Sequence 23670, A
	15	29.4	5.0	1497	6	US-10-953-349-14136	Sequence 14136, A
	16	29.4	5.0	1587	7	US-11-217-529-223	Sequence 223, App
	17	29.2	4.9	1384	6	US-10-953-349-17610	Sequence 17610, A
c	18	29.2	4.9	10735	6	US-10-839-442A-3	Sequence 3, Appli
c	19	29	4.9	657	7	US-11-217-529-4785	Sequence 4785, Ap
c	20	29	4.9	2184	7	US-11-217-529-166643	Sequence 166643,
c	21	28.8	4.9	841	6	US-10-953-349-30929	Sequence 30929, A
	22	28.8	4.9	6826	6	US-10-505-928-330	Sequence 330, App
	23	28.6	4.8	822	6	US-10-953-349-8031	Sequence 8031, Ap
	24	28.6	4.8	1947	7	US-11-217-529-4699	Sequence 4699, Ap
c	25	28.6	4.8	2015	7	US-11-293-697-1866	Sequence 1866, Ap
	26	28.6	4.8	3869	6	US-10-511-937-2853	Sequence 2853, Ap
	27	28.4	4.8	1614	6	US-10-953-349-12483	Sequence 12483, A
c	28	28.4	4.8	1631	6	US-10-953-349-10481	Sequence 10481, A
c	29	28.2	4.8	414	7	US-11-217-529-191170	Sequence 191170,
c	30	28.2	4.8	2030	7	US-11-315-766-27	Sequence 27, Appl
	31	28	4.7	1287	7	US-11-328-070-5	Sequence 5, Appli
	32	28	4.7	1463	6	US-10-953-349-31591	Sequence 31591, A
	33	28	4.7	1704	6	US-10-953-349-11021	Sequence 11021, A
	34	27.8	4.7	648	7	US-11-217-529-842	Sequence 842, App
	35	27.8	4.7	814	6	US-10-953-349-35671	Sequence 35671, A
c	36	27.6	4.7	333	7	US-11-216-033-9	Sequence 9, Appli
c	37	27.6	4.7	672	7	US-11-251-466-47	Sequence 47, Appl
c	38	27.6	4.7	672	7	US-11-264-784-74	Sequence 74, Appl
c	39	27.6	4.7	672	7	US-11-264-737-115	Sequence 115, App
c	40	27.6	4.7	672	7	US-11-265-761-87	Sequence 87, Appl
	41	27.6	4.7	1442	6	US-10-953-349-21635	Sequence 21635, A
c	42	27.6	4.7	12918	6	US-10-501-834-4	Sequence 4, Appli
	43	27.6	4.7	151830	6	US-10-519-335-37	Sequence 37, Appl
	44	27.4	4.6	1299	7	US-11-217-529-77793	Sequence 77793, A
	45	27.4	4.6	1314	7	US-11-217-529-190	Sequence 190, App

ALIGNMENTS

RESULT 1
US-10-471-571A-3681
; Sequence 3681, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 3681
; LENGTH: 2487
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-471-571A-3681

Query Match 5.9%; Score 35; DB 6; Length 2487;
Best Local Similarity 46.2%; Pred. No. 0.15;
Matches 116; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

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Qy       328 AAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGG 387
            || ||  | | | || |   || |    ||||   |||| |  ||| | | | ||  |
Db      2144 AATATAAAACGGTTGAATCACAGGAATCTGAAGCTAAAGATAGTAAGGAAACATACGACA 2203

Qy       388 CAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAAT 447
             ||    ||   | ||    ||| | ||  |   ||  ||        |  ||   |  |
Db      2204 CAACCTTTAAAGTATATCCACAAGGTGCAACAAATGTATCGAAACATCAAGATGCACATG 2263

Qy       448 GTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACT 507
             | ||| |   ||    | | | || |||     |  ||  |  | ||| |   || |
Db      2264 GGCAAGATGATGCACATTCAATAGTACTAGATGATAAAACGATGGCATTGTACCAAGAAG 2323

Qy       508 AAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGA 567
               || ||          | ||| |  | |||  |  || | |  |  ||  ||||| | |
Db      2324 TGAAACAGCAATCAGCAAGTTCATTGTTCTTATATGATGCTTTAATAGATTATCAAAACA 2383

Qy       568 ATGATGAGCTA 578
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Db      2384 AGCATCAACTA 2394
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RESULT 2
US-11-217-529-80999
; Sequence 80999, Application US/11217529

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; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80999
;   LENGTH: 1287
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-80999

  Query Match             5.7%;  Score 33.8;  DB 7;  Length 1287;
  Best Local Similarity   53.4%;  Pred. No. 0.25;
  Matches   71;  Conservative    0;  Mismatches   62;  Indels    0;  Gaps    0;

Qy        438 GGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTT 497
              | || |||||         ||||  | |  ||    ||| ||| ||  | ||| ||| |||
Db        327 GCCCATGAATAGATCAGATGTGGATTTAACAATATACTACTCTTTTAATGAAACGGTTTT 386

Qy        498 TTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGAC 557
              | ||  | || ||    |   |   | || |||| | |   |   || |  ||| |  |
Db        387 AGAGAACCCAAATATAGGTCAAAGTGCAGTTTTTCAGGATGGCTACATCCAAGCATTAGC 446

Qy        558 CATCAATAGAATG 570
              |||||  |  | ||
Db        447 CATCAGTCCAGTG 459


RESULT 3
US-11-217-529-79541
; Sequence 79541, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79541
;   LENGTH: 1710
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (1692)..(1692)
;   OTHER INFORMATION: a, c, g, t, unknown, or other
US-11-217-529-79541

  Query Match             5.6%;  Score 33.2;  DB 7;  Length 1710;
  Best Local Similarity   55.1%;  Pred. No. 0.45;
  Matches   65;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy         77 TCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAG 136
              |||  |||   ||||| ||   ||   | | | ||| |||| ||      ||    |||||
Db        290 TCAAGAACGATCTTCAAAATTTCATGAAGAATGTAGGATTTGACCAACACAAACTCGAAG 349

Qy        137 AGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACC 194
              |  | ||  |||| |||||   | ||||    || ||| |    ||  |     ||||
Db        350 ATGTAGACGATGACGATATAGAAGAAGAATCCACTAGCTCCAAAGAATCTAAAATACC 407


RESULT 4
US-11-293-697-1600
; Sequence 1600, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1600
;   LENGTH: 2338
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1600

  Query Match             5.5%;  Score 32.4;  DB 7;  Length 2338;
  Best Local Similarity   49.4%;  Pred. No. 0.98;
  Matches   84;  Conservative    0;  Mismatches   86;  Indels    0;  Gaps    0;

Qy        304 CTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCA 363
              || ||  | | | | | |  | |  ||||||||||||  | || |         || | |
Db       1001 CTCAGGCGGAGCAAAGTGTCCATTGAGATGTACCAGTCGCAGGTGGCAAAGCTGGAGGAT 1060

Qy        364 AAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATT 423
              |  | |  |  ||  |  ||  | ||  | | ||| |  |    | ||  |
Db       1061 GATATCTACAAAGAGGCCGAAGAGAAGGCCCTGCTGAAGGAGGCCCTGGAGCGCATGGAG 1120

Qy        424 GATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAA 473
              |  ||||||  ||||    ||  |||||||| |  |    ||  |||||
Db       1121 CACCAGCTGTGCCAGGAGAAGAGGGTCAACAGGGCCATCCGGCAGCAGAA 1170


RESULT 5
US-10-488-619-2605/c
; Sequence 2605, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations W
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2605
;   LENGTH: 654
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-488-619-2605

  Query Match             5.3%;  Score 31.4;  DB 6;  Length 654;
  Best Local Similarity   51.0%;  Pred. No. 0.99;
  Matches   74;  Conservative    0;  Mismatches   71;  Indels    0;  Gaps    0;

Qy        227 CTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTT 286
              |||| | ||  | ||    |||  |   |  |  || || |||| |   || | |  ||
Db        476 CTTCAAAAGTCACCTTCACGATCTCCTCTCTGCCTTCCCGGGCCACGTAAAGGGCGACTC 417

Qy        287 TTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGT 346
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                |   |    || ||||||  || ||  ||| || | | |||| |  |    |   || |
Db        416 TGTCGTTCTCCTTGTGCCGCAGGAGGTTCTCTGCGTAGTTGAGGCGGCTGCCTCTGAACC 357

Qy        347 TCAAGGCCATGAATGCAAAGCTGTT 371
              |  ||  |    |||||  |  ||
Db        356 ACTCGGGGACATCTGCAATCCCTTT 332
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RESULT 6
US-10-196-749-121/c
; Sequence 121, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 121
; LENGTH: 1532
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-196-749-121

Query Match 5.3%; Score 31.2; DB 6; Length 1532;
Best Local Similarity 49.4%; Pred. No. 1.9;
Matches 81; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

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Qy        170 CCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTT 229
              |||  |  || | |   |  |||  ||     ||  ||| ||     ||   || ||||
Db        633 CCAACGGAGGGTACATCGACTTCACAACATCATCCACCCTGGGGCTGATCCGCTTGGCCA 574

Qy        230 CCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTA 289
              |||  |  ||| || |||| |     ||     | | |     ||  | || ||  | | |
Db        573 CCACAATGATGTCGCTGACACTGGCTGAAGTCTTCATCTTGGCCCCAGAGCCCATTGTCA 514

Qy        290 TGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
              || | ||    | |  |  |||  | |   |   ||| ||||||
Db        513 TGGCAACAAGCTTCTCTGTCAGAGTGTGACAAATCTTCAAGATG 470
```

RESULT 7
US-10-953-349-2851
; Sequence 2851, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2851
; LENGTH: 588
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-2851

Query Match 5.2%; Score 30.8; DB 6; Length 588;
Best Local Similarity 43.6%; Pred. No. 1.5;
Matches 137; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

```
Qy        231 CAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTAT 290
              | |  |||||  |||   ||  |      |   |  | | |  || |||| |    |  |
Db        161 CCGCAAGATCCATCTCCGAATCAGGATCTGAACCGGGACGTGAAGCAAGATCAGAATCTT 220

Qy        291 GACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAA 350
              |  |   | |||    |||| |   |  || |   ||||  | |   ||||||| |  |
Db        221 CAACAGAATCTGCAGATGCAGAAGGAAGAAGAAGAGGAAGGAGAAGGTGGTGGAGGTGGA 280

Qy        351 GGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACAT 410
              |    ||    | ||| |  |  ||         |  | |       | ||| | | |
Db        281 GAGTTTGTGAACGAAGATACTGGTGAGATTGGAGGGCCTAGAGGTCCTGAACCGACTCGG 340

Qy        411 GCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACA 470
              | |   |    |  | |  || |  | || |||| |    | ||  |  |||  | |
Db        341 TACGGCGATTGGGAACAACGTGGTCGATGCTCTGATTTCTGAGAGGATTCATGTATCCCT 400

Qy        471 GAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCT 530
              |   |    ||||     |     || |  |||| |  ||  ||  ||    ||  | |
Db        401 GTGTTTTAGCTTGTTCTTATATATTTCTGGGAAAAATGGAAATAAATTCGTTTTATGTGT 460

Qy        531 TCATGCTTTCAGAA 544
              | |||  ||   ||
Db        461 TTATGTATTTGCAA 474

RESULT 8
US-10-471-571A-4253
; Sequence 4253, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 4253
; LENGTH: 1212
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-471-571A-4253

Query Match 5.2%; Score 30.8; DB 6; Length 1212;
Best Local Similarity 50.7%; Pred. No. 2.2;
Matches 74; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
```

```
Qy        327 GAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAG 386
              | ||||| |  ||||    ||   |   ||| | |  ||  ||||   | | | | || |
Db         25 GCAGATGAATTAGGTTTCTTTGGTGAATATGGAGGGCAATATGTTCCAGAAACATTAATG 84

Qy        387 GCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAA 446
              |||   ||  ||  |  ||| | ||| | |   |   | ||| |   |||    | ||
Db         85 CCAGCAATTATTGAGTTGAAAAAAGCTTATAAAGAGGCAAAAGCAGACCCAGAGTTTCAA 144

Qy        447 TGTCAACAGTGTGACTGTGCCACAGA 472
              |  ||| |    ||| |    ||||
Db        145 AGAGAACTGGAATACTATTTATCAGA 170


RESULT 9
US-11-293-697-683/c
; Sequence 683, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 683
;   LENGTH: 2920
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-683

  Query Match             5.2%;  Score 30.8;  DB 7;  Length 2920;
  Best Local Similarity   53.3%;  Pred. No. 3.6;
  Matches   65;  Conservative    0;  Mismatches   57;  Indels    0;  Gaps    0;

Qy         85 ACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGAT 144
              | | || ||| |   || | ||  |  |   | || ||| | ||||     |  || |||
Db       1411 AGGATTGAGACGCTGAGCCCAATGCAGGTGATGTAGTCCAGAACTTTGTCGGTCATCGAT 1352

Qy        145 CATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 204
                || || || | ||  || ||| || |||      ||  |  |||| | | | ||
Db       1351 TTGGAGGACATGAGAATGGAAAAAGACATCACCACACTGGTGTAGTTACAGCGGCATTTC 1292

Qy        205 AC 206
              ||
Db       1291 AC 1290


RESULT 10
US-10-953-349-31587/c
; Sequence 31587, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31587
;   LENGTH: 1422
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-10-953-349-31587

  Query Match             5.1%;  Score 30.2;  DB 6;  Length 1422;
  Best Local Similarity   49.7%;  Pred. No. 3.8;
  Matches   77;  Conservative    0;  Mismatches   78;  Indels    0;  Gaps    0;

Qy        247 ATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTT 306
              || || |  | ||| ||| | | |  |||||  ||||| || | |  ||    |||
Db        430 ATGACGATGGCGAGATGCGTCGGCGTCAGAATAACCTCCTTGAAGCGGATGATGTTGGGA 371

Qy        307 AGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAG 366
              || | | | |    |   |||| ||| |  |        ||||    | ||      |  |
Db        370 TGCCGCAGCGACCTGTGGTTGATGATCTCTCTCTGCACGTTCTCATCGATCTTCTCGCCG 311

Qy        367 CTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGA 401
              | ||  ||| |    | |  |  || ||  | |||
Db        310 CGGTCGATGTACTTGACAGCGACGAGCTCGCCGGA 276


RESULT 11
US-10-953-349-10993
; Sequence 10993, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10993
;   LENGTH: 1491
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-10993

  Query Match             5.1%;  Score 30.2;  DB 6;  Length 1491;
  Best Local Similarity   51.9%;  Pred. No. 3.9;
  Matches   68;  Conservative    0;  Mismatches   63;  Indels    0;  Gaps    0;

Qy        304 CTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCA 363
              || |  || |   | | ||    ||||| | |  | || ||   || |  || |||| |
Db        929 CTGAAGAGGAAAGAGGCGGCAAAGAAGAGGAAGAAAGTCGATCCCATGATCAAGAATCCT 988

Qy        364 AAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATT 423
              ||   |  | |||  |   | | | |||  | | ||   |||| ||  ||      |
Db        989 GAGAGATACCTCGATGATCCTAAGAATATCCATTTCGAGACAAACGTGAAGAATAGGTTA 1048

Qy        424 GATGAGCTGTT 434
              | ||||||||
Db       1049 TACGAGCTGTT 1059


RESULT 12
US-11-293-697-2144
; Sequence 2144, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2144
;   LENGTH: 1846
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-2144

  Query Match             5.0%;  Score 29.8;  DB 7;  Length 1846;
  Best Local Similarity   58.4%;  Pred. No. 5.9;
  Matches   52;  Conservative    0;  Mismatches   37;  Indels    0;  Gaps    0;
```

```
Qy         26 GCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACA 85
              ||  |||  |||| |||| | |  | |    | |    | ||||    | |   |||||
Db       1494 GCGAAGGTGTGTTTCAGTACATTCAAGAGGTGCGAGAAATTCTGCACAACTTGCACAACA 1553

Qy         86 CGCTTCAGAAGGCCAGACAAACTCTAGAA 114
                | | || ||||| | ||||| | |||||
Db       1554 GGATGCAAAAGGCAAAACAAAATATAGAA 1582


RESULT 13
US-11-293-697-2354/c
; Sequence 2354, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2354
;   LENGTH: 2267
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-2354

  Query Match             5.0%;  Score 29.8;  DB 7;  Length 2267;
  Best Local Similarity   49.7%;  Pred. No. 6.6;
  Matches   76;  Conservative    0;  Mismatches   77;  Indels    0;  Gaps    0;

Qy        265 CTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGAC 324
              | ||||  ||      | |||  | ||     | ||| | |  ||  |||| |   |
Db        963 CCGGCCATCAAGTTCCCTTCTGATCTGGGCTGCTTGTTCATCTGCGTTATCCAGCTGACA 904

Qy        325 TTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAA 384
              |  |  ||  |  || ||| |||| ||    | ||| |  ||    |  || | | |
Db        903 TGCATTATAAAGGAGCTGGTGTTCTAGTTTTTTAATACCCAGAATCTGCTGAAACATTTC 844

Qy        385 AGGCAGATCTTTCTGGATCAAAACATGCTGACA 417
              |   || | || || | ||| || | | | |
Db        843 ATAGAGTTGTTCCTTGCTCAGAATAAGTTCAGA 811


RESULT 14
US-10-953-349-23670/c
; Sequence 23670, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23670
;   LENGTH: 1336
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-23670

  Query Match             5.0%;  Score 29.6;  DB 6;  Length 1336;
  Best Local Similarity   52.4%;  Pred. No. 5.7;
  Matches   65;  Conservative    0;  Mismatches   59;  Indels    0;  Gaps    0;

Qy        240 CTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCT 299
              |||| | ||||  | ||| | | ||  ||   |      |||||  | | |  |    ||
Db        640 CTCTGTAATAAGCACTGGTAATGGCACGGTACCGCTCTTGACCTGCTGTGTCCCAGATCT 581

Qy        300 GTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAA 359
              |||| ||  |||| | |       || ||||||  |      |  ||  ||||  ||   |
Db        580 GTGCTTTCACAGTCTTTCCCTCTACCTGAAGAGTTCTGGTGGCGAACTCAACTCCGATAG 521

Qy        360 TGCA 363
              || |
Db        520 TGGA 517


RESULT 15
US-10-953-349-14136
; Sequence 14136, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14136
;   LENGTH: 1497
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-14136

  Query Match             5.0%;  Score 29.4;  DB 6;  Length 1497;
  Best Local Similarity   58.6%;  Pred. No. 7;
  Matches   51;  Conservative    0;  Mismatches   36;  Indels    0;  Gaps    0;

Qy        442 CTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTAT 501
              || |||||  || || | | | |  || | |   |  |||||| || || | |||||
Db        187 CTAAATGTATACCGTATTATTTTTACAAAAAGAACGAACTTGGATGAGCCCGTTTTTTCT 246

Qy        502 AAAACTAAAATCAAGCTCTGCATACTT 528
              ||  || | |  ||  | ||  |  ||
Db        247 AACCCTTATAAGAAAGTATGAGTGGTT 273


Search completed: June 10, 2006, 18:18:57
Job time : 11.2451 secs
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2006, 22:33:03 ; Search time 3743.84 Seconds
(without alignments)
10094.706 Million cell updates/sec

Title: US-10-821-670A-35
Perfect score: 591
Sequence: 1 aggaacctccccacacccac.....tgagctatctgaatgcttcc 591

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 6366136 seqs, 31973710525 residues

Word size : 1

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Maximum DB seq length: 2000000000

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1: gb_env:*
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10: gb_vi:*
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13: gb_in:*
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15: gb_ba:*

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SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		591	100.0	591	2	AR595954	AR595954 Sequence
2	c	591	100.0	591	2	AR595955	AR595955 Sequence
3		591	100.0	669	14	FCIL12P35	Y07761 Felis catus
4		558	94.4	1533	2	AR595959	AR595959 Sequence
5	c	558	94.4	1533	2	AR595960	AR595960 Sequence
6		558	94.4	1599	2	AR595956	AR595956 Sequence
7	c	558	94.4	1599	2	AR595957	AR595957 Sequence
8		540	91.4	666	2	AR595952	AR595952 Sequence
9	c	540	91.4	666	2	AR595953	AR595953 Sequence
10		534	90.4	669	14	FCU83185	U83185 Felis catus
11		507	85.8	561	2	AR596007	AR596007 Sequence
12	c	507	85.8	561	2	AR596008	AR596008 Sequence
13		480	81.2	591	2	AR242439	AR242439 Sequence
14		480	81.2	591	2	AR280207	AR280207 Sequence
15		480	81.2	591	2	AR322422	AR322422 Sequence
16		480	81.2	1441	2	AR242438	AR242438 Sequence
17		480	81.2	1441	2	AR280206	AR280206 Sequence
18		480	81.2	1441	2	AR322421	AR322421 Sequence
19		253	42.8	285	14	AF054605	AF054605 Felis cat
20		228	38.6	669	2	AX076201	AX076201 Sequence
21		228	38.6	669	2	AX076483	AX076483 Sequence
22		228	38.6	4201	2	AX076477	AX076477 Sequence
23		189	32.0	689	2	AR242451	AR242451 Sequence
24		189	32.0	689	2	AR280219	AR280219 Sequence
25		189	32.0	689	2	AR322434	AR322434 Sequence
26		178	30.1	660	2	AX154615	AX154615 Sequence
27		120	20.3	660	2	AX154616	AX154616 Sequence
28		115	19.5	660	2	AX154614	AX154614 Sequence
29		115	19.5	660	2	AX154621	AX154621 Sequence
30		102	17.3	660	2	AX154619	AX154619 Sequence
31		98	16.6	657	8	AY191828	AY191828 Synthetic
32		98	16.6	660	2	AX154617	AX154617 Sequence
33		84	14.2	660	2	AX154620	AX154620 Sequence
34		81	13.7	591	2	BD171284	BD171284 Novel can
35		81	13.7	591	2	AR595963	AR595963 Sequence
36	c	81	13.7	591	2	AR595964	AR595964 Sequence
37		81	13.7	666	2	AR595961	AR595961 Sequence
38	c	81	13.7	666	2	AR595962	AR595962 Sequence
39		81	13.7	669	2	AR151062	AR151062 Sequence
40		81	13.7	669	2	AR151072	AR151072 Sequence
41		81	13.7	669	2	BD014654	BD014654 Process f
42		81	13.7	669	2	BD014664	BD014664 Process f
43		81	13.7	669	2	E15018	E15018 Canine mRNA
44		81	13.7	669	2	AR316461	AR316461 Sequence
45		81	13.7	669	2	AR316471	AR316471 Sequence
46		81	13.7	669	14	CFU49085	U49085 Canis famil
47		81	13.7	1282	2	BD171283	BD171283 Novel can
48		81	13.7	1455	2	AR596009	AR596009 Sequence
49	c	81	13.7	1455	2	AR596010	AR596010 Sequence
50		81	13.7	1533	2	AR595973	AR595973 Sequence
51	c	81	13.7	1533	2	AR595974	AR595974 Sequence
52		81	13.7	1599	2	AR595971	AR595971 Sequence
53	c	81	13.7	1599	2	AR595972	AR595972 Sequence
54		71	12.0	71	2	AX076207	AX076207 Sequence
55		65	11.0	660	2	AR008951	AR008951 Sequence
56		65	11.0	660	2	BD007071	BD007071 IL-12 gen
57		65	11.0	660	2	BD007079	BD007079 Gene expr
58		65	11.0	660	2	BD136037	BD136037 Interfero
59		65	11.0	660	2	I28592	I28592 Sequence 3
60		65	11.0	660	2	AX154618	AX154618 Sequence
61		65	11.0	660	2	AX154634	AX154634 Sequence
62		65	11.0	702	2	CQ829447	CQ829447 Sequence
63		65	11.0	721	2	AR052862	AR052862 Sequence
64		65	11.0	721	2	AR288174	AR288174 Sequence
65		65	11.0	721	2	AR567161	AR567161 Sequence
66		65	11.0	762	2	BD105971	BD105971 Animal mo
67		65	11.0	762	2	CQ803343	CQ803343 Sequence
68		65	11.0	762	2	AR533401	AR533401 Sequence
69		65	11.0	762	5	AF101062	AF101062 Homo sapi
70		65	11.0	780	5	MMU19842	U19842 Macaca mula
71		65	11.0	823	5	AF180562	AF180562 Homo sapi
72		65	11.0	856	2	BD165801	BD165801 Antibody
73		65	11.0	1020	2	CQ716168	CQ716168 Sequence
74		65	11.0	1021	5	BC104982	BC104982 Homo sapi
75		65	11.0	1021	5	BC104984	BC104984 Homo sapi
76		65	11.0	1026	2	AR091390	AR091390 Sequence
77		65	11.0	1026	2	AR380496	AR380496 Sequence
78		65	11.0	1026	5	HUMCLMF35	M65271 Human cytot
79		65	11.0	1287	2	AR393790	AR393790 Sequence
80		65	11.0	1287	2	AX084108	AX084108 Sequence
81		65	11.0	1316	2	AR050785	AR050785 Sequence
82		65	11.0	1316	2	AR212036	AR212036 Sequence
83		65	11.0	1316	5	HUMNKSFP35	M65291 Human natur
84		65	11.0	1364	2	AR082685	AR082685 Sequence
85		65	11.0	1364	2	AR122961	AR122961 Sequence
86		65	11.0	1364	2	I28326	I28326 Sequence 3
87		65	11.0	1364	2	I89771	I89771 Sequence 3
88		65	11.0	1395	2	AR309637	AR309637 Sequence
89		65	11.0	1444	2	CS032085	CS032085 Sequence
90		65	11.0	1444	2	CS041037	CS041037 Sequence
91		65	11.0	1444	2	CS143811	CS143811 Sequence

92	65	11.0	1560	2	AR091395	AR091395 Sequence
93	65	11.0	1623	2	AR091394	AR091394 Sequence
94	65	11.0	1645	2	A92078	A92078 Sequence 2
95	65	11.0	1645	2	AR230689	AR230689 Sequence
96	65	11.0	3205	2	CS131489	CS131489 Sequence
97	65	11.0	5686	2	BD136048	BD136048 Interfero
98	65	11.0	6139	2	AR091393	AR091393 Sequence
99	65	11.0	11792	5	AF404773	AF404773 Homo sapi
100	65	11.0	157079	5	AC010370	AC010370 Homo sapi
101	65	11.0	176108	5	AC026118	AC026118 Homo sapi
102	65	11.0	300140	12	AC129109	AC129109 Homo sapi
103	60	10.2	666	2	AX154612	AX154612 Sequence
104	60	10.2	666	2	AX154613	AX154613 Sequence
105	55	9.3	786	5	CTU19835	U19835 Cercocebus
106	50	8.5	669	14	ECIL12P35	Y11130 Equus cabal
107	50	8.5	817	14	AY686642	AY686642 Equus cab
108	50	8.5	1626	8	AF401989	AF401989 Synthetic
c 109	45	7.6	76	2	AX076205	AX076205 Sequence
c 110	45	7.6	76	2	AX076208	AX076208 Sequence
111	45	7.6	669	14	AB107653	AB107653 Lama glam
112	45	7.6	669	14	AB246672	AB246672 Camelus b
113	43	7.3	79	2	AR242449	AR242449 Sequence
114	43	7.3	79	2	AR280217	AR280217 Sequence
115	43	7.3	79	2	AR322432	AR322432 Sequence
116	41	6.9	690	14	AB246272	AB246272 Bubalus c
117	41	6.9	690	14	AB246359	AB246359 Bubalus b
118	41	6.9	690	14	BTU14416	U14416 Bos taurus
119	41	6.9	703	2	E35793	E35793 Process for
120	38	6.4	1426	14	PIGIL12PSU	L35765 Sus scrofa
121	37	6.3	785	5	AY234219	AY234219 Papio anu
c 122	34	5.8	559	7	BV429425	BV429425 S237P6482
123	30	5.1	672	6	AF288520	AF288520 Marmota m
124	30	5.1	672	6	MMIL12P35	X97018 M.monax mRN
125	29	4.9	618	14	AY603407	AY603407 Capra hir
126	29	4.9	666	14	AF173557	AF173557 Ovis arie
127	29	4.9	666	14	AY232819	AY232819 Bubalus b
128	29	4.9	666	14	CEU57751	U57751 Cervus elap
129	29	4.9	690	14	AB246352	AB246352 Bubalus b
130	29	4.9	690	14	AF003542	AF003542 Capra hir
131	29	4.9	711	14	BTA271034	AJ271034 Bos tauru
132	29	4.9	714	14	OAR271035	AJ271035 Ovis arie
133	27	4.6	39	2	AR595997	AR595997 Sequence
c 134	27	4.6	322	7	BV094414	BV094414 RPAMMSEQ0
135	27	4.6	582	2	AR393785	AR393785 Sequence
136	27	4.6	582	2	AX084103	AX084103 Sequence
137	27	4.6	660	2	E26662	E26662 Improved me
138	27	4.6	700	6	S82412S4	S82418 interleukin
139	27	4.6	713	2	AR069652	AR069652 Sequence
140	27	4.6	713	6	AF128212	AF128212 Mus muscu
141	27	4.6	713	6	AF128213	AF128213 Mus muscu
142	27	4.6	786	6	AF128210	AF128210 Mus muscu
143	27	4.6	786	6	AF128211	AF128211 Mus muscu
144	27	4.6	793	6	AF177031	AF177031 Rattus no
145	27	4.6	827	6	AF421396	AF421396 Sigmodon
146	27	4.6	1265	6	MUSIL35A	M86672 Mus musculu
147	27	4.6	1278	2	AR393789	AR393789 Sequence
148	27	4.6	1278	2	AX084107	AX084107 Sequence
149	27	4.6	1569	2	AR393796	AR393796 Sequence
150	27	4.6	1569	2	AX084114	AX084114 Sequence
151	27	4.6	1669	8	AF411293	AF411293 Synthetic
152	27	4.6	2013	2	AR393795	AR393795 Sequence
153	27	4.6	2013	2	AX084113	AX084113 Sequence
154	27	4.6	2438	2	CQ812173	CQ812173 Sequence
155	27	4.6	2709	2	AR393797	AR393797 Sequence
156	27	4.6	2709	2	AX084115	AX084115 Sequence
157	27	4.6	5252	2	CQ803341	CQ803341 Sequence
158	27	4.6	5966	2	BD136050	BD136050 Interfero
159	27	4.6	9049	2	CQ803350	CQ803350 Sequence
160	27	4.6	10633	2	CQ803349	CQ803349 Sequence
161	27	4.6	11746	2	CQ803348	CQ803348 Sequence
162	27	4.6	38246	2	CQ803351	CQ803351 Sequence
c 163	27	4.6	195059	6	AC121306	AC121306 Mus muscu
c 164	27	4.6	223879	12	AC111877	AC111877 Rattus no
165	26	4.4	660	2	BD007080	BD007080 Gene expr
166	26	4.4	660	2	BD007081	BD007081 Gene expr
167	26	4.4	660	2	BD136038	BD136038 Interfero
168	26	4.4	660	2	BD136039	BD136039 Interfero
169	25	4.2	1239	6	AB085791	AB085791 Mesocrice
c 170	24	4.1	27	2	AR595996	AR595996 Sequence
c 171	24	4.1	36	2	AR242450	AR242450 Sequence
c 172	24	4.1	36	2	AR280218	AR280218 Sequence
c 173	24	4.1	36	2	AR322433	AR322433 Sequence
c 174	24	4.1	41	2	AR595998	AR595998 Sequence
c 175	24	4.1	144	14	AY388980S3	AY388982 Sus scrof
176	23	3.9	666	6	AB025723	AB025723 Cavia por
177	22	3.7	146	14	AY575615	AY575615 Ovis arie
178	22	3.7	146	14	AY575616	AY575616 Ovis arie
179	22	3.7	586	7	BV209307	BV209307 IL12A_306
180	22	3.7	221805	6	AC105515	AC105515 Rattus no
c 181	22	3.7	225611	12	AC111446	AC111446 Rattus no
c 182	22	3.7	237532	6	AC094950	AC094950 Rattus no
183	21	3.6	32	2	AR090263	AR090263 Sequence
184	21	3.6	32	2	AR197298	AR197298 Sequence
185	21	3.6	32	2	AR259452	AR259452 Sequence
c 186	21	3.6	733	7	BV616987	BV616987 S216P6464
187	21	3.6	60511	5	HS618F1	AL023878 Human DNA
188	21	3.6	114233	5	AP000783	AP000783 Homo sapi
c 189	21	3.6	136388	14	AC146679	AC146679 Felis cat
c 190	21	3.6	143814	12	AC151632	AC151632 Felis cat
c 191	21	3.6	158375	12	AC080039	AC080039 Homo sapi
c 192	21	3.6	163846	5	AC136619	AC136619 Homo sapi
193	21	3.6	168721	5	AC136431	AC136431 Homo sapi
194	21	3.6	173912	12	AC141075	AC141075 Homo sapi
195	21	3.6	175785	12	AC138897	AC138897 Homo sapi
c 196	21	3.6	179245	5	HUAC002492	AC002492 Human Chr
197	21	3.6	185030	5	AC008785	AC008785 Homo sapi
c 198	21	3.6	186535	12	AL589793	AL589793 Homo sapi
c 199	21	3.6	187721	5	AC126763	AC126763 Homo sapi
c 200	21	3.6	188256	12	AC160269	AC160269 Bos tauru

ALIGNMENTS

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RESULT 1
AR595954
LOCUS       AR595954                 591 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 35 from patent US 6818444.
ACCESSION   AR595954
VERSION     AR595954.1  GI:56646935
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 35 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 591;  DB 2;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-310;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
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Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
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Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
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Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
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Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591


RESULT 2
AR595955/c
LOCUS       AR595955                591 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 37 from patent US 6818444.
ACCESSION   AR595955
VERSION     AR595955.1  GI:56646936
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 37 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 591;  DB 2;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-310;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1


RESULT 3
FCIL12P35
LOCUS       FCIL12P35               669 bp    mRNA    linear   MAM 18-APR-2005
DEFINITION  Felis catus mRNA for interleukin-12 p35 chain.
ACCESSION   Y07761
VERSION     Y07761.1  GI:2102662
KEYWORDS    interleukin-12 subunit p35.
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1
  AUTHORS   Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
  TITLE     Molecular cloning of cat interleukin-12
  JOURNAL   Immunogenetics 45 (6), 462-463 (1997)
   PUBMED   9089110
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Schijns,V.E.C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
            Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
            Utrecht, NETHERLANDS
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Felis catus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
                     /cell_type="lymphocyte"
                     /tissue_type="peripheral blood"
     gene            1. .669
                     /gene="IL-12.p35"
     CDS             1. .669
                     /gene="IL-12.p35"
                     /function="heterodimer with IL-12 p40 chain"
                     /codon_start=1
                     /product="interleukin-12 p35 chain"
                     /protein_id="CAA69067.1"
                     /db_xref="GI:2102663"
                     /db_xref="GOA:O02743"
                     /db_xref="InterPro:IPR004281"
                     /db_xref="InterPro:IPR009079"
                     /db_xref="UniProtKB/Swiss-Prot:O02743"
                     /translation="MCPPRGLLLVTILVLLNHLDHLSLARNLPTPTPSPGMFQCLNHS
                     QTLLRAISNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
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                    LNAS"
ORIGIN

  Query Match           100.0%;  Score 591;  DB 14;  Length 669;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-310;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666


RESULT 4
AR595959
LOCUS       AR595959               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 43 from patent US 6818444.
ACCESSION   AR595959
VERSION     AR595959.1  GI:56646940
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 43 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           94.4%;  Score 558;  DB 2;  Length 1533;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-292;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        976 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 1035

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1036 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 1095

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1096 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 1155

Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1156 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 1215

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1216 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 1275

Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1276 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 1335

Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1336 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 1395

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1396 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 1455

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1456 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 1515

Qy        574 AGCTATCTGAATGCTTCC 591
              |||||||||||||||||
Db       1516 AGCTATCTGAATGCTTCC 1533


RESULT 5
AR595960/c
LOCUS       AR595960               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 45 from patent US 6818444.
ACCESSION   AR595960
VERSION     AR595960.1  GI:56646941
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 45 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           94.4%;  Score 558;  DB 2;  Length 1533;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-292;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        574 AGCTATCTGAATGCTTCC 591
              ||||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1
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RESULT 6
AR595956
LOCUS AR595956 1599 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 38 from patent US 6818444.
ACCESSION AR595956
VERSION AR595956.1 GI:56646937
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1599)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 38 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .1599
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 94.4%; Score 558; DB 2; Length 1599;
Best Local Similarity 100.0%; Pred. No. 1.7e-292;
Matches 558; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1042 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 1101

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1102 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 1161

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1162 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 1221

Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1222 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 1281

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1282 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 1341

Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1342 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 1401

Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1402 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 1461

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1462 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 1521

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1522 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 1581

Qy        574 AGCTATCTGAATGCTTCC 591
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Db       1582 AGCTATCTGAATGCTTCC 1599
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RESULT 7
AR595957/c
LOCUS AR595957 1599 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 40 from patent US 6818444.
ACCESSION AR595957
VERSION AR595957.1 GI:56646938
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1599)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 40 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .1599
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 94.4%; Score 558; DB 2; Length 1599;
Best Local Similarity 100.0%; Pred. No. 1.7e-292;
Matches 558; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259
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Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        574 AGCTATCTGAATGCTTCC 591
              ||||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1


RESULT 8
AR595952
LOCUS       AR595952                 666 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 32 from patent US 6818444.
ACCESSION   AR595952
VERSION     AR595952.1  GI:56646933
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 32 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             91.4%;  Score 540;  DB 2;  Length 666;
  Best Local Similarity   99.8%;  Pred. No. 1.2e-282;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666


RESULT 9
AR595953/c
LOCUS       AR595953                 666 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 34 from patent US 6818444.
ACCESSION   AR595953
VERSION     AR595953.1  GI:56646934
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 34 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             91.4%;  Score 540;  DB 2;  Length 666;
  Best Local Similarity   99.8%;  Pred. No. 1.2e-282;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        111 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1


RESULT 10
FCU83185
LOCUS       FCU83185                669 bp    mRNA    linear   MAM 16-JUL-1999
DEFINITION  Felis catus interleukin-12 p35 subunit (IL-12) mRNA, complete cds.
ACCESSION   U83185
VERSION     U83185.1  GI:2735052
KEYWORDS    .
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Nucleotide and predicted peptide sequence of feline interleukin-12
            (IL-12)
  JOURNAL   DNA Seq. 8 (1-2), 77-82 (1997)
   PUBMED   9522125
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal
            Veterinary Medicine, University of Zurich, Winterthurerstrasse 260,
            Zurich, ZH 8057, Switzerland
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Felis catus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
     CDS             1. .669
                     /note="cytokine"
                     /codon_start=1
                     /product="interleukin-12 p35 subunit"
                     /protein_id="AAB93836.1"
                     /db_xref="GI:2735053"
                     /translation="MCPPRGLLLVTILVLLNHLDHLSLARNLPTPTPSPGMFQCLNHS
                     QTLLRAISNTLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
                     REISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAMNAKLLMDPKRQIFLDQ
                     NMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSY
                     LNSS"
ORIGIN

  Query Match             90.4%;  Score 534;  DB 14;  Length 669;
  Best Local Similarity   99.8%;  Pred. No. 2.2e-279;
  Matches  584;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 585
              |||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660


RESULT 11
AR596007
LOCUS       AR596007                561 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 101 from patent US 6818444.
ACCESSION   AR596007
VERSION     AR596007.1  GI:56646988
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 561)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 101 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .561
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             85.8%;  Score 507;  DB 2;  Length 561;
  Best Local Similarity   99.8%;  Pred. No. 1.2e-264;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183

Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303

Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363

Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
                |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543

Qy        574 AGCTATCTGAATGCTTCC 591
                ||||||||||||||||||
Db        544 AGCTATCTGAATGCTTCC 561


RESULT 12
AR596008/c
LOCUS       AR596008                561 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 103 from patent US 6818444.
ACCESSION   AR596008
VERSION     AR596008.1  GI:56646989
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 561)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 103 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .561
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             85.8%;  Score 507;  DB 2;  Length 561;
  Best Local Similarity   99.8%;  Pred. No. 1.2e-264;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
                |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        574 AGCTATCTGAATGCTTCC 591
                ||||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1


RESULT 13
AR242439
LOCUS       AR242439                591 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 9 from patent US 6472509.
ACCESSION   AR242439
VERSION     AR242439.1  GI:27288856
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 9 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             81.2%;  Score 480;  DB 2;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-250;
  Matches  480;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTTATGACGACCCTG 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTTATGACGACCCTG 300

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480


RESULT 14
AR280207
LOCUS       AR280207                591 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 9 from patent US 6518045.
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ACCESSION   AR280207
VERSION     AR280207.1  GI:29715597
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 9 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             81.2%;  Score 480;  DB 2;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-250;
  Matches  480;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480


RESULT 15
AR322422
LOCUS       AR322422                 591 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 9 from patent US 6566097.
ACCESSION   AR322422
VERSION     AR322422.1  GI:33708175
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 9 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             81.2%;  Score 480;  DB 2;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-250;
  Matches  480;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480


RESULT 16
AR242438
LOCUS       AR242438                 1441 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 8 from patent US 6472509.
ACCESSION   AR242438
VERSION     AR242438.1  GI:27288855
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1441)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 8 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .1441
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             81.2%;  Score 480;  DB 2;  Length 1441;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-250;
  Matches  480;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 277
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Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 337

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 397

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 457

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 517

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 577

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        578 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 637

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        638 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 697
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RESULT 17
AR280206
LOCUS AR280206 1441 bp mRNA linear PAT 10-APR-2003
DEFINITION Sequence 8 from patent US 6518045.
ACCESSION AR280206
VERSION AR280206.1 GI:29715596
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1441)
AUTHORS Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
TITLE Feline cytokine protein
JOURNAL Patent: US 6518045-A 8 11-FEB-2003;
Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
Kumamoto-ken;
EPX;
FEATURES Location/Qualifiers
source 1. .1441
/organism="unknown"
/mol_type="mRNA"
ORIGIN

Query Match 81.2%; Score 480; DB 2; Length 1441;
Best Local Similarity 100.0%; Pred. No. 6.2e-250;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 277

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 337

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 397

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 457

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 517

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 577

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        578 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 637

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        638 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 697
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RESULT 18
AR322421
LOCUS AR322421 1441 bp mRNA linear PAT 17-AUG-2003
DEFINITION Sequence 8 from patent US 6566097.
ACCESSION AR322421
VERSION AR322421.1 GI:33708174
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1441)
AUTHORS Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
TITLE Feline cytokine protein
JOURNAL Patent: US 6566097-A 8 20-MAY-2003;
Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;;
EPX;
FEATURES Location/Qualifiers
source 1. .1441
/organism="unknown"
/mol_type="mRNA"
ORIGIN

Query Match 81.2%; Score 480; DB 2; Length 1441;
Best Local Similarity 100.0%; Pred. No. 6.2e-250;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 277

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 337

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 397

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 457

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 517

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 577

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        578 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 637

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
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Db        638 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 697


RESULT 19
AF054605
LOCUS       AF054605                 285 bp    mRNA    linear   MAM 26-JUL-2000
DEFINITION  Felis catus interleukin 12 p35 subunit mRNA, partial cds.
ACCESSION   AF054605
VERSION     AF054605.1  GI:3126818
KEYWORDS    .
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Harley,R., Helps,C.R., Harbour,D.A., Gruffydd-Jones,T.J. and
            Day,M.J.
  TITLE     Cytokine mRNA expression in lesions in cats with chronic
            gingivostomatitis
  JOURNAL   Clin. Diagn. Lab. Immunol. 6 (4), 471-478 (1999)
   PUBMED   10391845
REFERENCE   2  (bases 1 to 285)
  AUTHORS   Harley,R., Helps,C.R., Gruffydd-Jones,T.J., Day,M.J. and
            Harbour,D.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-1998) Clinical Veterinary Science, University of
            Bristol, Langford House, Langford, Bristol BS40 7DU, U.K.
FEATURES             Location/Qualifiers
     source          1. .285
                     /organism="Felis catus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
                     /cell_line="FL4"
                     /cell_type="T cell"
                     /note="persistant FIV infection"
     CDS             <1. .>285
                     /codon_start=3
                     /product="interleukin 12 p35 subunit"
                     /protein_id="AAC15978.1"
                     /db_xref="GI:3126819"
                     /translation="LLRAISNTLHKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLP
                     LELTMNESCLASREISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVE"
ORIGIN

  Query Match             42.8%;  Score 253;  DB 14;  Length 285;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-126;
  Matches  253;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          33 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 92

Qy         154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          93 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 152

Qy         214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         153 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 212

Qy         274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         213 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 272

Qy         334 TACCAGGTGGAGT 346
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Db         273 TACCAGGTGGAGT 285


RESULT 20
AX076201
LOCUS       AX076201                 669 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 2 from Patent WO0104155.
ACCESSION   AX076201
VERSION     AX076201.1  GI:12710826
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 2 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="feline IL-12 p35"
ORIGIN

  Query Match             38.6%;  Score 228;  DB 2;  Length 669;
  Best Local Similarity   99.1%;  Pred. No. 1.8e-112;
  Matches  428;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy           1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy          61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy         121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         196 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy         181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
               |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db         256 GAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy         241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
               |||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db         316 TCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy         301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy         361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy         421 ATTGATGAGCTG 432
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Db         496 ATTGATGAGCTG 507


RESULT 21
AX076483
LOCUS       AX076483                 669 bp    DNA     linear   PAT 07-FEB-2001
DEFINITION  Sequence 9 from Patent WO0104280.
ACCESSION   AX076483
VERSION     AX076483.1  GI:12711035
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
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            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 9 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Sequence coding for SEQ ID NO 3, IL-12 p35"
ORIGIN

  Query Match            38.6%;  Score 228;  DB 2;  Length 669;
  Best Local Similarity   99.1%;  Pred. No. 1.8e-112;
  Matches  428;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              |||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATTGATGAGCTG 432
              ||||||||||||
Db        496 ATTGATGAGCTG 507


RESULT 22
AX076477
LOCUS       AX076477               4201 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 3 from Patent WO0104280.
ACCESSION   AX076477
VERSION     AX076477.1  GI:12711029
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 3 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .4201
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="IL-12p35 (pMOLfIL-12p35 (e-,_e31-)clone61)"
ORIGIN

  Query Match            38.6%;  Score 228;  DB 2;  Length 4201;
  Best Local Similarity   99.1%;  Pred. No. 1.7e-112;
  Matches  428;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3122 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 3181

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3182 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 3241

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3242 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 3301

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       3302 GAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 3361

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              |||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db       3362 TCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCTTTTATGACGACCCTG 3421

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3422 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 3481

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3482 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 3541

Qy        421 ATTGATGAGCTG 432
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Db       3542 ATTGATGAGCTG 3553


RESULT 23
AR242451
LOCUS       AR242451               689 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 26 from patent US 6472509.
ACCESSION   AR242451
VERSION     AR242451.1  GI:27288868
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 26 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .689
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match            32.0%;  Score 189;  DB 2;  Length 689;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-91;
  Matches  189;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 141

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 201
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Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 261

Qy        181 GAGGCCTGC 189
              |||||||||
Db        262 GAGGCCTGC 270


RESULT 24
AR280219
LOCUS       AR280219                689 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 26 from patent US 6518045.
ACCESSION   AR280219
VERSION     AR280219.1  GI:29715609
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 26 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .689
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             32.0%;  Score 189;  DB 2;  Length 689;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-91;
  Matches  189;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 141

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 201

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 261

Qy        181 GAGGCCTGC 189
              |||||||||
Db        262 GAGGCCTGC 270


RESULT 25
AR322434
LOCUS       AR322434                689 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 26 from patent US 6566097.
ACCESSION   AR322434
VERSION     AR322434.1  GI:33708187
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 26 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .689
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             32.0%;  Score 189;  DB 2;  Length 689;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-91;
  Matches  189;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 141

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 201

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 261

Qy        181 GAGGCCTGC 189
              |||||||||
Db        262 GAGGCCTGC 270


RESULT 26
AX154615
LOCUS       AX154615                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 19 from Patent WO0140257.
ACCESSION   AX154615
VERSION     AX154615.1  GI:14536190
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 19 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match             30.1%;  Score 178;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-85;
  Matches  178;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        237 GATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGAC 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 GATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGAC 362

Qy        297 CCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCAT 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 CCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCAT 422

Qy        357 GAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 GAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480


RESULT 27
AX154616
LOCUS       AX154616                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 20 from Patent WO0140257.
ACCESSION   AX154616
VERSION     AX154616.1  GI:14536191
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
```

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            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 20 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match             20.3%;  Score 120;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-53;
  Matches  120;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        295 ACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCC 354
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCC 420

Qy        355 ATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480


RESULT 28
AX154614
LOCUS       AX154614                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 18 from Patent WO0140257.
ACCESSION   AX154614
VERSION     AX154614.1  GI:14536189
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 18 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match             19.5%;  Score 115;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-51;
  Matches  115;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 216

Qy        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAA 205
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        217 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAA 271


RESULT 29
AX154621
LOCUS       AX154621                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 25 from Patent WO0140257.
ACCESSION   AX154621
VERSION     AX154621.1  GI:14536196
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 25 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match             19.5%;  Score 115;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-51;
  Matches  115;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 216

Qy        151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAA 205
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        217 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAA 271


RESULT 30
AX154619
LOCUS       AX154619                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 23 from Patent WO0140257.
ACCESSION   AX154619
VERSION     AX154619.1  GI:14536194
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 23 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match             17.3%;  Score 102;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-44;
  Matches  102;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        313 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 438

Qy        373 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 414
              |||||||||||||||||||||||||||||||||||||||||
Db        439 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480


RESULT 31
AY191828
LOCUS       AY191828                657 bp    mRNA    linear   SYN 04-FEB-2003
DEFINITION  Synthetic construct evolved IL-12 p35 precursor, mRNA, partial cds.
ACCESSION   AY191828
VERSION     AY191828.1  GI:27729523
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 657)
```

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  AUTHORS   Leong,S.R., Chang,J.C.C., Ong,R., Dawes,G., Stemmer,W.P.C. and
            Punnonen,J.
  TITLE     Optimized expression and specific activity of IL-12 by directed
            molecular evolution
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (3), 1163-1168 (2003)
   PUBMED   12529500
REFERENCE   2  (bases 1 to 657)
  AUTHORS   Leong,S.R., Chang,J.C.C., Ong,R., Dawes,G., Stemmer,W.P.C. and
            Punnonen,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-DEC-2002) Vaccines, Maxygen, Inc., 515 Galveston
            Drive, Redwood City, CA 94063, USA
FEATURES             Location/Qualifiers
     source          1. .657
                     /organism="synthetic construct"
                     /mol_type="mRNA"
                     /db_xref="taxon:32630"
     CDS             1. .>657
                     /codon_start=1
                     /transl_table=11
                     /product="evolved IL-12 p35 precursor"
                     /protein_id="AAO19111.1"
                     /db_xref="GI:27729524"
                     /translation="MCPARSLLLVATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNL
                     LRAVSNMLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASRGI
                     SLITNGSCLASRKTSFMTTLCLGSIYEDLKMYQVEFKTMNAKLLMNPKRQIFLDQNML
                     TAIDELLQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNS
                     S"
     sig_peptide     1. .66
     mat_peptide     67. .657
                     /product="evolved IL-12 p35"
ORIGIN

  Query Match            16.6%;  Score 98;  DB 8;  Length 657;
  Best Local Similarity  100.0%;  Pred. No. 1.5e-41;
  Matches   98;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         157 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 216

Qy         151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 188
               ||||||||||||||||||||||||||||||||||||||
Db         217 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 254


RESULT 32
AX154617
LOCUS       AX154617                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 21 from Patent WO0140257.
ACCESSION   AX154617
VERSION     AX154617.1  GI:14536192
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 21 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match            16.6%;  Score 98;  DB 2;  Length 660;
  Best Local Similarity  100.0%;  Pred. No. 1.5e-41;
  Matches   98;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 150
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         157 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 216

Qy         151 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 188
               ||||||||||||||||||||||||||||||||||||||
Db         217 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 254


RESULT 33
AX154620
LOCUS       AX154620                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 24 from Patent WO0140257.
ACCESSION   AX154620
VERSION     AX154620.1  GI:14536195
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 24 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match            14.2%;  Score 84;  DB 2;  Length 660;
  Best Local Similarity  99.3%;  Pred. No. 6.3e-34;
  Matches  134;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         237 GATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGAC 296
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         303 GATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGAC 362

Qy         297 CCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCAT 356
               |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db         363 CCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCAT 422

Qy         357 GAATGCAAAGCTGTT 371
               |||||||||||||||
Db         423 GAATGCAAAGCTGTT 437


RESULT 34
BD171284
LOCUS       BD171284                591 bp    DNA     linear   PAT 18-FEB-2003
DEFINITION  Novel canine cytokine protein.
ACCESSION   BD171284
VERSION     BD171284.1  GI:28412574
KEYWORDS    JP 2002241398-A/4.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Imamura,T., Maeda,H., Tokiyoshi,Y. and Eda,Y.
  TITLE     Novel canine cytokine protein
  JOURNAL   Patent: JP 2002241398-A 4 28-AUG-2002;
            CHEMO SERO THERAPEUT RES INST
COMMENT     OS   Canine splenocyte
            PN   JP 2002241398-A/4
            PD   28-AUG-2002
            PF   03-JUN-1997 JP 1997161936
            PI   TAKAYUKI IMAMURA,HIROAKI MAEDA,YUKIO TOKIYOSHI,YASUYUKI EDA PC
              C07K14/52,A61K38/00,A61K39/395,C07K16/24,C12N5/10,C12N15/09, PC
            C12P21/02//
            PC   C12P21/08,(C12P21/02,C12R1:91),A61K37/02,C12N5/00,C12N15/00 CC
              Strandedness: Double;
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           CC   Topology: Linear;
           FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             13.7%;  Score 81;  DB 2;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        223 CTGGCTTCCAGAGAGATCTCT 243


RESULT 35
AR595963
LOCUS       AR595963                591 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 49 from patent US 6818444.
ACCESSION   AR595963
VERSION     AR595963.1  GI:56646944
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 49 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             13.7%;  Score 81;  DB 2;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        223 CTGGCTTCCAGAGAGATCTCT 243


RESULT 36
AR595964/c
LOCUS       AR595964                591 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 51 from patent US 6818444.
ACCESSION   AR595964
VERSION     AR595964.1  GI:56646945
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 51 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             13.7%;  Score 81;  DB 2;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 37
AR595961
LOCUS       AR595961                666 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 46 from patent US 6818444.
ACCESSION   AR595961
VERSION     AR595961.1  GI:56646942
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 46 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             13.7%;  Score 81;  DB 2;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 38
AR595962/c
LOCUS       AR595962                666 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 48 from patent US 6818444.
ACCESSION   AR595962
VERSION     AR595962.1  GI:56646943
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 48 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             13.7%;  Score 81;  DB 2;  Length 666;
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  Best Local Similarity   100.0%;  Pred. No. 2.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 39
AR151062
LOCUS       AR151062                669 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 2 from patent US 6231850.
ACCESSION   AR151062
VERSION     AR151062.1  GI:15117112
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12
  JOURNAL   Patent: US 6231850-A 2 15-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            13.7%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 40
AR151072
LOCUS       AR151072                669 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 12 from patent US 6231850.
ACCESSION   AR151072
VERSION     AR151072.1  GI:15117122
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12
  JOURNAL   Patent: US 6231850-A 12 15-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            13.7%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 41
BD014654
LOCUS       BD014654                669 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy.
ACCESSION   BD014654
VERSION     BD014654.1  GI:22555437
KEYWORDS    JP 2001161378-A/2.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F.
  TITLE     Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy
  JOURNAL   Patent: JP 2001161378-A 2 19-JUN-2001;
            TORAY INDUSTRIES INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 2001161378-A/2
            PD   19-JUN-2001
            PF   26-SEP-2000 JP 2000292946
            PI   FUMIYOSHI OKANO
            PC   C12N15/09,A61K38/00,A61P17/00,A61P17/00,A61P31/04,A61P31/04,
            PC   A61P35/00,
            PC   A61P37/00,C07K1/18,C07K1/22,C07K14/54,C12P21/02//(C12P21/02,
            PC   C12R1:91),
            PC   (C12P21/02,C12R1:93),C12N15/00,A61K37/02
            CC   Process for producing highly pure protein, interleukin 12,  CC
                 protein
            CC   inhibiting interleukin-12 activity, remedies for mammalian  CC
                 immunopathy and
            CC   method of treating immunopathy
            FH   Key             Location/Qualifiers
            FT   CDS             (1). .(666)
            FT   mat_peptide     (76). .(666).
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Canis sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9616"
ORIGIN

  Query Match            13.7%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 42
BD014664
LOCUS       BD014664                669 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy.
ACCESSION   BD014664
VERSION     BD014664.1  GI:22555447
KEYWORDS    JP 2001161378-A/12.
```

```
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F.
  TITLE     Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy
  JOURNAL   Patent: JP 2001161378-A 12 19-JUN-2001;
            TORAY INDUSTRIES INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 2001161378-A/12
            PD   19-JUN-2001
            PF   26-SEP-2000 JP 2000292946
            PI   FUMIYOSHI OKANO
            PC   C12N15/09,A61K38/00,A61P17/00,A61P17/00,A61P31/04,A61P31/04,
            PC   A61P35/00,
            PC   A61P37/00,C07K1/18,C07K1/22,C07K14/54,C12P21/02//(C12P21/02,
            PC   C12R1:91),
            PC   (C12P21/02,C12R1:93),C12N15/00,A61K37/02
            CC   Process for producing highly pure protein, interleukin 12,  CC
                 protein
            CC   inhibiting interleukin-12 activity, remedies for mammalian  CC
                 immunopathy and
            CC   method of treating immunopathy
            FH   Key             Location/Qualifiers
            FT   CDS             (1). .(666)
            FT   mat_peptide     (76). .(666).
FEATURES            Location/Qualifiers
     source         1. .669
                    /organism="Canis sp."
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9616"
ORIGIN

  Query Match            13.7%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 43
E15018
LOCUS       E15018                   669 bp    DNA     linear   PAT 28-JUL-1999
DEFINITION  Canine mRNA for interleukin 12 35kDa subunit,complete cds.
ACCESSION   E15018
VERSION     E15018.1  GI:5709701
KEYWORDS    JP 1998036397-A/2.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F.
  TITLE     CANINE INTERLEUKIN 12 AND ITS PRODUCTION
  JOURNAL   Patent: JP 1998036397-A 2 10-FEB-1998;
            TORAY IND INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 1998036397-A/2
            PD   10-FEB-1998
            PF   08-NOV-1996 JP 1996296789
            PR   08-NOV-1995 JP 95P   289729, 23-MAY-1996 JP 96P   128104 PI
            OKANO FUMIYOSHI
            PC   C07K14/54,C07H21/04,C12N5/10,C12N15/09,C12P21/02,(C12N5/10, PC
              C12R1:91),
            PC   (C12P21/02,C12R1:91);
            CC   strandedness: Double;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .669
            FT                   /organism='Canis sp.'
            FT                   /tissue_type='liver'
            FT   CDS             1. .669
            FT                   /product='interleukin12 35kDa subunit'.
FEATURES            Location/Qualifiers
     source         1. .669
                    /organism="Canis sp."
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9616"
ORIGIN

  Query Match            13.7%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 44
AR316461
LOCUS       AR316461                 669 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 2 from patent US 6562334.
ACCESSION   AR316461
VERSION     AR316461.1  GI:33695289
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12 administration as an immune disease treatment
  JOURNAL   Patent: US 6562334-A 2 13-MAY-2003;
            Toray Industries, Inc.;;
            JPX;
FEATURES            Location/Qualifiers
     source         1. .669
                    /organism="unknown"
                    /mol_type="mRNA"
ORIGIN

  Query Match            13.7%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 45
AR316471
LOCUS       AR316471                 669 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 12 from patent US 6562334.
ACCESSION   AR316471
VERSION     AR316471.1  GI:33695299
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12 administration as an immune disease treatment
  JOURNAL   Patent: US 6562334-A 12 13-MAY-2003;
            Toray Industries, Inc.;;
            JPX;
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             13.7%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 46
CFU49085
LOCUS       CFU49085                669 bp    mRNA    linear   MAM 13-MAR-1996
DEFINITION  Canis familiaris interleukin-12 p35 subunit mRNA, complete cds.
ACCESSION   U49085
VERSION     U49085.1  GI:1223905
KEYWORDS    .
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Belke-Louis,G.F. and Buettner,M.
  TITLE     Cloning and sequence analysis of the p35 and p40 subunits of canine
            interleukin-12
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Belke-Louis,G.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-FEB-1996) Georg F. Belke-Louis, Institute of Med.
            Microbiology, Veterinaerstr. 13, Muenchen, D-80539, Germany
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Canis familiaris"
                     /mol_type="mRNA"
                     /db_xref="taxon:9615"
     CDS             1. .669
                     /codon_start=1
                     /product="interleukin-12 p35 subunit"
                     /protein_id="AAA92058.1"
                     /db_xref="GI:1223906"
                     /translation="MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHS
                     QNLLRAVSNTLQKARQTLDYIPCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
                     REISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQ
                     NMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSY
                     LNSS"
ORIGIN

  Query Match             13.7%;  Score 81;  DB 14;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 47
BD171283
LOCUS       BD171283                1282 bp    DNA     linear   PAT 18-FEB-2003
DEFINITION  Novel canine cytokine protein.
ACCESSION   BD171283
VERSION     BD171283.1  GI:28412573
KEYWORDS    JP 2002241398-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 1282)
  AUTHORS   Imamura,T., Maeda,H., Tokiyoshi,Y. and Eda,Y.
  TITLE     Novel canine cytokine protein
  JOURNAL   Patent: JP 2002241398-A 3 28-AUG-2002;
            CHEMO SERO THERAPEUT RES INST
COMMENT     OS   Canine splenocyte
            PN   JP 2002241398-A/3
            PD   28-AUG-2002
            PF   03-JUN-1997 JP 1997161936
            PI   TAKAYUKI IMAMURA,HIROAKI MAEDA,YUKIO TOKIYOSHI,YASUYUKI EDA PC
              C07K14/52,A61K38/00,A61K39/395,C07K16/24,C12N5/10,C12N15/09, PC
            C12P21/02//
            PC   C12P21/08,(C12P21/02,C12R1:91),A61K37/02,C12N5/00,C12N15/00 CC
              Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .1282
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             13.7%;  Score 81;  DB 2;  Length 1282;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 362

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        363 CTGGCTTCCAGAGAGATCTCT 383


RESULT 48
AR596009
LOCUS       AR596009                1455 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 104 from patent US 6818444.
ACCESSION   AR596009
VERSION     AR596009.1  GI:56646990
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1455)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 104 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1455
                     /organism="unknown"
                     /mol_type="genomic DNA"
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ORIGIN

  Query Match            13.7%;  Score 81;  DB 2;  Length 1455;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 528

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        529 CTGGCTTCCAGAGAGATCTCT 549


RESULT 49
AR596010/c
LOCUS       AR596010               1455 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 106 from patent US 6818444.
ACCESSION   AR596010
VERSION     AR596010.1  GI:56646991
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1455)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 106 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1455
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match            13.7%;  Score 81;  DB 2;  Length 1455;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 928

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        927 CTGGCTTCCAGAGAGATCTCT 907


RESULT 50
AR595973
LOCUS       AR595973               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 66 from patent US 6818444.
ACCESSION   AR595973
VERSION     AR595973.1  GI:56646954
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 66 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match            13.7%;  Score 81;  DB 2;  Length 1533;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1105 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1164

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db       1165 CTGGCTTCCAGAGAGATCTCT 1185


RESULT 51
AR595974/c
LOCUS       AR595974               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 68 from patent US 6818444.
ACCESSION   AR595974
VERSION     AR595974.1  GI:56646955
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 68 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match            13.7%;  Score 81;  DB 2;  Length 1533;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 52
AR595971
LOCUS       AR595971               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 61 from patent US 6818444.
ACCESSION   AR595971
VERSION     AR595971.1  GI:56646952
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 61 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match            13.7%;  Score 81;  DB 2;  Length 1599;
  Best Local Similarity  100.0%;  Pred. No. 2.6e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1230
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```
Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db       1231 CTGGCTTCCAGAGAGATCTCT 1251


RESULT 53
AR595972/c
LOCUS       AR595972               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 63 from patent US 6818444.
ACCESSION   AR595972
VERSION     AR595972.1  GI:56646953
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 63 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match            13.7%;  Score 81;  DB 2;  Length 1599;
  Best Local Similarity  100.0%;  Pred. No. 2.6e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 54
AX076207
LOCUS       AX076207                 71 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 8 from Patent WO0104155.
ACCESSION   AX076207
VERSION     AX076207.1  GI:12710832
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 8 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .71
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer f12p35-1-lang"
ORIGIN

  Query Match            12.0%;  Score 71;  DB 2;  Length 71;
  Best Local Similarity  100.0%;  Pred. No. 8.3e-27;
  Matches   71;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        410 TGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCAC 469
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCAC 60

Qy        470 AGAACTCCTCC 480
              ||||||||||||
Db         61 AGAACTCCTCC 71


RESULT 55
AR008951
LOCUS       AR008951               660 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 3 from patent US 5756085.
ACCESSION   AR008951
VERSION     AR008951.1  GI:3967756
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Sykes,M. and Wolf,S.F.
  TITLE     Use of interleukin-12 to prevent graft versus host disease
  JOURNAL   Patent: US 5756085-A 3 26-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            11.0%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity  100.0%;  Pred. No. 1.5e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        544 ATTCG 548
              |||||
Db        610 ATTCG 614


RESULT 56
BD007071
LOCUS       BD007071               660 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  IL-12 gene expression and delivery systems and uses.
ACCESSION   BD007071
VERSION     BD007071.1  GI:18635442
KEYWORDS    JP 2001503257-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Nodosutoromu,J., Freemark,B. and Dishupande,D.
  TITLE     IL-12 gene expression and delivery systems and uses
  JOURNAL   Patent: JP 2001503257-A 2 13-MAR-2001;
            BARENTISU INC,SYNTEX INC
COMMENT     OS   Unidentified
            PN   JP 2001503257-A/2
            PD   13-MAR-2001
            PF   10-OCT-1997 JP 1998519514
            PR   18-OCT-1996 US    60/028676
            PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
            C12N15/09,A61K31/711,A61K38/00,A61K47/18,A61K47/28,A61K48/00, PC
            A61P11/06,
            PC   C12N15/00,A61K37/02
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .660
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN
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  Query Match           11.0%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        544 ATTCG 548
              |||||
Db        610 ATTCG 614


RESULT 57
BD007079
LOCUS       BD007079                660 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Gene expression and delivery systems and uses.
ACCESSION   BD007079
VERSION     BD007079.1  GI:18635450
KEYWORDS    JP 2001503258-A/4.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Nodosutoromu,J., Freemark,B. and Dishupande,D.
  TITLE     Gene expression and delivery systems and uses
  JOURNAL   Patent: JP 2001503258-A 4 13-MAR-2001;
            BARENTISU INC
COMMENT     OS   Unidentified
            PN   JP 2001503258-A/4
            PD   13-MAR-2001
            PF   10-OCT-1997 JP 1998519520
            PR   18-OCT-1996 US    60/028687
            PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
            C12N15/09,A61K48/00,A61P11/06,A61P35/00,A61P43/00//C07K14/54, PC
            C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .660
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .660
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
ORIGIN

  Query Match           11.0%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        544 ATTCG 548
              |||||
Db        610 ATTCG 614


RESULT 58
BD136037
LOCUS       BD136037                660 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Interferon alpha plasmid and delivery system and method of
            preparing and using the same.
ACCESSION   BD136037
VERSION     BD136037.1  GI:23230982
KEYWORDS    JP 2002506647-A/4.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.
  TITLE     Interferon alpha plasmid and delivery system and method of
            preparing and using the same
  JOURNAL   Patent: JP 2002506647-A 4 05-MAR-2002;
            VALENTIS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002506647-A/4
            PD   05-MAR-2002
            PF   12-MAR-1999 JP 2000536861
            PR   19-MAR-1998 US    60/078654
            PI   JEFF NORDSTROM,FEDERICA PERICLE,ALAIN ROLLAND,ROBERT RALSTON
            PC   C12N15/09,A61K38/21,A61K48/00,A61P35/00,C07K14/54,C07K14/56,
            PC   C12N1/15,
            PC   C12N1/19,C12N1/21,C12N5/10//A61K9/127,C12N15/00,A61K37/66, PC
             C12N5/00
            CC   Interferon alpha plasmid and delivery system and method of  CC
                      preparing and
            CC   using the same
            FH   Key             Location/Qualifiers
            FT   source          1. .660
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .660
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
ORIGIN

  Query Match           11.0%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        544 ATTCG 548
              |||||
Db        610 ATTCG 614


RESULT 59
I28592
LOCUS       I28592                  660 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 3 from patent US 5573764.
ACCESSION   I28592
VERSION     I28592.1  GI:1819368
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Sykes,M. and Wolf,S.F.
  TITLE     Use of interleukin-12 to prevent graft versus host disease
  JOURNAL   Patent: US 5573764-A 3 12-NOV-1996;
FEATURES              Location/Qualifiers
     source           1. .660
                      /organism="unknown"
                      /mol_type="unassigned DNA"
ORIGIN

  Query Match           11.0%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        544 ATTCG 548
              |||||
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Db        610 ATTCG 614


RESULT 60
AX154618
LOCUS       AX154618                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 22 from Patent WO0140257.
ACCESSION   AX154618
VERSION     AX154618.1  GI:14536193
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 22 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match            11.0%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity  100.0%;  Pred. No. 1.5e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        141 TGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGA 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 TGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGA 266

Qy        201 ATTAA 205
              |||||
Db        267 ATTAA 271


RESULT 61
AX154634
LOCUS       AX154634                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 38 from Patent WO0140257.
ACCESSION   AX154634
VERSION     AX154634.1  GI:14536198
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 38 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match            11.0%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity  100.0%;  Pred. No. 1.5e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        544 ATTCG 548
              |||||
Db        610 ATTCG 614


RESULT 62
CQ829447
LOCUS       CQ829447                702 bp    DNA     linear   PAT 05-JUL-2004
DEFINITION  Sequence 6 from Patent WO2004052929.
ACCESSION   CQ829447
VERSION     CQ829447.1  GI:49732783
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Vandenbroeck,K. and Alloza,I.
  TITLE     Recombinant cell line
  JOURNAL   Patent: WO 2004052929-A 6 24-JUN-2004;
            The Queen's University of Belfast (GB)
FEATURES             Location/Qualifiers
     source          1. .702
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="cDNA for alpha chain of IL-12"
ORIGIN

  Query Match            11.0%;  Score 65;  DB 2;  Length 702;
  Best Local Similarity  100.0%;  Pred. No. 1.5e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 624

Qy        544 ATTCG 548
              |||||
Db        625 ATTCG 629


RESULT 63
AR052862
LOCUS       AR052862                721 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 199 from patent US 5833975.
ACCESSION   AR052862
VERSION     AR052862.1  GI:5977724
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 721)
  AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
  TITLE     Canarypox virus expressing cytokine and/or tumor-associated antigen
            DNA sequence
  JOURNAL   Patent: US 5833975-A 199 10-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .721
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            11.0%;  Score 65;  DB 2;  Length 721;
  Best Local Similarity  100.0%;  Pred. No. 1.5e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy        544 ATTCG 548
              |||||
Db        671 ATTCG 675
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RESULT 64
AR288174
LOCUS       AR288174                721 bp    mRNA    linear   PAT 12-JUN-2003
DEFINITION  Sequence 199 from patent US 6537594.
ACCESSION   AR288174
VERSION     AR288174.1  GI:31675453
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 721)
  AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
  TITLE     Vaccina virus comprising cytokine and/or tumor associated antigen
            genes
  JOURNAL   Patent: US 6537594-A 199 25-MAR-2003;
            Virogenetics Corporation; Troy, NY
FEATURES             Location/Qualifiers
     source          1. .721
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match            11.0%;  Score 65;  DB 2;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy        544 ATTCG 548
              |||||
Db        671 ATTCG 675


RESULT 65
AR567161
LOCUS       AR567161                721 bp    mRNA    linear   PAT 08-OCT-2004
DEFINITION  Sequence 199 from patent US 6780407.
ACCESSION   AR567161
VERSION     AR567161.1  GI:53984803
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 721)
  AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
  TITLE     Pox virus comprising DNA sequences encoding CEA and B7 antigen
  JOURNAL   Patent: US 6780407-A 199 24-AUG-2004;
            Aventis Pasteur; Swiftwater, PA
FEATURES             Location/Qualifiers
     source          1. .721
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match            11.0%;  Score 65;  DB 2;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy        544 ATTCG 548
              |||||
Db        671 ATTCG 675


RESULT 66
BD105971
LOCUS       BD105971                762 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Animal model for evaluation of vaccines.
ACCESSION   BD105971
VERSION     BD105971.1  GI:23200789
KEYWORDS    JP 2002501375-A/21.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Chang,L.J.
  TITLE     Animal model for evaluation of vaccines
  JOURNAL   Patent: JP 2002501375-A 21 15-JAN-2002;
            LUNG JI CHANG
COMMENT     PN   JP 2002501375-A/21
            PD   15-JAN-2002
            PF   09-APR-1998 JP 1998543062
            PR   09-APR-1997 US    08/838702,01-MAY-1997 US    08/848760 PR
            09-DEC-1997 US    60/069163
            PI   LUNG JI CHANG
            PC   A01K67/027,C12N7/01,C12N1/10,C07K14/16,A61K39/008,C12N1/36, PC
              C12N7/04,
            PC   A61K39/21
            CC   Strandedness: Double;
            CC   Topology: Linear;
            CC   /desc = 'DNA'
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .762
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match            11.0%;  Score 65;  DB 2;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        544 ATTCG 548
              |||||
Db        712 ATTCG 716


RESULT 67
CQ803343
LOCUS       CQ803343                762 bp    DNA     linear   PAT 10-MAY-2004
DEFINITION  Sequence 3 from Patent WO2004035799.
ACCESSION   CQ803343
VERSION     CQ803343.1  GI:47110209
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Waehler,R. and Schnieders,F.
  TITLE     Viral vectors and the use of the same for gene therapy
  JOURNAL   Patent: WO 2004035799-A 3 29-APR-2004;
            Universitaetsklinikum Hamburg-Eppendorf (DE)
FEATURES             Location/Qualifiers
     source          1. .762
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match            11.0%;  Score 65;  DB 2;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        544 ATTCG 548
                  |||||
Db        712 ATTCG 716


RESULT 68
AR533401
LOCUS       AR533401                762 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 21 from patent US 6730512.
ACCESSION   AR533401
VERSION     AR533401.1  GI:53923067
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Chang,L.-J.
  TITLE     Combination immunogene therapy
  JOURNAL   Patent: US 6730512-A 21 04-MAY-2004;
            Amdl, Inc.; Tustin, CA
FEATURES             Location/Qualifiers
     source          1. .762
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             11.0%;  Score 65;  DB 2;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
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Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        544 ATTCG 548
                  |||||
Db        712 ATTCG 716


RESULT 69
AF101062
LOCUS       AF101062                762 bp    mRNA    linear   PRI 03-MAR-1999
DEFINITION  Homo sapiens interleukin 12 mRNA, complete cds.
ACCESSION   AF101062
VERSION     AF101062.1  GI:4323578
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Liu,y., Guo,Y. and Wu,M.
  TITLE     Human Interleukin-12 (or Natural Killer Cell Stimulatory Factor, or
            Cytotoxic Lymphocyte Maturation Factor) 35kDa subunit mRNA
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 762)
  AUTHORS   Liu,Y., Guo,Y. and Wu,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-OCT-1998) Molecular Biology Department, Cancer
            Institute of Second Military Medical University, 800 XianYin Road,
            Shanghai 200433, P.R. China
FEATURES             Location/Qualifiers
     source          1. .762
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="3"
                     /map="3p12-q13.2"
                     /cell_line="lymphoblastoid B-cell line NC37"
                     /note="cells induced by phorbol 12-myristate 13 acetate
                     (PMA) and ionophore A23187"
     CDS             1. .762
                     /note="natural killer cell stimulatory factor; cytotoxic
                     lymphocyte maturation factor 35kDa subunit; p35"
                     /codon_start=1
                     /product="interleukin 12"
                     /protein_id="AAD16432.1"
                     /db_xref="GI:4323579"
                     /translation="MWPPGSASQPPPSPAAATGLHPAARPVSLQCRLSMCPARSLLLV
                     ATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEE
                     IDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSS
                     IYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLE
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     variation       732
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ORIGIN

  Query Match             11.0%;  Score 65;  DB 5;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
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Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        544 ATTCG 548
                  |||||
Db        712 ATTCG 716


RESULT 70
MMU19842
LOCUS       MMU19842                780 bp    mRNA    linear   PRI 03-FEB-1996
DEFINITION  Macaca mulatta interleukin-12 beta p35 subunit (IL-12b) mRNA,
            complete cds.
ACCESSION   U19842
VERSION     U19842.1  GI:644801
KEYWORDS    .
SOURCE      Macaca mulatta (rhesus monkey)
  ORGANISM  Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 780)
  AUTHORS   Villinger,F., Brar,S.S., Mayne,A., Chikkala,N. and Ansari,A.A.
  TITLE     Comparative sequence analysis of cytokine genes from human and
            nonhuman primates
  JOURNAL   J. Immunol. 155 (8), 3946-3954 (1995)
   PUBMED   7561102
REFERENCE   2  (bases 1 to 780)
  AUTHORS   Villinger,F.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JAN-1995) Francois J. Villinger, Emory University,
            Pathology, 1327 Clifton Rd, Atlanta, GA 30322, USA
FEATURES             Location/Qualifiers
     source          1. .780
                     /organism="Macaca mulatta"
                     /mol_type="mRNA"
                     /db_xref="taxon:9544"
                     /clone="RNc IL-12b"
                     /cell_type="peripheral blood mononuclear cells"
                     /tissue_type="blood"
     gene            1. .780
                     /gene="IL-12b"
     CDS             10. .771
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                     /function="NK cell stimulatory factor"
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                     /product="interleukin-12 beta p35 subunit"
                     /protein_id="AAA86707.1"
                     /db_xref="GI:644802"
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                     ATLVLLDYLSLARNLSVATPGPEMFPCLHHSQNLLKAASNTLQKARQILEFYPCTSEE
                     IDHEDITKDKTSTVEACLPLELIKNESCLNSRETSFITNGSCLASRKTSFMMALCLRS
                     IYEDLKMYQVEFKTMNAKLLRDPKRQIFLDQNILGVIDELMQALNFNSETVPQKSSLE
                     EPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS"
ORIGIN

  Query Match             11.0%;  Score 65;  DB 5;  Length 780;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 720

Qy        544 ATTCG 548
              |||||
Db        721 ATTCG 725


RESULT 71
AF180562
LOCUS       AF180562                823 bp    mRNA    linear   PRI 26-SEP-1999
DEFINITION  Homo sapiens interleukin 12, P35 mRNA, complete cds.
ACCESSION   AF180562
VERSION     AF180562.1  GI:5923852
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 823)
  AUTHORS   Hongyuan,J. and Meiyun,Z.
  TITLE     Cloning and sequence analysis of IL-12 cDNA from Chinese
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 823)
  AUTHORS   Hongyuan,J. and Meiyun,Z.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-AUG-1999) Hepatitis, Institute of Virology, CAPM, 100
            Yingxinjie, Xuanwuqu, Beijing 100052, China
FEATURES             Location/Qualifiers
     source          1. .823
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="3"
                     /map="3p12-q13.2"
                     /cell_type="peripheral mononuclear"
     CDS             60. .821
                     /note="NKSF/CLMF; IL12p35; 35kD"
                     /codon_start=1
                     /product="interleukin 12, P35"
                     /protein_id="AAD56385.1"
                     /db_xref="GI:5923853"
                     /translation="MWPPGSASQPPPSPAAATGLHPAARPVSLQCRLSMCPARSLLLV
                     ATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEE
                     IDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSS
                     IYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLE
                     EPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS"
ORIGIN

  Query Match             11.0%;  Score 65;  DB 5;  Length 823;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        711 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 770

Qy        544 ATTCG 548
              |||||
Db        771 ATTCG 775


RESULT 72
BD165801
LOCUS       BD165801                856 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Antibody against cytotoxic lymphocyte maturing factors.
ACCESSION   BD165801
VERSION     BD165801.1  GI:27871613
KEYWORDS    JP 2002167400-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 856)
  AUTHORS   Chizzonite,R.A., Gately,M.K., Gubler,U.A., Hulmes,J.D., Pan,Y.C.E.,
            Podlanski,F.J. and Stern,A.S.
  TITLE     Antibody against cytotoxic lymphocyte maturing factors
  JOURNAL   Patent: JP 2002167400-A 2 11-JUN-2002;
            PROTEIN DESIGN LABS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002167400-A/2
            PD   11-JUN-2002
            PF   14-AUG-2001 JP 2001246031
            PR   22-DEC-1989 US       455708,09-MAY-1990 US       520935 PR
            27-AUG-1990 US       572284
            PI   RICHARD ANTHONY CHIZZONITE,MAURICE KENT GATELY,ULRICH ANDREAS
            PI   GUBLER,
            PI   JEFFREY DAVID HULMES,YU CHING EUGENE PAN,FRANK JOHN PODLANSKI,
            PI   ALVIN SETH STERN
            PC   C07K16/24,C12N15/02,C12N15/02,C12P21/08,C12N15/00,C12N15/00 CC
              Antibody against cytotoxic lymphocyte maturing factors FH   Key
                     Location/Qualifiers
            FT   CDS             (170). .(826).
FEATURES             Location/Qualifiers
     source          1. .856
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ORIGIN

  Query Match             11.0%;  Score 65;  DB 2;  Length 856;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 778

Qy        544 ATTCG 548
              |||||
Db        779 ATTCG 783


RESULT 73
CQ716168
LOCUS       CQ716168                1020 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 2102 from Patent WO02068579.
ACCESSION   CQ716168
VERSION     CQ716168.1  GI:42277025
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 2102 06-SEP-2002;
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            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
     source          1. .1020
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             11.0%;  Score 65;  DB 2;  Length 1020;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        712 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 771

Qy        544 ATTCG 548
              |||||
Db        772 ATTCG 776


RESULT 74
BC104982
LOCUS       BC104982               1021 bp    mRNA    linear   PRI 19-JAN-2006
DEFINITION  Homo sapiens interleukin 12A (natural killer cell stimulatory
            factor 1, cytotoxic lymphocyte maturation factor 1, p35), mRNA
            (cDNA clone MGC:132642 IMAGE:8143985), complete cds.
ACCESSION   BC104982
VERSION     BC104982.1  GI:85397857
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1021)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1021)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (13-SEP-2005) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Mike Brownstein, NIMH
            cDNA Library Preparation: British Columbia Cancer Research Center
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
            Martin Hirst, Thomas Zeng, Ryan Morin, Michelle Moksa, Johnson
            Pang, Diana Mah, Jing Wang, Kieth Fichter, Eric Chuah, Allen
            Delaney, Rob Kirkpatrick, Agnes Baross, Sarah Barber, Mabel
            Brown-John, Steve S. Chand, William Chow, Ryan Babakaiff, Dave
            Wong, Corey Matsuo, Jaclyn Beland, Susan Gibson, Luis delRio, Ruth
            Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
            Kim MacDonald,  Mike R. Mayo, Josh Moran, Diana Palmquist, JR
            Santos, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang,
            Jacquie Schein, Asim Siddiqui,Steven Jones, Rob Holt, Marco Marra.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRCB Plate: 3 Row: j Column: 15.
FEATURES             Location/Qualifiers
     source          1. .1021
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:132642 IMAGE:8143985"
                     /tissue_type="Brain, cerebral cortex, PCR rescued clones"
                     /clone_lib="NIH_MGC_287"
                     /note="Vector: pCR4-TOPO with reversed insert; Clone
                     identification sequence tag: TCGTTGCT"
     gene            1. .1021
                     /gene="IL12A"
                     /note="synonyms: IL-12A, NFSK, CLMF"
                     /db_xref="GeneID:3592"
                     /db_xref="HGNC:5969"
                     /db_xref="IMGT/GENE-DB:5969"
                     /db_xref="MIM:161560"
     CDS             154. .915
                     /gene="IL12A"
                     /codon_start=1
                     /product="interleukin 12A, precursor"
                     /protein_id="AAI04983.1"
                     /db_xref="GI:85397858"
                     /db_xref="GeneID:3592"
                     /db_xref="HGNC:5969"
                     /db_xref="IMGT/GENE-DB:5969"
                     /db_xref="MIM:161560"
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                     IYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLE
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ORIGIN

  Query Match             11.0%;  Score 65;  DB 5;  Length 1021;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 864

Qy        544 ATTCG 548
              |||||
Db        865 ATTCG 869


RESULT 75
BC104984
LOCUS       BC104984               1021 bp    mRNA    linear   PRI 19-JAN-2006
DEFINITION  Homo sapiens interleukin 12A (natural killer cell stimulatory
            factor 1, cytotoxic lymphocyte maturation factor 1, p35), mRNA
            (cDNA clone MGC:132644 IMAGE:8143987), complete cds.
ACCESSION   BC104984
VERSION     BC104984.1  GI:85397860
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1021)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1021)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (13-SEP-2005) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Mike Brownstein, NIMH
            cDNA Library Preparation: British Columbia Cancer Research Center
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
            Martin Hirst, Thomas Zeng, Ryan Morin, Michelle Moksa, Johnson
            Pang, Diana Mah, Jing Wang, Kieth Fichter, Eric Chuah, Allen
            Delaney, Rob Kirkpatrick, Agnes Baross, Sarah Barber, Mabel
            Brown-John, Steve S. Chand, William Chow, Ryan Babakaiff, Dave
            Wong, Corey Matsuo, Jaclyn Beland, Susan Gibson, Luis delRio, Ruth
            Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
            Kim MacDonald,  Mike R. Mayo, Josh Moran, Diana Palmquist, JR
            Santos, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang,
            Jacquie Schein, Asim Siddiqui,Steven Jones, Rob Holt, Marco Marra.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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FEATURES             Location/Qualifiers
     source          1. .1021
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                     /clone="MGC:132644 IMAGE:8143987"
                     /tissue_type="Brain, cerebral cortex, PCR rescued clones"
                     /clone_lib="NIH_MGC_287"
                     /note="Vector: pCR4-TOPO with reversed insert; Clone
                     identification sequence tag: AAATAGCC"
     gene            1. .1021
                     /gene="IL12A"
                     /note="synonyms: IL-12A, NFSK, CLMF"
                     /db_xref="GeneID:3592"
                     /db_xref="HGNC:5969"
                     /db_xref="IMGT/GENE-DB:5969"
                     /db_xref="MIM:161560"
     CDS             154. .915
                     /gene="IL12A"
                     /codon_start=1
                     /product="interleukin 12A, precursor"
                     /protein_id="AAI04985.1"
                     /db_xref="GI:85397861"
                     /db_xref="GeneID:3592"
                     /db_xref="HGNC:5969"
                     /db_xref="IMGT/GENE-DB:5969"
                     /db_xref="MIM:161560"
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ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 1.4e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 864

Qy        544 ATTCG 548
              |||||
Db        865 ATTCG 869


RESULT 76
AR091390
LOCUS       AR091390               1026 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 1 from patent US 5994104.
ACCESSION   AR091390
VERSION     AR091390.1  GI:10018145
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1026)
  AUTHORS   Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
  TITLE     Interleukin-12 fusion protein
  JOURNAL   Patent: US 5994104-A 1 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .1026
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            11.0%;  Score 65;  DB 2;  Length 1026;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 778

Qy        544 ATTCG 548
              |||||
Db        779 ATTCG 783


RESULT 77
AR380496
LOCUS       AR380496               1026 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1041 from patent US 6607879.
ACCESSION   AR380496
VERSION     AR380496.1  GI:40088130
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1026)
  AUTHORS   Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.
```

```
  TITLE     Compositions for the detection of blood cell and immunological
            response gene expression
  JOURNAL   Patent: US 6607879-A 1041 19-AUG-2003;
            Incyte Corporation; Palo Alto, CA
FEATURES             Location/Qualifiers
     source          1. .1026
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match            11.0%;  Score 65;  DB 2;  Length 1026;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-23;
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Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 778

Qy        544 ATTCG 548
              |||||
Db        779 ATTCG 783


RESULT 78
HUMCLMF35
LOCUS       HUMCLMF35               1026 bp    mRNA    linear   PRI 27-APR-1993
DEFINITION  Human cytotoxic lymphocyte maturation factor 35 kDa subunit mRNA,
            complete cds.
ACCESSION   M65271 M38443
VERSION     M65271.1  GI:180623
KEYWORDS    cytotoxic lymphocyte maturation factor 35 kDa subunit; interleukin.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1026)
  AUTHORS   Gubler,U., Chua,A.O., Schoenhaut,D.S., Dwyer,C.M., McComas,W.,
            Motyka,R., Nabavi,N., Wolitzky,A.G., Quinn,P.M., Familletti,P.C.
            and Gately,M.K.
  TITLE     Coexpression of two distinct genes is required to generate secreted
            bioactive cytotoxic lymphocyte maturation factor
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 88 (10), 4143-4147 (1991)
   PUBMED   1674604
COMMENT     Original source text: Human, cDNA to mRNA.
FEATURES             Location/Qualifiers
     source          1. .1026
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     CDS             170. .829
                     /codon_start=1
                     /product="cytotoxic lymphocyte maturation factor 35 kDa
                     subunit"
                     /protein_id="AAA35694.1"
                     /db_xref="GI:180624"
                     /translation="MCPARSLLLVATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNL
                     LRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRET
                     SFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNML
                     AVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVTSYLNA
                     S"
ORIGIN

  Query Match            11.0%;  Score 65;  DB 5;  Length 1026;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 778

Qy        544 ATTCG 548
              |||||
Db        779 ATTCG 783


RESULT 79
AR393790
LOCUS       AR393790                1287 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 6 from patent US 6617135.
ACCESSION   AR393790
VERSION     AR393790.1  GI:40120794
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1287)
  AUTHORS   Gillies,S.D. and Lo,K.-M.
  TITLE     Multiple cytokine protein complexes
  JOURNAL   Patent: US 6617135-A 6 09-SEP-2003;
            EMD Lexigen Research Center Corp.; Billerica, MA
FEATURES             Location/Qualifiers
     source          1. .1287
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match            11.0%;  Score 65;  DB 2;  Length 1287;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1177 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1236

Qy        544 ATTCG 548
              |||||
Db       1237 ATTCG 1241


RESULT 80
AX084108
LOCUS       AX084108                1287 bp    DNA     linear   PAT 28-FEB-2001
DEFINITION  Sequence 6 from Patent WO0110912.
ACCESSION   AX084108
VERSION     AX084108.1  GI:13185658
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Gillies,S.D. and Lo,K.M.
  TITLE     Multiple cytokine-antibody complexes
  JOURNAL   Patent: WO 0110912-A 6 15-FEB-2001;
            Lexigen Pharmaceuticals Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .1287
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="human Fc-p35 fusion protein coding sequence"
ORIGIN

  Query Match            11.0%;  Score 65;  DB 2;  Length 1287;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
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Db       1177 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1236

Qy        544 ATTCG 548
              |||||
Db       1237 ATTCG 1241
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RESULT 81
AR050785
LOCUS       AR050785               1316 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 3 from patent US 5830451.
ACCESSION   AR050785
VERSION     AR050785.1  GI:5974149
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1316)
  AUTHORS   Devergne,O. and Kieff,E.D.
  TITLE     Haematopoietic cytokine Epstein Barr virus-induced protein
  JOURNAL   Patent: US 5830451-A 3 03-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .1316
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           11.0%;  Score 65;  DB 2;  Length 1316;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 812

Qy        544 ATTCG 548
              |||||
Db        813 ATTCG 817


RESULT 82
AR212036
LOCUS       AR212036               1316 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 3 from patent US 6399379.
ACCESSION   AR212036
VERSION     AR212036.1  GI:21515515
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1316)
  AUTHORS   Baker,B.F. and Freier,S.M.
  TITLE     Antisense modulation of interleukin 12 p35 subunit expression
  JOURNAL   Patent: US 6399379-A 3 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .1316
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           11.0%;  Score 65;  DB 2;  Length 1316;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 812

Qy        544 ATTCG 548
              |||||
Db        813 ATTCG 817


RESULT 83
HUMNKSFP35
LOCUS       HUMNKSFP35             1316 bp    mRNA    linear   PRI 07-JAN-1995
DEFINITION  Human natural killer cell stimulatory factor (NKSF) mRNA, complete
            cds, clone p35.
ACCESSION   M65291
VERSION     M65291.1  GI:189233
KEYWORDS    cytokine; natural killer cell stimulatory factor.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1316)
  AUTHORS   Wolf,S.F., Temple,P.A., Kobayashi,M., Young,D., Dicig,M., Lowe,L.,
            Dzialo,R., Fitz,L., Ferenz,C., Hewick,R.M., Kelleher,K.,
            Herrmann,S.H., Clark,S.C., Azzoni,L., Chan,S.H., Trinchieri,G. and
            Perussia,B.
  TITLE     Cloning of cDNA for natural killer cell stimulatory factor, a
            heterodimeric cytokine with multiple biologic effects on T and
            natural killer cells
  JOURNAL   J. Immunol. 146 (9), 3074-3081 (1991)
  PUBMED    1673147
COMMENT     Original source text: Human EBV-transformed B cell line RPMI 8866,
            cDNA to mRNA, clone p35.
FEATURES             Location/Qualifiers
     source          1. .1316
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /map="Unassigned"
                     /cell_line="EBV-transformed B cell line RPMI 8866"
     gene            1. .1316
                     /gene="NKSF1"
     CDS             102. .863
                     /gene="NKSF1"
                     /codon_start=1
                     /product="natural killer cell stimulatory factor"
                     /protein_id="AAA59937.1"
                     /db_xref="GI:189234"
                     /db_xref="GDB:G00-127-869"
                     /translation="MWPPGSASQPPPSPAAATGLHPAARPVSLQCRLSMCPARSLLLV
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                     EPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS"
     sig_peptide     102. .269
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                     /note="G00-127-869"
     mat_peptide     270. .860
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                     /product="natural killer cell stimulatory factor"
                     /note="G00-127-869"
ORIGIN

  Query Match           11.0%;  Score 65;  DB 5;  Length 1316;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-23;
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Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
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Db        753 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 812

Qy        544 ATTCG 548
              |||||
Db        813 ATTCG 817


RESULT 84
AR082685
LOCUS       AR082685               1364 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 3 from patent US 5976539.
ACCESSION   AR082685
VERSION     AR082685.1  GI:10009475
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1364)
  AUTHORS   Scott,P. and Trinchieri,G.
```

```
  TITLE     Compositions and methods for use of IL-12 as an adjuvant
  JOURNAL   Patent: US 5976539-A 3 02-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .1364
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             11.0%;  Score 65;  DB 2;  Length 1364;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 811

Qy        544 ATTCG 548
              |||||
Db        812 ATTCG 816


RESULT 85
AR122961
LOCUS       AR122961                1364 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 3 from patent US 6168923.
ACCESSION   AR122961
VERSION     AR122961.1  GI:14107927
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1364)
  AUTHORS   Scott,P. and Trinchieri,G.
  TITLE     Compositions and methods for use of IL-12 as an adjuvant
  JOURNAL   Patent: US 6168923-A 3 02-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .1364
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             11.0%;  Score 65;  DB 2;  Length 1364;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 811

Qy        544 ATTCG 548
              |||||
Db        812 ATTCG 816


RESULT 86
I28326
LOCUS       I28326                  1364 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 3 from patent US 5571515.
ACCESSION   I28326
VERSION     I28326.1  GI:1819102
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1364)
  AUTHORS   Scott,P. and Trinchieri,G.
  TITLE     Compositions and methods for use of IL-12 as an adjuvant
  JOURNAL   Patent: US 5571515-A 3 05-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .1364
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             11.0%;  Score 65;  DB 2;  Length 1364;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 811

Qy        544 ATTCG 548
              |||||
Db        812 ATTCG 816


RESULT 87
I89771
LOCUS       I89771                  1364 bp    DNA     linear   PAT 10-AUG-1998
DEFINITION  Sequence 3 from patent US 5723127.
ACCESSION   I89771
VERSION     I89771.1  GI:3409711
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1364)
  AUTHORS   Scott,P. and Trinchieri,G.
  TITLE     Compositions and methods for use of IL-12 as an adjuvant
  JOURNAL   Patent: US 5723127-A 3 03-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .1364
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             11.0%;  Score 65;  DB 2;  Length 1364;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 811

Qy        544 ATTCG 548
              |||||
Db        812 ATTCG 816


RESULT 88
AR309637
LOCUS       AR309637                1395 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 5 from patent US 6555658.
ACCESSION   AR309637
VERSION     AR309637.1  GI:31701688
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1395)
  AUTHORS   Trinchieri,G., Perussia,B., Clark,S.C., Wong,G.G., Hewick,R. and
            Kobayashi,M.
  TITLE     Antibodies to natural killer stimulatory factor
  JOURNAL   Patent: US 6555658-A 5 29-APR-2003;
            Wyeth and The Wistar Institute; Madison, NJ
FEATURES             Location/Qualifiers
     source          1. .1395
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             11.0%;  Score 65;  DB 2;  Length 1395;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        765 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 824

Qy        544 ATTCG 548
              |||||
Db        825 ATTCG 829


RESULT 89
CS032085
LOCUS       CS032085               1444 bp    DNA     linear   PAT 10-MAR-2005
DEFINITION  Sequence 1591 from Patent WO2005016962.
ACCESSION   CS032085
VERSION     CS032085.1  GI:60731804
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Abbas,A., Clark,H., Ouyang,W., Williams,M.P., Wood,W.I. and Wu,T.D.
  TITLE     Compositions and methods for the treatment of immune related
            diseases
  JOURNAL   Patent: WO 2005016962-A 1591 24-FEB-2005;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1444
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match            11.0%;  Score 65;  DB 2;  Length 1444;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 926

Qy        544 ATTCG 548
              |||||
Db        927 ATTCG 931


RESULT 90
CS041037
LOCUS       CS041037               1444 bp    DNA     linear   PAT 22-MAR-2005
DEFINITION  Sequence 1591 from Patent WO2005019258.
ACCESSION   CS041037
VERSION     CS041037.1  GI:61848609
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Abbas,A., Clark,H., Ouyang,W., Williams,P.M., Wood,W.I. and Wu,T.D.
  TITLE     Compositions and methods for the treatment of immune related
            diseases
  JOURNAL   Patent: WO 2005019258-A 1591 03-MAR-2005;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1444
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match            11.0%;  Score 65;  DB 2;  Length 1444;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 926

Qy        544 ATTCG 548
              |||||
Db        927 ATTCG 931


RESULT 91
CS143811
LOCUS       CS143811               1444 bp    DNA     linear   PAT 19-AUG-2005
DEFINITION  Sequence 53 from Patent WO2005073411.
ACCESSION   CS143811
VERSION     CS143811.1  GI:73658825
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ried,T.
  TITLE     Composition for detecting the response of rectal adenocarcinomas to
            radiochemotherapy
  JOURNAL   Patent: WO 2005073411-A 53 11-AUG-2005;
            DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES             Location/Qualifiers
     source          1. .1444
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match            11.0%;  Score 65;  DB 2;  Length 1444;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 926

Qy        544 ATTCG 548
              |||||
Db        927 ATTCG 931


RESULT 92
AR091395
LOCUS       AR091395               1560 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 11 from patent US 5994104.
ACCESSION   AR091395
VERSION     AR091395.1  GI:10018150
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1560)
  AUTHORS   Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
  TITLE     Interleukin-12 fusion protein
  JOURNAL   Patent: US 5994104-A 11 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .1560
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            11.0%;  Score 65;  DB 2;  Length 1560;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
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Db       1450 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1509

Qy        544 ATTCG 548
              |||||
Db       1510 ATTCG 1514


RESULT 93
AR091394
LOCUS       AR091394               1623 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 9 from patent US 5994104.
ACCESSION   AR091394
VERSION     AR091394.1  GI:10018149
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1623)
  AUTHORS   Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
  TITLE     Interleukin-12 fusion protein
  JOURNAL   Patent: US 5994104-A 9 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .1623
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 1.4e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1513 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1572

Qy        544 ATTCG 548
              |||||
Db       1573 ATTCG 1577


RESULT 94
A92078
LOCUS       A92078                 1645 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 2 from Patent WO9821322.
ACCESSION   A92078
VERSION     A92078.1  GI:6740882
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 1645)
  AUTHORS   Junghans,C. and Wittig,B.
  TITLE     DESIGN PRINCIPLE FOR CONSTRUCTING EXPRESSION CONSTRUCTS FOR GENE
            THERAPY
  JOURNAL   Patent: WO 9821322-A 2 22-MAY-1998;
            JUNGHANS CLAAS (DE); SOFT GENE GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .1645
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match            11.0%;  Score 65;  DB 2;  Length 1645;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1284 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1343

Qy        544 ATTCG 548
              |||||
Db       1344 ATTCG 1348


RESULT 95
AR230689
LOCUS       AR230689               1645 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 2 from patent US 6451593.
ACCESSION   AR230689
VERSION     AR230689.1  GI:27271470
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1645)
  AUTHORS   Wittig,B. and Junghans,C.
  TITLE     Design principle for construction of expression constructs for gene
            therapy
  JOURNAL   Patent: US 6451593-A 2 17-SEP-2002;
            Soft Gene GmbH; Berlin;
            DEX;
FEATURES             Location/Qualifiers
     source          1. .1645
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match            11.0%;  Score 65;  DB 2;  Length 1645;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1284 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1343

Qy        544 ATTCG 548
              |||||
Db       1344 ATTCG 1348


RESULT 96
CS131489
LOCUS       CS131489               3205 bp    DNA     linear   PAT 02-AUG-2005
DEFINITION  Sequence 8 from Patent WO2005066348.
ACCESSION   CS131489
VERSION     CS131489.1  GI:71794157
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Gillies,S.
  TITLE     Compounds for targeting
  JOURNAL   Patent: WO 2005066348-A 8 21-JUL-2005;
            Antisoma PLC (GB); EMD Lexigen Research Center Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .3205
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HuBC1 heavy chain fused to huIL12 p35 subunit"
ORIGIN

  Query Match            11.0%;  Score 65;  DB 2;  Length 3205;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3095 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 3154
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Qy        544 ATTCG 548
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Db       3155 ATTCG 3159


RESULT 97
BD136048
LOCUS       BD136048               5686 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Interferon alpha plasmid and delivery system and method of
            preparing and using the same.
ACCESSION   BD136048
VERSION     BD136048.1  GI:23230993
KEYWORDS    JP 2002506647-A/15.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 5686)
  AUTHORS   Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.
  TITLE     Interferon alpha plasmid and delivery system and method of
            preparing and using the same
  JOURNAL   Patent: JP 2002506647-A 15 05-MAR-2002;
            VALENTIS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002506647-A/15
            PD   05-MAR-2002
            PF   12-MAR-1999 JP 2000536861
            PR   19-MAR-1998 US    60/078654
            PI   JEFF NORDSTROM,FEDERICA PERICLE,ALAIN ROLLAND,ROBERT RALSTON
            PC   C12N15/09,A61K38/21,A61K48/00,A61P35/00,C07K14/54,C07K14/56,
            PC   C12N1/15,
            PC   C12N1/19,C12N1/21,C12N5/10//A61K9/127,C12N15/00,A61K37/66, PC
             C12N5/00
            CC   Sequence source: synthetic construct
            FH   Key             Location/Qualifiers
            FT   source          1. .5686
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .5686
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             11.0%;  Score 65;  DB 2;  Length 5686;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2094 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 2153

Qy        544 ATTCG 548
              |||||
Db       2154 ATTCG 2158


RESULT 98
AR091393
LOCUS       AR091393               6139 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 7 from patent US 5994104.
ACCESSION   AR091393
VERSION     AR091393.1  GI:10018148
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 6139)
  AUTHORS   Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
  TITLE     Interleukin-12 fusion protein
  JOURNAL   Patent: US 5994104-A 7 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .6139
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             11.0%;  Score 65;  DB 2;  Length 6139;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4734 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 4793

Qy        544 ATTCG 548
              |||||
Db       4794 ATTCG 4798


RESULT 99
AF404773
LOCUS       AF404773              11792 bp    DNA     linear   PRI 09-AUG-2001
DEFINITION  Homo sapiens interleukin 12A (natural killer cell stimulatory
            factor 1, cytotoxic lymphocyte maturation factor 1, p35) (IL12A)
            gene, complete cds.
ACCESSION   AF404773
VERSION     AF404773.1  GI:15128214
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 11792)
  AUTHORS   Rieder,M.J., Carrington,D.P., Chung,M.-W., Lee,K.L., Poel,C.L.,
            Yi,Q. and Nickerson,D.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2001) Molecular Biotechnology, University of
            Washington, 1705 NE Pacific, Seattle, WA 98195, USA
COMMENT     To cite this work please use:  SeattleSNPs. NHLBI Program for
            Genomic Applications, UW-FHCRC, Seattle, WA (URL:
            http://pga.mbt.washington.edu).
FEATURES             Location/Qualifiers
     source          1. .11792
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     repeat_region   489. .535
                     /rpt_family="MIR3"
                     /rpt_type=dispersed
     repeat_region   719. .857
                     /rpt_family="L2"
                     /rpt_type=dispersed
     variation       913
                     /frequency="0.01"
                     /replace="c"
     variation       1108
                     /frequency="0.07"
                     /replace="g"
     variation       1250
                     /frequency="0.01"
                     /replace="t"
     variation       1526
                     /frequency="0.04"
                     /replace="g"
     variation       1716. .1721
                     /frequency="0.01"
                     /replace=""
     gene            2030. .8791
                     /gene="IL12A"
     mRNA            join(2030. .2207,3200. .3345,6045. .6158,6484. .6525,
                     6601. .6642,6734. .6877,8439. .8791)
                     /gene="IL12A"
                     /product="interleukin 12A (natural killer cell stimulatory
                     factor 1, cytotoxic lymphocyte maturation factor 1, p35)"
     CDS             join(2192. .2207,3200. .3345,6045. .6158,6484. .6525,
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                6601. .6642,6734. .6877,8439. .8594)
                /gene="IL12A"
                /codon_start=1
                /product="interleukin 12A (natural killer cell stimulatory
                factor 1, cytotoxic lymphocyte maturation factor 1, p35)"
                /protein_id="AAK84425.1"
                /db_xref="GI:15128215"
                /translation="MCPARSLLLVATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNL
                LRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRET
                SFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNML
                AVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNA
                S"
repeat_region   2379. .2491
                /rpt_family="MIR"
                /rpt_type=dispersed
repeat_region   2533. .2830
                /rpt_family="AluSx"
                /rpt_type=dispersed
variation       2651
                /gene="IL12A"
                /frequency="0.01"
                /replace="g"
variation       2709
                /gene="IL12A"
                /frequency="0.01"
                /replace="c"
variation       2765
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variation       3025
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                /frequency="0.01"
                /replace="t"
variation       3362
                /gene="IL12A"
                /frequency="0.01"
                /replace="g"
variation       4071
                /gene="IL12A"
                /frequency="0.01"
                /replace="a"
variation       4238
                /gene="IL12A"
                /frequency="0.02"
                /replace="c"
repeat_region   4387. .4550
                /rpt_family="Charlie8"
                /rpt_type=dispersed
repeat_region   4618. .5111
                /rpt_family="MLT1D"
                /rpt_type=dispersed
variation       4897
                /gene="IL12A"
                /frequency="0.19"
                /replace="c"
variation       4909
                /gene="IL12A"
                /frequency="0.01"
                /replace="t"
variation       4926
                /gene="IL12A"
                /frequency="0.01"
                /replace="t"
variation       5071
                /gene="IL12A"
                /frequency="0.03"
                /replace="a"
repeat_region   5152. .5462
                /rpt_family="L2"
                /rpt_type=dispersed
variation       5247
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                /frequency="0.42"
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variation       5344
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                /frequency="0.44"
                /replace="a"
variation       5571
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                /frequency="0.08"
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variation       5574
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variation       5636
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                /replace="g"
variation       5757
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                /frequency="0.10"
                /replace="a"
variation       6229
                /gene="IL12A"
                /frequency="0.01"
                /replace="g"
variation       6238
                /gene="IL12A"
                /frequency="0.03"
                /replace="a"
repeat_region   6331. .6412
                /rpt_family="L1MB2"
                /rpt_type=dispersed
repeat_region   7112. .7214
                /rpt_family="MIR"
                /rpt_type=dispersed
variation       7300
                /gene="IL12A"
                /frequency="0.44"
                /replace="g"
variation       7304
                /gene="IL12A"
                /frequency="0.23"
                /replace="c"
variation       7476
                /gene="IL12A"
                /frequency="0.03"
                /replace="t"
variation       7519
                /gene="IL12A"
                /frequency="0.02"
                /replace="t"
repeat_region   7749. .7908
                /rpt_family="MIR"
                /rpt_type=dispersed
variation       7824
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                /replace="a"
variation       8241
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                /frequency="0.36"
                /replace="c"
variation       8335
                /gene="IL12A"
                /frequency="0.04"
                /replace="c"
misc_feature    8500. .8820
                /note="Region not scanned for variation"
variation       9094
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  Query Match             11.0%;  Score 65;  DB 5;  Length 11792;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 8543

Qy        544 ATTCG 548
              |||||
Db       8544 ATTCG 8548


RESULT 100
AC010370
LOCUS       AC010370               157079 bp    DNA     linear   PRI 23-JAN-2002
DEFINITION  Homo sapiens chromosome 3 clone CTD-2049J23, complete sequence.
ACCESSION   AC010370
VERSION     AC010370.5  GI:14573679
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 157079)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 157079)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE   3  (bases 1 to 157079)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
REFERENCE   4  (bases 1 to 157079)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JAN-2002) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
COMMENT     On Jun 28, 2001 this sequence version replaced gi:12830118.
            Draft Sequence Produced by DOE Joint Genome Institute
            www.jgi.doe.gov
            Finishing Completed at Stanford Human Genome Center
            www-shgc.stanford.edu
            Quality: Phrap Quality >=40 99.7% of Sequence;
            Estimated Total Number of Errors is 0.4.
FEATURES             Location/Qualifiers
     source          1. .157079
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="3"
                     /clone="CTD-2049J23"
ORIGIN

  Query Match             11.0%;  Score 65;  DB 5;  Length 157079;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Search completed: June 10, 2006, 06:52:42
Job time : 3747.84 secs
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 9, 2006, 22:34:58 ; Search time 3620.39 Seconds
(without alignments)
9128.382 Million cell updates/sec

Title: US-10-821-670A-35
Perfect score: 591
Sequence: 1 aggaacctccccacacccac.....tgagctatctgaatgcttcc 591

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 48236798 seqs, 27959665780 residues

Word size : 1

Total number of hits satisfying chosen parameters: 96473154

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 200 summaries

Database : EST:*
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2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
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6: gb_htc:*
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8: gb_est7:*
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10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	3	65	11.0	935	4	CD013914	CD013914 90138124
	4	65	11.0	1136	4	CD013915	CD013915 90138132
	5	65	11.0	1938	6	BC035571	BC035571 Homo sapi
	6	57	9.6	762	14	DQ033873	DQ033873 Pan trogl
	7	56	9.5	581	3	BP260963	BP260963 BP260963
	8	56	9.5	832	2	BI523569	BI523569 603175938
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	17	27	4.6	427	10	DT930939	DT930939 S13.1784
	18	27	4.6	456	10	DT913216	DT913216 S13.1426
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	20	27	4.6	563	3	BU698113	BU698113 LL2in1206
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126	19	3.2	507	2	BM366269	BM366269 BS3200240
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c 136	19	3.2	541	8	CR565401	CR565401 CR565401
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ALIGNMENTS

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VERSION     DQ033872.1  GI:66885081
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     A Scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
  JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
   PUBMED   15869325
REFERENCE   2  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
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FEATURES             Location/Qualifiers
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  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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DEFINITION  90138296 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD013916
VERSION     CD013916.1  GI:37777446
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 863)
  AUTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
            Au-Young,J. and Stuve,L.L.
  TITLE     PCR isolation and cloning of novel splice variant mRNAs from known
            drug target genes
  JOURNAL   Genomics 83 (4), 566-571 (2004)
   PUBMED   15028279
COMMENT     Contact: Jin, P.
            Incyte Corporation
            3160 Porter Drive, Palo Alto, CA 94304, USA
            Tel: 650 621 8639
            Fax: 650 621 8965
            Email: pjin@incyte.com.
FEATURES             Location/Qualifiers
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                     /clone_lib="Single gene library"
                     /note="Vector: pDrive Cloning Vector; RT-PCR was performed
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                     frame. PCR products were subcloned into pDrive Cloning
                     Vector and sequenced completely using M13 forward and
                     reverse primers. Sequencing gaps were closed by
                     re-sequencig using primers flanking the gapped areas."
ORIGIN

  Query Match             11.0%;  Score 65;  DB 4;  Length 863;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        701 ATTCG 705


RESULT 3
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LOCUS       CD013914                935 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION  90138124 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD013914
VERSION     CD013914.1  GI:37777444
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 935)
  AUTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
            Au-Young,J. and Stuve,L.L.
  TITLE     PCR isolation and cloning of novel splice variant mRNAs from known
            drug target genes
  JOURNAL   Genomics 83 (4), 566-571 (2004)
   PUBMED   15028279
COMMENT     Contact: Jin, P.
            Incyte Corporation
            3160 Porter Drive, Palo Alto, CA 94304, USA
            Tel: 650 621 8639
            Fax: 650 621 8965
            Email: pjin@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .935
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Single gene library"
                     /note="Vector: pDrive Cloning Vector; RT-PCR was performed
                     using gene-specific primers flanking the open-reading
                     frame. PCR products were subcloned into pDrive Cloning
                     Vector and sequenced completely using M13 forward and
                     reverse primers. Sequencing gaps were closed by
                     re-sequencig using primers flanking the gapped areas."
ORIGIN

  Query Match             11.0%;  Score 65;  DB 4;  Length 935;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        713 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 772

Qy        544 ATTCG 548
              |||||
Db        773 ATTCG 777


RESULT 4
CD013915
LOCUS       CD013915                1136 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION  90138132 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD013915
VERSION     CD013915.1  GI:37777445
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1136)
  AUTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
            Au-Young,J. and Stuve,L.L.
  TITLE     PCR isolation and cloning of novel splice variant mRNAs from known
            drug target genes
  JOURNAL   Genomics 83 (4), 566-571 (2004)
   PUBMED   15028279
COMMENT     Contact: Jin, P.
```

```
           Incyte Corporation
           3160 Porter Drive, Palo Alto, CA 94304, USA
           Tel: 650 621 8639
           Fax: 650 621 8965
           Email: pjin@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .1136
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Single gene library"
                     /note="Vector: pDrive Cloning Vector; RT-PCR was performed
                     using gene-specific primers flanking the open-reading
                     frame. PCR products were subcloned into pDrive Cloning
                     Vector and sequenced completely using M13 forward and
                     reverse primers. Sequencing gaps were closed by
                     re-sequencig using primers flanking the gapped areas."
ORIGIN

  Query Match            11.0%;  Score 65;  DB 4;  Length 1136;
  Best Local Similarity  100.0%;  Pred. No. 8.1e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        914 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 973

Qy        544 ATTCG 548
              |||||
Db        974 ATTCG 978


RESULT 5
BC035571
LOCUS       BC035571               1938 bp    mRNA    linear   HTC 04-MAR-2003
DEFINITION  Homo sapiens, clone IMAGE:5240216, mRNA.
ACCESSION   BC035571
VERSION     BC035571.1  GI:23958681
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1938)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 69 Row: b Column: 15
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 4504638
            This clone has the following problem: retained intron.
FEATURES             Location/Qualifiers
     source          1. .1938
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240216"
                     /tissue_type="Brain, fetal, whole pooled"
                     /clone_lib="NIH_MGC_121"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
ORIGIN

  Query Match            11.0%;  Score 65;  DB 6;  Length 1938;
  Best Local Similarity  100.0%;  Pred. No. 9e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1335 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1394

Qy        544 ATTCG 548
              |||||
Db       1395 ATTCG 1399


RESULT 6
DQ033873
LOCUS       DQ033873               762 bp    DNA     linear   GSS 02-JUN-2005
DEFINITION  Pan troglodytes IL12A gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   DQ033873
VERSION     DQ033873.1  GI:66885082
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     A Scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
  JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
   PUBMED   15869325
REFERENCE   2  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.  Translation starts at the beginning of
            alignment.
FEATURES             Location/Qualifiers
     source          1. .762
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     gene            <1. .>762
                     /gene="IL12A"
                     /locus_tag="HC3464"
ORIGIN

  Query Match             9.6%;  Score 57;  DB 14;  Length 762;
  Best Local Similarity  100.0%;  Pred. No. 2e-19;
  Matches   57;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy        492 GGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 GGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 716


RESULT 7
BP260963
LOCUS       BP260963                581 bp    mRNA    linear   EST 16-SEP-2004
DEFINITION  BP260963 Sugano cDNA library, small intestine Homo sapiens cDNA
            clone HSI02082, mRNA sequence.
ACCESSION   BP260963
VERSION     BP260963.1  GI:52176194
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 581)
  AUTHORS   Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
            Mizushima-Sugano,J., Nakai,K. and Sugano,S.
  TITLE     Sequence comparison of human and mouse genes reveals a homologous
            block structure in the promoter regions
  JOURNAL   Genome Res. 14 (9), 1711-1718 (2004)
   PUBMED   15342556
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Tel: 81-3-5449-5343
            Fax: 81-3-5449-5416
            Email: ysuzuki@hgc.jp.
FEATURES             Location/Qualifiers
     source          1. .581
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HSI02082"
                     /tissue_type="small intestine"
                     /clone_lib="Sugano cDNA library, small intestine"
ORIGIN

  Query Match             9.5%;  Score 56;  DB 3;  Length 581;
  Best Local Similarity   100.0%;  Pred. No. 6.9e-19;
  Matches   56;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        517 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 572


RESULT 8
BI523569
LOCUS       BI523569                832 bp    mRNA    linear   EST 29-AUG-2001
DEFINITION  603175938F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 5',
            mRNA sequence.
ACCESSION   BI523569
VERSION     BI523569.1  GI:15348361
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 832)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11605  row: 1  column: 09
            High quality sequence start: 23
            High quality sequence stop: 821.
FEATURES             Location/Qualifiers
     source          1. .832
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240216"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_121"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 017. Note:
                     this is a NIH_MGC Library."
ORIGIN

  Query Match             9.5%;  Score 56;  DB 2;  Length 832;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-19;
  Matches   56;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        520 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 575


RESULT 9
CE159257
LOCUS       CE159257                592 bp    DNA     linear   GSS 25-SEP-2003
DEFINITION  tigr-gss-dog-17000371408491 Dog Library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION   CE159257
VERSION     CE159257.1  GI:35287296
KEYWORDS    GSS.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 592)
  AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
            Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
            Venter,J.C.
  TITLE     The dog genome: survey sequencing and comparative analysis
  JOURNAL   Science 301 (5641), 1898-1903 (2003)
   PUBMED   14512627
COMMENT     Contact: Kirkness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirknes@tigr.org
            Class: shotgun.
FEATURES             Location/Qualifiers
     source          1. .592
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /strain="Standard Poodle"
                     /db_xref="taxon:9615"
                     /clone_lib="Dog Library"
                     /note="Site_1: BstXI; Libraries were prepared from
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peripheral blood"
ORIGIN

Query Match 8.1%; Score 48; DB 12; Length 592;
Best Local Similarity 100.0%; Pred. No. 1.9e-14;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 210
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 66 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 113

RESULT 10
BG702253
LOCUS BG702253 812 bp mRNA linear EST 07-MAY-2001
DEFINITION 602683459F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4816118 5', mRNA sequence.
ACCESSION BG702253
VERSION BG702253.1 GI:13973409
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 812)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10714 row: e column: 15
High quality sequence stop: 804.
FEATURES Location/Qualifiers
source 1. .812
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4816118"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_95"
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
ORIGIN

Query Match 8.0%; Score 47; DB 2; Length 812;
Best Local Similarity 100.0%; Pred. No. 7.1e-14;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 142 GATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 188
|||||||||||||||||||||||||||||||||||||||||||||||
Db 624 GATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 670

RESULT 11
BM257856
LOCUS BM257856 342 bp mRNA linear EST 17-DEC-2001
DEFINITION 521721 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BM257856
VERSION BM257856.1 GI:17893455
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 342)
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.
TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
JOURNAL Genome Res. 11 (4), 626-630 (2001)
PUBMED 11282978
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
PCR PRimers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 125 row: E column: 18
Seq primer: ATTTAGGTGACACTATAG.
FEATURES Location/Qualifiers
source 1. .342
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 3BOV"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."
ORIGIN

Query Match 6.9%; Score 41; DB 2; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 91 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTC 131
|||||||||||||||||||||||||||||||||||||||||
Db 294 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTC 334

RESULT 12
BI824638
LOCUS BI824638 447 bp mRNA linear EST 04-OCT-2001
DEFINITION 603033580F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175018 5', mRNA sequence.
ACCESSION BI824638
VERSION BI824638.1 GI:15936188
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 447)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

```
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11435  row: o  column: 19
            High quality sequence start: 3
            High quality sequence stop: 445.
FEATURES             Location/Qualifiers
     source          1. .447
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5175018"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_115"
                     /note="Organ: pooled brain, lung, testis; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of 6 male brains, age range 23-27; 1
                     male lung, age 27; and 1 male testis, age 69.  Library is
                     oligo-dT primed and directionally cloned (EcoRV site is
                     destroyed upon  cloning).  Average insert size 1.8 kb,
                     insert size range 1-3 kb. Library is normalized and
                     enriched for full-length clones and was  constructed by C.
                     Gruber (Invitrogen).  Research Genetics tracking  code
                     021. Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             6.9%;  Score 41;  DB 2;  Length 447;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-10;
  Matches   41;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        508 AAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 548
              |||||||||||||||||||||||||||||||||||||||||
Db          1 AAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 41


RESULT 13
BI523344/c
LOCUS       BI523344                1099 bp    mRNA    linear   EST 29-AUG-2001
DEFINITION  603175938T1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 3',
            mRNA sequence.
ACCESSION   BI523344
VERSION     BI523344.1  GI:15348136
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1099)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11605  row: l  column: 09
            High quality sequence start: 40
            High quality sequence stop: 727.
FEATURES             Location/Qualifiers
     source          1. .1099
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240216"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_121"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 017. Note:
                     this is a NIH_MGC Library."
ORIGIN

  Query Match             6.8%;  Score 40;  DB 2;  Length 1099;
  Best Local Similarity   100.0%;  Pred. No. 5.7e-10;
  Matches   40;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        509 AAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 548
              ||||||||||||||||||||||||||||||||||||||||
Db        524 AAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 485


RESULT 14
CR813130
LOCUS       CR813130                539 bp    DNA     linear   GSS 27-SEP-2004
DEFINITION  GR0AAA37CD06RM1 INRA BAC Bos taurus genomic clone INRAb_622G01, DNA
            sequence, genomic survey sequence.
ACCESSION   CR813130
VERSION     CR813130.1  GI:52749218
KEYWORDS    GSS.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 539)
  AUTHORS   Eggen,A., Schibler,L. and Roy,A.
  TITLE     Bovine BAC End Sequences from the INRA bovine BAC library
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 539)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-SEP-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Contact: Andre Eggen
            Department of Animal Genetics - LGbC
            INRA
            78350 Jouy-en-Josas, France
            Tel: 33 1 34 65 24 24
            Fax: 33 1 34 65 24 78
            Email: eggen@jouy.inra.fr
            Clones are derived from the INRA bovine BAC library
            (http://locus.jouy.inra.fr/fpc/cattle_bac_map.htm). For BAC library
            availability, please contact Andre Eggen (eggen@jouy.inra.fr). This
            work  was undertaken as part of the International Bovine BAC
            Mapping Consortium (IBBMC) by INRA (Jouy-en-Josas) and Genoscope
            (Evry) Plate: 622 row: G column: 01
            Seq primer: M13 Reverse
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .539
                     /organism="Bos taurus"
                     /mol_type="genomic DNA"
                     /strain="breed: Holstein"
                     /db_xref="taxon:9913"
                     /clone="INRAb_622G01"
                     /sex="Male"
```

```
                     /cell_type="fibroblast"
                     /clone_lib="INRA bovine BAC"
                     /note="Vector: pBeloBAC11; Site_1: HindIII; Holstein bull;
                     INRA Bovine BAC library (Male) produced by Andre Eggen
                     Genoscope sequence ID : GR0AAA37CD06RM1"
ORIGIN

  Query Match             4.9%;  Score 29;  DB 14;  Length 539;
  Best Local Similarity   100.0%;  Pred. No. 0.00062;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        210 GAATGAGAGTTGCCTGGCTTCCAGAGAGA 238
              |||||||||||||||||||||||||||||
Db        330 GAATGAGAGTTGCCTGGCTTCCAGAGAGA 358


RESULT 15
CR795312
LOCUS       CR795312                568 bp    DNA     linear   GSS 24-SEP-2004
DEFINITION  GR0AAA12DG09RM1 INRA BAC Bos taurus genomic clone INRAb_238E06, DNA
            sequence, genomic survey sequence.
ACCESSION   CR795312
VERSION     CR795312.1  GI:52676311
KEYWORDS    GSS.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 568)
  AUTHORS   Eggen,A., Schibler,L. and Roy,A.
  TITLE     Bovine BAC End Sequences from the INRA bovine BAC library
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 568)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-SEP-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Contact: Andre Eggen
            Department of Animal Genetics - LGbC
            INRA
            78350 Jouy-en-Josas, France
            Tel: 33 1 34 65 24 24
            Fax: 33 1 34 65 24 78
            Email: eggen@jouy.inra.fr
            Clones are derived from the INRA bovine BAC library
            (http://locus.jouy.inra.fr/fpc/cattle_bac_map.htm). For BAC library
            availability, please contact Andre Eggen (eggen@jouy.inra.fr). This
            work  was undertaken as part of the International Bovine BAC
            Mapping Consortium (IBBMC) by INRA (Jouy-en-Josas) and Genoscope
            (Evry) Plate: 238 row: E column: 06
            Seq primer: M13 Reverse
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .568
                     /organism="Bos taurus"
                     /mol_type="genomic DNA"
                     /strain="breed: Holstein"
                     /db_xref="taxon:9913"
                     /clone="INRAb_238E06"
                     /sex="Male"
                     /cell_type="fibroblast"
                     /clone_lib="INRA bovine BAC"
                     /note="Vector: pBeloBAC11; Site_1: HindIII; Holstein bull;
                     INRA Bovine BAC library (Male) produced by Andre Eggen
                     Genoscope sequence ID : GR0AAA12DG09RM1"
ORIGIN

  Query Match             4.9%;  Score 29;  DB 14;  Length 568;
  Best Local Similarity   100.0%;  Pred. No. 0.00063;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        210 GAATGAGAGTTGCCTGGCTTCCAGAGAGA 238
              |||||||||||||||||||||||||||||
Db        329 GAATGAGAGTTGCCTGGCTTCCAGAGAGA 357


RESULT 16
BF552757
LOCUS       BF552757                373 bp    mRNA    linear   EST 12-DEC-2000
DEFINITION  UI-R-C0-iz-d-02-0-UI.r1 UI-R-C0 Rattus norvegicus cDNA clone
            UI-R-C0-iz-d-02-0-UI 5', mRNA sequence.
ACCESSION   BF552757
VERSION     BF552757.1  GI:11662487
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 373)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  PUBMED    8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156  MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            cDNA Library Preparation: M.B. Soares Lab Clone distribution:
            clones will be available through Research Genetics (www.resgen.com)
            This clone is also available through the I.M.A.G.E. Consortium at
            LLNL (info@image.llnl.gov). IMAGE ID= 1782759
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .373
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="UI-R-C0-iz-d-02-0-UI"
                     /dev_stage="adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="UI-R-C0"
                     /note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI;
                     The UI-R-C0 library is a subtracted library derived from
                     the UI-R-A1 and UI-R-E1 libraries. The UI-R-A1 library
                     consisted of a mixture of individually tagged normalized
                     libraries constructed from rat  placenta, adult lung,
                     brain, liver, kidney, heart, spleen, ovary,  and muscle.
                     The UI-R-E1 library  consisted of a mixture of
                     individually tagged normalized libraries constructed from
                     8, 12 and 18-day embryo. The tag is a string of 3-5
                     nucleotides present between the Not I  site and the
                     oligo-dT track which allows identification of the library
                     of origin of a clone within the mixture. The subtracted
                     library (UI-R-C0) was constructed as follows: PCR
                     amplified cDNA inserts from a pool of UI-R-A1 and UI-R-E1
                     clones from which 3' ESTs had been derived was used as a
                     driver in a hybridization with the pooled UI-R-A1 and
                     UI-R-E1 library in the form of single-stranded circles.
                     The remaining single-stranded circles (subtracted library)
                     was purified by hydroxyapatite column chromatography,
                     converted to double-stranded circles and electroporated
                     into DH10B bacteria (Life Technologies) to generate the
                     UI-R-C0 library. This procedure has been previously
                     described (Bonaldo, Lennon and Soares, Genome Research 6:
                     791-806, 1996)"
ORIGIN

  Query Match             4.6%;  Score 27;  DB 7;  Length 373;
```

```
  Best Local Similarity   100.0%;  Pred. No. 0.0074;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        313 ATCTATGAGGACTTGAAGATGTACCAG 339
              |||||||||||||||||||||||||||
Db        101 ATCTATGAGGACTTGAAGATGTACCAG 127


RESULT 17
DT930939
LOCUS       DT930939                427 bp    mRNA    linear   EST 20-SEP-2005
DEFINITION  S13.1784 Hematopoietic stem cells Mus musculus cDNA, mRNA sequence.
ACCESSION   DT930939
VERSION     DT930939.1  GI:75963455
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 427)
  AUTHORS   Pritsker,M., Doniger,T.T., Kramer,L.C., Westcot,S.E. and
            Lemischka,I.R.
  TITLE     Diversification of Stem Cell Molecular Repertoire by Alternative
            Splicing
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. (2005) In press
COMMENT     Contact: Pritsker M
            Lab of Ihor Lemischka, Department of Molecular Biology
            Princeton University
            Princeton, NJ 08544, USA
            Tel: 609 258 5657
            Fax: 609 258 1704
            Email: pritsker@molbio.princeton.edu.
FEATURES             Location/Qualifiers
     source          1. .427
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /tissue_type="Hematopoietic stem cells"
                     /cell_type="Hematopoietic stem cells"
                     /clone_lib="Hematopoietic stem cells"
                     /note="cDNA library was made from FACS-purified
                     hematopoietic stem cells"
ORIGIN

  Query Match             4.6%;  Score 27;  DB 10;  Length 427;
  Best Local Similarity   100.0%;  Pred. No. 0.0076;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        313 ATCTATGAGGACTTGAAGATGTACCAG 339
              |||||||||||||||||||||||||||
Db        385 ATCTATGAGGACTTGAAGATGTACCAG 411


RESULT 18
DT913216
LOCUS       DT913216                456 bp    mRNA    linear   EST 19-SEP-2005
DEFINITION  S13.1426 Hematopoietic stem cells Mus musculus cDNA, mRNA sequence.
ACCESSION   DT913216
VERSION     DT913216.1  GI:75893697
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   Pritsker,M., Doniger,T.T., Kramer,L.C., Westcot,S.E. and
            Lemischka,I.R.
  TITLE     Diversification of Stem Cell Molecular Repertoire by Alternative
            Splicing
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. (2005) In press
COMMENT     Contact: Pritsker M
            Lab of Ihor Lemischka, Department of Molecular Biology
            Princeton University
            Princeton, NJ 08544, USA
            Tel: 609 258 5657
            Fax: 609 258 1704
            Email: pritsker@molbio.princeton.edu.
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /tissue_type="Hematopoietic stem cells"
                     /cell_type="Hematopoietic stem cells"
                     /clone_lib="Hematopoietic stem cells"
                     /note="cDNA library was made from FACS-purified
                     hematopoietic stem cells"
ORIGIN

  Query Match             4.6%;  Score 27;  DB 10;  Length 456;
  Best Local Similarity   100.0%;  Pred. No. 0.0077;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        313 ATCTATGAGGACTTGAAGATGTACCAG 339
              |||||||||||||||||||||||||||
Db        385 ATCTATGAGGACTTGAAGATGTACCAG 411


RESULT 19
BU699383
LOCUS       BU699383                561 bp    mRNA    linear   EST 09-OCT-2002
DEFINITION  LL2in11573T7 Hematopoietic Stem Cell Subtracted Library Mus
            musculus cDNA 5' similar to interleukin 12 p35 subunit, mRNA
            sequence.
ACCESSION   BU699383
VERSION     BU699383.1  GI:23615967
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 561)
  AUTHORS   Phillips,R.L., Ernst,R.E., Brunk,B.P., Ivanova,N., Mahan,M.A.,
            Deanehan,J.K., Moore,K.A., Overton,G.C. and Lemischka,I.R.
  TITLE     The genetic program of hematopoietic stem cells
  JOURNAL   Science 288 (5471), 1635-1640 (2000)
   PUBMED   10834841
COMMENT     Contact: Lemischka, Ihor R.
            Department of Molecular Biology
            Princeton University
            Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544, USA
            Tel: 609 258 2838
            Fax: 609 258 2759
            Email: ilemischka@molbio.princeton.edu
            These ESTs are derived from a subtracted cDNA library enriched for
            gene products expressed in day 14-14.5 fetal liver hematopoietic
            stem cells defined as Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E
            (Sca-1)pos
            Seq primer: M13Reverse or T7.
FEATURES             Location/Qualifiers
     source          1. .561
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /tissue_type="Hematopoietic"
                     /cell_type="Stem Cells; Lineageneg/lo, AA4.1pos, cKitpos,
                     Ly6A/E (Sca-1)pos"
                     /dev_stage="Embryonic day 14-14.5"
                     /lab_host="DH10B"
                     /clone_lib="Hematopoietic Stem Cell Subtracted Library"
                     /note="Organ: Fetal Liver; Vector: Sport 1; Site_1: Sal I;
                     Site_2: Not I; Two directionally cloned cDNA libraries
```

were made from fetal liver hematopoietic stem cells enriched to be Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E (Sca-1)pos called Scapos and from AA4.1neg fetal liver cells. Subtractive hybridization was performed by hybridization of the target, Scapos, single stranded cDNA library in pSport1 to biotinylated RNA transcribed from the driver, AA4.1neg cDNA library in pSport2 with inserts cloned in the complementary orientation. For detailed protocols and additional information please see our website at http://stemcell.princeton.edu."

ORIGIN

Query Match 4.6%; Score 27; DB 3; Length 561;
Best Local Similarity 100.0%; Pred. No. 0.008;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 313 ATCTATGAGGACTTGAAGATGTACCAG 339
||||||||||||||||||||||||||
Db 302 ATCTATGAGGACTTGAAGATGTACCAG 328

RESULT 20
BU698113
LOCUS BU698113 563 bp mRNA linear EST 09-OCT-2002
DEFINITION LL2in12067T7 Hematopoietic Stem Cell Subtracted Library Mus musculus cDNA 5' similar to interleukin 12 p35 subunit, mRNA sequence.
ACCESSION BU698113
VERSION BU698113.1 GI:23610620
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 563)
AUTHORS Phillips,R.L., Ernst,R.E., Brunk,B.P., Ivanova,N., Mahan,M.A., Deanehan,J.K., Moore,K.A., Overton,G.C. and Lemischka,I.R.
TITLE The genetic program of hematopoietic stem cells
JOURNAL Science 288 (5471), 1635-1640 (2000)
PUBMED 10834841
COMMENT Contact: Lemischka, Ihor R.
Department of Molecular Biology
Princeton University
Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544, USA
Tel: 609 258 2838
Fax: 609 258 2759
Email: ilemischka@molbio.princeton.edu
These ESTs are derived from a subtracted cDNA library enriched for gene products expressed in day 14-14.5 fetal liver hematopoietic stem cells defined as Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E (Sca-1)pos
Seq primer: M13Reverse or T7.
FEATURES Location/Qualifiers
source 1. .563
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/tissue_type="Hematopoietic"
/cell_type="Stem Cells; Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E (Sca-1)pos"
/dev_stage="Embryonic day 14-14.5"
/lab_host="DH10B"
/clone_lib="Hematopoietic Stem Cell Subtracted Library"
/note="Organ: Fetal Liver; Vector: Sport 1; Site_1: Sal I; Site_2: Not I; Two directionally cloned cDNA libraries were made from fetal liver hematopoietic stem cells enriched to be Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E (Sca-1)pos called Scapos and from AA4.1neg fetal liver cells. Subtractive hybridization was performed by hybridization of the target, Scapos, single stranded cDNA library in pSport1 to biotinylated RNA transcribed from the driver, AA4.1neg cDNA library in pSport2 with inserts cloned in the complementary orientation. For detailed protocols and additional information please see our website at http://stemcell.princeton.edu."
ORIGIN

Query Match 4.6%; Score 27; DB 3; Length 563;
Best Local Similarity 100.0%; Pred. No. 0.008;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 313 ATCTATGAGGACTTGAAGATGTACCAG 339
||||||||||||||||||||||||||
Db 318 ATCTATGAGGACTTGAAGATGTACCAG 344

RESULT 21
AI050362
LOCUS AI050362 589 bp mRNA linear EST 09-JUL-1998
DEFINITION ub30a07.r1 Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:1379220 5' similar to gb:M65291 INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (HUMAN); gb:M86672 Mus musculus interleukin 12 p35 subunit, complete cds (MOUSE);, mRNA sequence.
ACCESSION AI050362
VERSION AI050362.1 GI:3299479
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 589)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:901688
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 60.
FEATURES Location/Qualifiers
source 1. .589
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1379220"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares_thymus_2NbMT"
/note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGGAGCGGCCGCGTTTTTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
ORIGIN

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  Query Match             4.6%;  Score 27;  DB 1;  Length 589;
  Best Local Similarity   100.0%;  Pred. No. 0.0081;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        313 ATCTATGAGGACTTGAAGATGTACCAG 339
              |||||||||||||||||||||||||||
Db        327 ATCTATGAGGACTTGAAGATGTACCAG 353


RESULT 22
CJ137697
LOCUS       CJ137697                692 bp    mRNA    linear   EST 23-SEP-2005
DEFINITION  CJ137697 RIKEN full-length enriched mouse cDNA library, C57BL/6J
            thymus 3 days neonate Mus musculus cDNA clone A630064E02 5', mRNA
            sequence.
ACCESSION   CJ137697
VERSION     CJ137697.1  GI:76238025
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 692)
  AUTHORS   The FANTOM Consortium and RIKEN Genome Exploration Research Group
            and Genome Science Group (Genome Network Project Core Group).
  TITLE     The transcriptional landscape of the mammalian genome
  JOURNAL   Science 309 (5740), 1559-1563 (2005)
   PUBMED   16141072
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. Tissues were provided by Dr. John Todd (
            Dept. of Medical Genetics Wellcome Trust Centre for Molecular
            Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes
            Hospital Cambridge ) whose assistance we gratefully acknowledge.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
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                     C57BL/6J thymus 3 days neonate"
ORIGIN

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  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        313 ATCTATGAGGACTTGAAGATGTACCAG 339
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Db        521 ATCTATGAGGACTTGAAGATGTACCAG 547


RESULT 23
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LOCUS       AK153729                1299 bp    mRNA    linear   HTC 21-SEP-2005
DEFINITION  Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
            library, clone:A630064E02 product:interleukin 12a, full insert
            sequence.
ACCESSION   AK153729
VERSION     AK153729.1  GI:74148962
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
            Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
            Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
            Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
            Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
            Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
            Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
            Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
            Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  CONSRTM   RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
   PUBMED   11217851
REFERENCE   5
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
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Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420 (6915), 563-573 (2002)

PUBMED 12466851

REFERENCE 6

AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE The transcriptional landscape of the mammalian genome

JOURNAL Science 309 (5740), 1559-1563 (2005)

PUBMED 16141072

REFERENCE 7

AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.

CONSRTM RIKEN Genome Exploration Research Group

TITLE Antisense transcription in the mammalian transcriptome

JOURNAL Science 309 (5740), 1564-1566 (2005)

PUBMED 16141073

REFERENCE 8 (bases 1 to 1299)

AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

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ORIGIN

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RESULT 24
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DEFINITION Sus scrofa genomic clone PigE-253A7, genomic survey sequence.
ACCESSION CT080894
VERSION CT080894.1 GI:78647963
KEYWORDS GSS.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 777)
AUTHORS Humphray,S.J., Plumb,R.W. and Durham,J.L.
TITLE Direct Submission
JOURNAL Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished
COMMENT This sequence was generated from the SP6 end of BAC 253A7. 253A7 is part of the PigEBAC BAC Library created by Roslin Institute/RFCGR. Further details: http://www.sanger.ac.uk/Projects/S_scrofa/.
FEATURES Location/Qualifiers
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/note="vector pBeloBAC11
sex male"

ORIGIN

Query Match 4.1%; Score 24; DB 14; Length 777;
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 294 GACCCTGTGCCTTAGCAGTATCTA 317
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Db 551 GACCCTGTGCCTTAGCAGTATCTA 574

RESULT 25
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LOCUS BY230958 354 bp mRNA linear EST 10-DEC-2002
DEFINITION BY230958 RIKEN full-length enriched, adult inner ear Mus musculus cDNA clone F930017D02 5', mRNA sequence.
ACCESSION BY230958
VERSION BY230958.1 GI:26412068
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 354)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Kirk W. Beisel (Boys Town National Research Hospital 555 North 30th Street Omaha,NE 68131 USA) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
FEATURES Location/Qualifiers
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/db_xref="taxon:10090"
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ORIGIN

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Qy 313 ATCTATGAGGACTTGAAGATGTA 335
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RESULT 26
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DEFINITION qq19a07.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1932948 3' similar to gb:M65291 INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION AI332701
VERSION AI332701.1 GI:4069260
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 528)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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High quality sequence stop: 451.
FEATURES Location/Qualifiers
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                     pregnant uterus"
                     /lab_host="DH10B"
                     /clone_lib="Soares_NhHMPu_S1"
                     /note="Organ: mixed (see below); Vector: pT7T3D-PacI;
                     Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid
                     DNA from three normalized libraries (melanocyte 2NbHM,
                     pregnant uterus NbHPU, and fetal heart NbHH19W) were
                     mixed, and ss circles were made in vitro. Following HAP
                     purification, this DNA was used as tracer in a subtractive
                     hybridization reaction. The driver was PCR-amplified cDNAs
                     from pools of 5,000 clones made from the same 3 libraries.
                     The pools consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."
ORIGIN

  Query Match             3.9%;  Score 23;  DB 1;  Length 528;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        569 TGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||
Db        482 TGATGAGCTATCTGAATGCTTCC 460


RESULT 27
BZ261813
LOCUS       BZ261813                840 bp    DNA     linear   GSS 15-OCT-2002
DEFINITION  CH230-420O11.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone
            CH230-420O11, genomic survey sequence.
ACCESSION   BZ261813
VERSION     BZ261813.1  GI:23972184
KEYWORDS    GSS.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 840)
  AUTHORS   Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
            Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D.,
            Riggs,F., de Jong,P. and Fraser,C.M.
  TITLE     Rat BAC End Sequences from Library CHORI-230 MboI segment
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the rat BAC library CHORI-230
            (http://www.chori.org/bacpac/rat230.htm). For BAC library
            availability, please contact Pieter de Jong (pdejong@mail.cho.org).
            Clones may be purchased from BACPAC Resources
            (http://www.chori.org/bacpac/or ering_information.htm). BAC end
            page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
            Plate: 420  row: O  column: 11
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .840
                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /strain="BN/SsNHsd/MCW"
                     /db_xref="taxon:10116"
                     /clone="CH230-420O11"
                     /sex="Female"
                     /cell_type="Brain"
                     /clone_lib="CHORI-230 Segment 2"
                     /note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
                     CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
                     Pieter de Jong"
ORIGIN

  Query Match             3.9%;  Score 23;  DB 11;  Length 840;
  Best Local Similarity   100.0%;  Pred. No. 1.4;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        179 TGGAGGCCTGCTTACCACTGGAA 201
              |||||||||||||||||||||||
Db        377 TGGAGGCCTGCTTACCACTGGAA 399


RESULT 28
CE841948/c
LOCUS       CE841948                588 bp    DNA     linear   GSS 01-OCT-2003
DEFINITION  tigr-gss-dog-17000332674172 Dog Library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION   CE841948
VERSION     CE841948.1  GI:37204217
KEYWORDS    GSS.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 588)
  AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
            Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
            Venter,J.C.
  TITLE     The dog genome: survey sequencing and comparative analysis
  JOURNAL   Science 301 (5641), 1898-1903 (2003)
   PUBMED   14512627
COMMENT     Contact: Kirkness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirknes@tigr.org
            Class: shotgun.
FEATURES             Location/Qualifiers
     source          1. .588
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /strain="Standard Poodle"
                     /db_xref="taxon:9615"
                     /clone_lib="Dog Library"
                     /note="Site_1: BstXI; Libraries were prepared from
                     peripheral blood"
ORIGIN

  Query Match             3.7%;  Score 22;  DB 12;  Length 588;
  Best Local Similarity   100.0%;  Pred. No. 4.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        494 ATTTTTATAAAACTAAAATCAA 515
              ||||||||||||||||||||||
Db        166 ATTTTTATAAAACTAAAATCAA 145


RESULT 29
CT100632
LOCUS       CT100632                758 bp    DNA     linear   GSS 01-NOV-2005
DEFINITION  Sus scrofa genomic clone CH242-93N13, genomic survey sequence.
ACCESSION   CT100632
VERSION     CT100632.1  GI:78654237
KEYWORDS    GSS.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 758)
  AUTHORS   Humphray,S.J., Plumb,R.W. and Durham,J.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Unpublished
COMMENT     This sequence was generated from the SP6 end of BAC 93N13. 93N13 is
            part of the CHORI-242 BAC Library created by P. de Jong. Further
            details: http://www.sanger.ac.uk/Projects/S_scrofa/.
FEATURES             Location/Qualifiers
     source          1. .758
                     /organism="Sus scrofa"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9823"
                     /clone="CH242-93N13"
                     /tissue_type="White blood cells"
                     /note="vector pTARBAC1.3_BamHI
                     sex female"
ORIGIN

  Query Match             3.7%;  Score 22;  DB 14;  Length 758;
  Best Local Similarity   100.0%;  Pred. No. 5;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        416 CAGCTATTGATGAGCTGTTACA 437
              ||||||||||||||||||||||
Db        351 CAGCTATTGATGAGCTGTTACA 372


RESULT 30
AQ100596
LOCUS       AQ100596                380 bp    DNA     linear   GSS 27-AUG-1998
DEFINITION  HS_3064_B1_F08_MR CIT Approved Human Genomic Sperm Library D Homo
            sapiens genomic clone Plate=3064 Col=15 Row=L, genomic survey
            sequence.
ACCESSION   AQ100596
VERSION     AQ100596.1  GI:3471625
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 380)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
   PUBMED   10449764
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Sequence Tagged Connector
            Plate: 3064  row: L  column: 15
            Class: BAC ends
            High quality sequence stop: 380.
FEATURES             Location/Qualifiers
     source          1. .380
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="Plate=3064 Col=15 Row=L"
                     /sex="male"
                     /clone_lib="CIT Approved Human Genomic Sperm Library D"
                     /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                     E-Coli DH10B"
ORIGIN

  Query Match             3.6%;  Score 21;  DB 11;  Length 380;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        250 ACTAATGGGAGTTGCCTGGCC 270
              |||||||||||||||||||||
Db         42 ACTAATGGGAGTTGCCTGGCC 62


RESULT 31
AQ393691/c
LOCUS       AQ393691                489 bp    DNA     linear   GSS 06-MAR-1999
DEFINITION  CITBI-E1-2544N3.TF CITBI-E1 Homo sapiens genomic clone 2544N3,
            genomic survey sequence.
ACCESSION   AQ393691
VERSION     AQ393691.1  GI:4364714
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 489)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
            Venter,J.C.
  TITLE     Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Other_GSSs: CITBI-E1-2544N3.TR
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are available from Research Genetics (info@resgen.com). BAC
            end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: M13-21
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .489
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="2544N3"
                     /sex="male"
                     /cell_type="sperm"
                     /clone_lib="CITBI-E1"
                     /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
                     CalTech Human BAC Library D"
ORIGIN

  Query Match             3.6%;  Score 21;  DB 11;  Length 489;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        212 ATGAGAGTTGCCTGGCTTCCA 232
              |||||||||||||||||||||
Db        441 ATGAGAGTTGCCTGGCTTCCA 421


RESULT 32
CV068291/c
LOCUS       CV068291                540 bp    mRNA    linear   EST 24-AUG-2004
DEFINITION  Le_mx0_43b06_SP6 Little Skate Multiple Tissues, Normalized
            Leucoraja erinacea cDNA clone Le_mx0_43b06 5' similar to
            emb|CAG02559.1| unnamed protein product - Tetraodon nigroviridis.
            Score = 248 bits (632), Expect = 6e-65, mRNA sequence.
```

```
ACCESSION   CV068291
VERSION     CV068291.1  GI:51531455
KEYWORDS    EST.
SOURCE      Leucoraja erinacea (little skate)
  ORGANISM  Leucoraja erinacea
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
            Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
            Rajiformes; Rajidae; Leucoraja.
REFERENCE   1  (bases 1 to 540)
  AUTHORS   Towle,D.W. and Smith,C.M.
  TITLE     Expressed sequence tags in a normalized cDNA library prepared from
            multiple tissues of adult little skate, Leucoraja erinacea
  JOURNAL   Unpublished (2004)
COMMENT     Contact: David W. Towle
            Marine DNA Sequencing and Analysis Center
            Mount Desert Island Biological Laboratory
            Old Bar Harbor Road, Salsbury Cove, ME 04672 USA
            Tel: 207-288-9880 x474
            Fax: 207-288-2130
            Email: dtowle@mdibl.org
            Plate: 43  row: b  column: 06
            Seq primer: SP6
            High quality sequence stop: 501.
FEATURES             Location/Qualifiers
     source          1. .540
                     /organism="Leucoraja erinacea"
                     /mol_type="mRNA"
                     /db_xref="taxon:7782"
                     /clone="Le_mx0_43b06"
                     /tissue_type="Liver, kidney, brain, testis, ovary, gill,
                     heart, spleen, rectal gland"
                     /dev_stage="Adult"
                     /clone_lib="Little Skate Multiple Tissues, Normalized"
                     /note="Vector: pCMV Sport 6.1; Total RNA samples were
                     prepared individually from each tissue, checked for
                     quality, then pooled for construction and normalization of
                     cDNA library by Invitrogen. Plasmids were isolated and
                     inserts end-sequenced by the Marine DNA Sequencing and
                     Analysis Facility at Mount Desert Island Biological
                     Laboratory. Traces were processed for submission to dbEST
                     by trace2dbest software (Parkinson, Anthony and Blaxter,
                     unpublished software)."
ORIGIN

  Query Match             3.6%;  Score 21;  DB 8;  Length 540;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 CCCACACCCACACCAAGCCCA 30
              ||||||||||||||||||||
Db        528 CCCACACCCACACCAAGCCCA 508


RESULT 33
BU002107
LOCUS       BU002107                679 bp    mRNA    linear   EST 03-OCT-2005
DEFINITION  QGG30D21.yg.ab1 QG_EFGHJ lettuce serriola Lactuca serriola cDNA
            clone QGG30D21, mRNA sequence.
ACCESSION   BU002107
VERSION     BU002107.1  GI:22436502
KEYWORDS    EST.
SOURCE      Lactuca serriola
  ORGANISM  Lactuca serriola
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
            Cichorieae; Lactuca.
REFERENCE   1  (bases 1 to 679)
  AUTHORS   Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
            Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J.,
            Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,
            Lai,Z., Church,S., Jackson,L. and Bradford,K.
  TITLE     Lettuce and Sunflower ESTs from the Compositae Genome Project
            http://compgenomics.ucdavis.edu/
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Alexander Kozik [R.W.Michelmore]
            Department of Vegetable Crops, R.W.Michelmore Lab
            University of California at Davis (UCD)
            Asmundson Hall, UCD, Davis, CA 95616, USA
            Tel: 1-(530)-742-1742
            Fax: 1-(530)-752-9659
            Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
            singleton, see http://cgpdb.ucdavis.edu/ for details.
            Plate: QGG30  row: D  column: 21.
FEATURES             Location/Qualifiers
     source          1. .679
                     /organism="Lactuca serriola"
                     /mol_type="mRNA"
                     /db_xref="taxon:75943"
                     /clone="QGG30D21"
                     /lab_host="E.coli"
                     /clone_lib="QG_EFGHJ lettuce serriola"
                     /note="Vector: pBRcDNASfiAB; The library was constructed
                     from 10 different sources of RNA from a single genotype.
                     Separate cDNAs were generated using primers that
                     incorporated unique 5' and 3' tags to distinguish each
                     source of RNA. cDNAs were then pooled, size-fractionated,
                     directionally cloned into a custom medium-copy vector and
                     transformations made with four size classes to minimize
                     size bias. Details of each source of RNA and library
                     construction can be obtained at http://cgpdb.ucdavis.edu/
                     TAG_TISSUE=flowers pre-fertilized
                     TAG_LIB=QG_EFGHJ lettuce serriola
                     TAG_SEQ=GCTTGACGGG"
ORIGIN

  Query Match             3.6%;  Score 21;  DB 3;  Length 679;
  Best Local Similarity   100.0%;  Pred. No. 18;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        198 GGAATTAACCATGAATGAGAG 218
              ||||||||||||||||||||
Db          8 GGAATTAACCATGAATGAGAG 28


RESULT 34
AQ631366/c
LOCUS       AQ631366                733 bp    DNA     linear   GSS 17-JUN-1999
DEFINITION  RPCI-11-482B16.TV RPCI-11 Homo sapiens genomic clone
            RPCI-11-482B16, genomic survey sequence.
ACCESSION   AQ631366
VERSION     AQ631366.1  GI:5094001
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 733)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
            Venter,J.C.
  TITLE     Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genet cs (info@resgen.com). BAC end search page:
```

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            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: T7
            Class: BAC ends.
FEATURES              Location/Qualifiers
     source           1. .733
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="GDB:7684743"
                      /db_xref="taxon:9606"
                      /clone="RPCI-11-482B16"
                      /sex="Male"
                      /cell_type="Lymphocytes"
                      /clone_lib="RPCI-11"
                      /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                      RPCI11 Human Male BAC Library"
ORIGIN

  Query Match             3.6%;  Score 21;  DB 11;  Length 733;
  Best Local Similarity   100.0%;  Pred. No. 18;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        494 ATTTTTATAAAACTAAAATCA 514
              |||||||||||||||||||||
Db        145 ATTTTTATAAAACTAAAATCA 125


RESULT 35
W29456/c
LOCUS       W29456                 1109 bp    mRNA    linear   EST 11-SEP-1996
DEFINITION  mc03e02.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone
            IMAGE:337850 5' similar to SW:IF4G_RABIT P41110 EUKARYOTIC
            INITIATION FACTOR 4 GAMMA ;, mRNA sequence.
ACCESSION   W29456
VERSION     W29456.1  GI:1309666
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1109)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:219250
            Seq primer: ETPrimer
            High quality sequence stop: 285.
FEATURES              Location/Qualifiers
     source           1. .1109
                      /organism="Mus musculus"
                      /mol_type="mRNA"
                      /db_xref="taxon:10090"
                      /clone="IMAGE:337850"
                      /dev_stage="19.5 dpc total fetus"
                      /lab_host="DH10B (ampicillin resistant)"
                      /clone_lib="Soares mouse p3NMF19.5"
                      /note="Vector: pT7T3D (Pharmacia) with a modified
                      polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                      was primed with a Not I - oligo(dT) primer [5'
                      TGTTACCAATCTGAAGTGGGAGCGGCCGCATTTTTTTTTTTTTTTTTT 3'],
                      double-stranded cDNA was size selected, ligated to Eco RI
                      adapters (Pharmacia), digested with Not I and cloned into
                      the Not I and Eco RI sites of a modified pT7T3 vector
                      (Pharmacia). Library went through one round of
                      normalization to a Cot = 5. Library constructed by Bento
                      Soares and M.Fatima Bonaldo. RNA was kindly provided by
                      Dr. Minoru Ko (Wayne State University)."
ORIGIN

  Query Match             3.6%;  Score 21;  DB 10;  Length 1109;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 CCCCACACCCACACCAAGCCC 29
              |||||||||||||||||||||
Db       1078 CCCCACACCCACACCAAGCCC 1058


RESULT 36
AZ901502/c
LOCUS       AZ901502                 229 bp    DNA     linear   GSS 05-MAR-2001
DEFINITION  RPCI-24-154C7.TJ RPCI-24 Mus musculus genomic clone RPCI-24-154C7,
            genomic survey sequence.
ACCESSION   AZ901502
VERSION     AZ901502.1  GI:13220447
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 229)
  AUTHORS   Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
            Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
            Russell,D., de Jong,P. and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-24
  JOURNAL   Unpublished (1999)
COMMENT     Other_GSSs: RPCI-24-154C7.TV
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-24. For BAC
            library availability, please contact Pieter de Jong
            (pdejong@mail.cho.org). Clones may be purchased from BACPAC
            Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
            page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 154  row: C  column: 7
            Seq primer: SP6
            Class: BAC ends.
FEATURES              Location/Qualifiers
     source           1. .229
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="RPCI-24-154C7"
                      /sex="Male"
                      /cell_type="Spleen/Brain"
                      /clone_lib="RPCI-24"
                      /note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
                      RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
                      library was  cloned in the pTARBAC1 cloning vector at the
                      BamH1 sites using MboI  partially digested male C57BL/6J
                      DNA."
ORIGIN

  Query Match             3.4%;  Score 20;  DB 11;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 51;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          8 TCCCCACACCCACACCAAGC 27
              ||||||||||||||||||||
Db        229 TCCCCACACCCACACCAAGC 210


RESULT 37
AZ891891/c
LOCUS       AZ891891                 241 bp    DNA     linear   GSS 05-MAR-2001
DEFINITION  RPCI-24-201J11.TV RPCI-24 Mus musculus genomic clone
            RPCI-24-201J11, genomic survey sequence.
ACCESSION   AZ891891
VERSION     AZ891891.1  GI:13210836
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 241)
  AUTHORS   Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
            Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
            Russell,D., de Jong,P. and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-24
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-24. For BAC
            library availability, please contact Pieter de Jong
            (pdejong@mail.cho.org). Clones may be purchased from BACPAC
            Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
            page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 201  row: J  column: 11
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .241
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="RPCI-24-201J11"
                     /sex="Male"
                     /cell_type="Spleen/Brain"
                     /clone_lib="RPCI-24"
                     /note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
                     RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
                     library was  cloned in the pTARBAC1 cloning vector at the
                     BamH1 sites using MboI  partially digested male C57BL/6J
                     DNA."
ORIGIN

  Query Match             3.4%;  Score 20;  DB 11;  Length 241;
  Best Local Similarity   100.0%;  Pred. No. 51;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        494 ATTTTTATAAAACTAAAATC 513
              ||||||||||||||||||||
Db         20 ATTTTTATAAAACTAAAATC 1


RESULT 38
BX537236
LOCUS       BX537236                 344 bp    DNA     linear   GSS 05-JUN-2003
DEFINITION  INRA porcine BAC library, clone 0849A01 BAC end sequence (Uni M13),
            genomic survey sequence.
ACCESSION   BX537236
VERSION     BX537236.1  GI:31455351
KEYWORDS    GSS; genome survey sequence.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1
  AUTHORS   Rogel-Gaillard,C., Bourgeaux,N., Billault,A., Vaiman,M. and
            Chardon,P.
  TITLE     Construction of a swine BAC library: application to the
            characterization and mapping of porcine type C endoviral elements
  JOURNAL   Cytogenet. Cell Genet. 85 (3-4), 205-211 (1999)
   PUBMED   10449899
REFERENCE   2  (bases 1 to 344)
  AUTHORS   Robic,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JUN-2003) Robic A., INRA, Laboratoire de Genetique
            Cellulaire, chemin de Borde rouge, BP27, Auzeville, 31626, FRANCE
            Phone : 05 61 28 51 15 Fax : 05 61 28 53 08 Email :
            arobic@toulouse.inra.fr
FEATURES             Location/Qualifiers
     source          1. .344
                     /organism="Sus scrofa"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9823"
                     /clone="0849A01"
                     /note="library Rogel gaillard et al 1999, clone 0849A01
                     Clone distribution : AGENAE Resource center. Francois
                     PIUMI, Francois.Piumi@jouy.inra.fr, INRA, CEA
                     Radiobiologie et Etude du genome (LREG), Domaine de
                     Vilvert, 78352, Jouy-en-Josas cedex, FRANCE"
ORIGIN

  Query Match             3.4%;  Score 20;  DB 14;  Length 344;
  Best Local Similarity   100.0%;  Pred. No. 55;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        385 AGGCAGATCTTTCTGGATCA 404
              ||||||||||||||||||||
Db         22 AGGCAGATCTTTCTGGATCA 41


RESULT 39
BY394944
LOCUS       BY394944                 389 bp    mRNA    linear   EST 12-DEC-2002
DEFINITION  BY394944 RIKEN full-length enriched, CRL-1722 L5178Y-R Mus musculus
            cDNA clone I730003H17 3', mRNA sequence.
ACCESSION   BY394944
VERSION     BY394944.1  GI:26624432
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 389)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
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            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
            Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
            Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
            Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
            Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
            Hayashizaki,Y. Direct Submission
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
             cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES              Location/Qualifiers
     source           1. .389
                      /organism="Mus musculus"
                      /mol_type="mRNA"
                      /strain="DBA/2"
                      /db_xref="taxon:10090"
                      /clone="I730003H17"
                      /cell_line="CRL-1722 L5178Y-R"
                      /clone_lib="RIKEN full-length enriched, CRL-1722 L5178Y-R"
ORIGIN

  Query Match             3.4%;  Score 20;  DB 4;  Length 389;
  Best Local Similarity   100.0%;  Pred. No. 56;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 CCCCACACCCACACCAAGCC 28
              ||||||||||||||||||||
Db        179 CCCCACACCCACACCAAGCC 198


RESULT 40
BW935403
LOCUS       BW935403                452 bp    mRNA    linear   EST 24-DEC-2005
DEFINITION  BW935403 Amphioxus Branchiostoma floridae unpublished cDNA library,
            neurula whole animal Branchiostoma floridae cDNA clone bfne121g22
            3', mRNA sequence.
ACCESSION   BW935403
VERSION     BW935403.1  GI:66569299
KEYWORDS    EST.
SOURCE      Branchiostoma floridae (Florida lancelet)
  ORGANISM  Branchiostoma floridae
            Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
            Branchiostoma.
REFERENCE   1  (bases 1 to 452)
  AUTHORS   Yu,J., Holland,L.Z., Shin-i,T., Kohara,Y., Satou,Y. and Satoh,N.
  TITLE     Expressed genes in Branchiostoma floridae
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp
            If you want to have a cDNA clone for this EST or if you have any
            questions, please send an e-mail to Nori Satoh
            (satoh@ascidian.zool.kyoto-u.ac.jp) and its cc to Yutaka Satou
            (yutaka@ascidian.zool.kyoto-u.ac.jp).
FEATURES              Location/Qualifiers
     source           1. .452
                      /organism="Branchiostoma floridae"
                      /mol_type="mRNA"
                      /db_xref="taxon:7739"
                      /clone="bfne121g22"
                      /tissue_type="whole animal"
                      /dev_stage="neurula"
                      /clone_lib="Amphioxus Branchiostoma floridae unpublished
                      cDNA library, neurula whole animal"
ORIGIN

  Query Match             3.4%;  Score 20;  DB 4;  Length 452;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        143 ATCATGAAGATATCACAAAA 162
              ||||||||||||||||||||
Db        375 ATCATGAAGATATCACAAAA 394


RESULT 41
AQ478437/c
LOCUS       AQ478437                516 bp    DNA     linear   GSS 23-APR-1999
DEFINITION  RPCI-11-248M18.TJ RPCI-11 Homo sapiens genomic clone
            RPCI-11-248M18, genomic survey sequence.
ACCESSION   AQ478437
VERSION     AQ478437.1  GI:4660556
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 516)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
            Venter,J.C.
  TITLE     Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genet cs (info@resgen.com). BAC end search page:
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            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: SP6
            Class: BAC ends.
FEATURES              Location/Qualifiers
     source           1. .516
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="GDB:7595153"
                      /db_xref="taxon:9606"
                      /clone="RPCI-11-248M18"
                      /sex="Male"
                      /cell_type="Lymphocytes"
                      /clone_lib="RPCI-11"
                      /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                      RPCI11 Human Male BAC Library"
ORIGIN

  Query Match             3.4%;  Score 20;  DB 11;  Length 516;
  Best Local Similarity   100.0%;  Pred. No. 60;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         85 ACGCTTCAGAAGGCCAGACA 104
              ||||||||||||||||||||
Db         57 ACGCTTCAGAAGGCCAGACA 38


RESULT 42
AZ855572/c
LOCUS       AZ855572                574 bp    DNA     linear   GSS 21-FEB-2001
DEFINITION  2M0159K08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0159K08 R, genomic survey sequence.
ACCESSION   AZ855572
VERSION     AZ855572.1  GI:13045870
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 574)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0159  row: K  column: 08
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 574.
FEATURES              Location/Qualifiers
     source           1. .574
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC2M0159K08"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
ORIGIN

  Query Match             3.4%;  Score 20;  DB 11;  Length 574;
  Best Local Similarity   100.0%;  Pred. No. 61;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        353 CCATGAATGCAAAGCTGTTA 372
              ||||||||||||||||||||
Db        232 CCATGAATGCAAAGCTGTTA 213


RESULT 43
CNS01PJI
LOCUS       CNS01PJI                603 bp    DNA     linear   GSS 14-JUN-2001
DEFINITION  Anopheles gambiae GSS SP6 end of clone 28L22 of NotreDame1 library
            from strain PEST of Anopheles gambiae (African malaria mosquito),
            genomic survey sequence.
ACCESSION   AL154894
VERSION     AL154894.1  GI:7015813
KEYWORDS    GSS.
SOURCE      Anopheles gambiae (African malaria mosquito)
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Culicidae; Anophelinae; Anopheles.
REFERENCE   1  (bases 1 to 603)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
REFERENCE   2  (bases 1 to 603)
  AUTHORS   Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.
            Roux, Paris 75015, France
COMMENT     This clone is from an A. gambiae BAC library provided by F.H.
            Collins and sequenced by Genoscope in collaboration with the
            Laboratory of Biochem. and Biol. Molec. of Insects, Institut
            Pasteur.
FEATURES              Location/Qualifiers
     source           1. .603
                      /organism="Anopheles gambiae"
                      /mol_type="genomic DNA"
                      /strain="PEST"
                      /db_xref="taxon:7165"
                      /clone="28L22"
                      /clone_lib="NotreDame1"
                      /note="end : SP6"
ORIGIN

  Query Match             3.4%;  Score 20;  DB 14;  Length 603;
  Best Local Similarity   100.0%;  Pred. No. 62;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        226 GCTTCCAGAGAGATCTCTCT 245
              ||||||||||||||||||||
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Db        496 GCTTCCAGAGAGATCTCTCT 515


RESULT 44
W63576/c
LOCUS       W63576                  604 bp    mRNA    linear   EST 11-OCT-1996
DEFINITION  zc55h09.r1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA
            clone IMAGE:326273 5', mRNA sequence.
ACCESSION   W63576
VERSION     W63576.1  GI:1371149
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 604)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 566   Std Error: 0.00
            Seq primer: ETPrimer
            High quality sequence stop: 400.
FEATURES             Location/Qualifiers
     source          1. .604
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:1257786"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:326273"
                     /tissue_type="senescent fibroblast"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares_senescent_fibroblasts_NbHSF"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco
                     RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                     primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo."
ORIGIN

  Query Match             3.4%;  Score 20;  DB 10;  Length 604;
  Best Local Similarity   100.0%;  Pred. No. 62;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        401 ATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||
Db        357 ATCAAAACATGCTGACAGCT 338


RESULT 45
AW107212
LOCUS       AW107212                610 bp    mRNA    linear   EST 20-OCT-1999
DEFINITION  um12c12.x1 Sugano mouse kidney mkia Mus musculus cDNA clone
            IMAGE:2182870 3', mRNA sequence.
ACCESSION   AW107212
VERSION     AW107212.1  GI:6078012
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 610)
  AUTHORS   Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     The WashU-NCI Mouse EST Project 1999
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: um12c12.y1
            Contact: Marra M/WashU-NCI Mouse EST Project 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:1004538
            Seq primer: custom primer used
            High quality sequence stop: 516.
FEATURES             Location/Qualifiers
     source          1. .610
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:2182870"
                     /sex="female"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="Sugano mouse kidney mkia"
                     /note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII
                     (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
                     was primed with an oligo(dT) primer
                     [ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
                     ligated to a  DraIII adaptor [TGTTGGCCTACTGG], digested
                     and cloned into distinct DraIII sites of the pME18S-FL3
                     vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
                     be used to isolate the cDNA insert.  Size selection was
                     performed to exclude fragments <1.5kb.  Library
                     constructed by Dr. Sumio Sugano (University of Tokyo
                     Institute of Medical Science).  Custom primers  for
                     sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
                     primer CGACCTGCAGCTCGAGCACA."
ORIGIN

  Query Match             3.4%;  Score 20;  DB 7;  Length 610;
  Best Local Similarity   100.0%;  Pred. No. 62;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TCCCCACACCCACACCAAGC 27
              ||||||||||||||||||||
Db        488 TCCCCACACCCACACCAAGC 507


RESULT 46
BH373165/c
LOCUS       BH373165                691 bp    DNA     linear   GSS 10-DEC-2001
DEFINITION  AG-ND-159L10.TR ND-TAM Anopheles gambiae genomic clone
            AG-ND-159L10, genomic survey sequence.
ACCESSION   BH373165
VERSION     BH373165.1  GI:17319307
KEYWORDS    GSS.
SOURCE      Anopheles gambiae (African malaria mosquito)
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Culicidae; Anophelinae; Anopheles.
REFERENCE   1  (bases 1 to 691)
  AUTHORS   Hong,Y.S., Hogan,J.R., Wang,X., Sarkar,A., Sim,C., Loftus,B.J.,
            Ren,C., Huff,E.R., Carlile,J.L., Black,K., Zhang,H.-B.,
            Gardner,M.J. and Collins,F.H.
  TITLE     Construction of a BAC library and generation of BAC end
            sequence-tagged connectors for genome sequencing of the African
            malaria mosquito Anopheles gambiae
  JOURNAL   Mol. Genet. Genomics 268 (6), 720-728 (2003)
   PUBMED   12655398
COMMENT     Other_GSSs: AG-ND-159L10.TF
            Contact: Brendan J Loftus
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0208
            Fax: 301 838 3543
            Email: bjloftus@tigr.org
            This clone is from an A. gambiae BAC library (ND-TAM) provided by
            F.H. Collins and sequenced by The Institute for Genomic Research
            (TIGR). The BAC library was generated from A. gambiae PEST strain
            DNA. All DNA was extracted from newly hatched first instar larvae
            to minimize the inclusion of DNA from microorganisms that inhabit
            the gut. The DNA is derived from mixed sexes of larvae. The BAC
            library was constructed at Texas A&M Universty BAC Center
            University, College Station, Texas 77843-2123, USA using a HindIII
            partial digest.
            Seq primer: M13 Rev
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .691
                     /organism="Anopheles gambiae"
                     /mol_type="genomic DNA"
                     /strain="PEST"
                     /db_xref="taxon:7165"
                     /clone="AG-ND-159L10"
                     /clone_lib="ND-TAM"
                     /note="Vector: pECBAC1; Site_1: HindIII"
ORIGIN

  Query Match             3.4%;  Score 20;  DB 11;  Length 691;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        360 TGCAAAGCTGTTAATGGATC 379
              ||||||||||||||||||||
Db        384 TGCAAAGCTGTTAATGGATC 365


RESULT 47
BW754129
LOCUS       BW754129                724 bp    mRNA    linear   EST 22-OCT-2005
DEFINITION  BW754129 Amphioxus Branchiostoma floridae unpublished cDNA library,
            egg whole animal Branchiostoma floridae cDNA clone bfeg020c16 3',
            mRNA sequence.
ACCESSION   BW754129
VERSION     BW754129.1  GI:66340777
KEYWORDS    EST.
SOURCE      Branchiostoma floridae (Florida lancelet)
  ORGANISM  Branchiostoma floridae
            Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
            Branchiostoma.
REFERENCE   1  (bases 1 to 724)
  AUTHORS   Yu,J., Holland,L.Z., Shin-i,T., Kohara,Y., Satou,Y. and Satoh,N.
  TITLE     Expressed genes in Branchiostoma floridae
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp
            If you want to have a cDNA clone for this EST or if you have any
            questions, please send an e-mail to Nori Satoh
            (satoh@ascidian.zool.kyoto-u.ac.jp) and its cc to Yutaka Satou
            (yutaka@ascidian.zool.kyoto-u.ac.jp).
FEATURES             Location/Qualifiers
     source          1. .724
                     /organism="Branchiostoma floridae"
                     /mol_type="mRNA"
                     /db_xref="taxon:7739"
                     /clone="bfeg020c16"
                     /tissue_type="whole animal"
                     /dev_stage="egg"
                     /clone_lib="Amphioxus Branchiostoma floridae unpublished
                     cDNA library, egg whole animal"
ORIGIN

  Query Match             3.4%;  Score 20;  DB 4;  Length 724;
  Best Local Similarity   100.0%;  Pred. No. 64;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        143 ATCATGAAGATATCACAAAA 162
              ||||||||||||||||||||
Db        366 ATCATGAAGATATCACAAAA 385


RESULT 48
BZ028162/c
LOCUS       BZ028162                734 bp    DNA     linear   GSS 08-OCT-2002
DEFINITION  oeg78e09.g1 B.oleracea002 Brassica oleracea genomic, genomic survey
            sequence.
ACCESSION   BZ028162
VERSION     BZ028162.1  GI:23591436
KEYWORDS    GSS.
SOURCE      Brassica oleracea
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 734)
  AUTHORS   Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
            Nash,W., Rabinowicz,P.D. and Wilson,R.K.
  TITLE     Whole genome shotgun reads from Brassica oleracea
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Richard K. Wilson
            Genome Sequencing Center
            Washington University School of Medicine
            Email: submissions@watson.wustl.edu
            Plate: oeg78  row: e  column: 09
            Seq primer: -28RPpOT reverse
            Class: shotgun
            High quality sequence start: 8
            High quality sequence stop: 551.
FEATURES             Location/Qualifiers
     source          1. .734
                     /organism="Brassica oleracea"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:3712"
                     /clone_lib="B.oleracea002"
                     /note="Vector: pOTw13; Whole genome shotgun library from
                     flowering buds. DNA was purified  from a crude nuclear
                     prep using Brassica oleracea TO1000DH3 buds  provided by
                     Thosmas Osborn at the University of Wisconsin. Genomic
                     DNA was provided by Pablo Rabinowicz (CSHL) and the
                     shotgun library  prepared at Washington University Genome
                     Sequencing Center."
ORIGIN

  Query Match             3.4%;  Score 20;  DB 11;  Length 734;
  Best Local Similarity   100.0%;  Pred. No. 64;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        494 ATTTTTATAAAACTAAAATC 513
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                    ||||||||||||||||||||
Db        722 ATTTTTATAAAACTAAAATC 703


RESULT 49
CD357085/c
LOCUS       CD357085                822 bp    mRNA    linear   EST 29-MAY-2003
DEFINITION  AGENCOURT_14284510 NIH_MGC_187 Homo sapiens cDNA clone
            IMAGE:30402141 5', mRNA sequence.
ACCESSION   CD357085
VERSION     CD357085.1  GI:31128496
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 822)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDCM183  row: p  column: 22
            High quality sequence stop: 252.
FEATURES             Location/Qualifiers
     source          1. .822
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:30402141"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_187"
                     /note="Organ: Blood vessels - aorta, basilar and artery;
                     Vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc); Site_2:
                     SfiI (ggccgcctcggcc); 5' and 3' adaptors were used in
                     cloning as follows: 5' adaptor sequence:
                     5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C, G, or T). Average insert size 1.4 kb
                     (range 0.5-4.0 kb). 14/15 colonies contained inserts by
                     PCR. This library was enriched for full-length clones and
                     was constructed by Clontech Laboratories (Palo Alto, CA).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             3.4%;  Score 20;  DB 5;  Length 822;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        162 AGATAAAACCAGCACAGTGG 181
              ||||||||||||||||||||
Db        130 AGATAAAACCAGCACAGTGG 111


RESULT 50
AQ574005
LOCUS       AQ574005                855 bp    DNA     linear   GSS 02-JUN-1999
DEFINITION  nbxb0083O17f CUGI Rice BAC Library Oryza sativa (japonica
            cultivar-group) genomic clone nbxb0083O17f, genomic survey
            sequence.
ACCESSION   AQ574005
VERSION     AQ574005.1  GI:4973806
KEYWORDS    GSS.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 855)
  AUTHORS   Wing,R.A. and Dean,R.A.
  TITLE     A BAC End Sequencing Framework to Sequence the Rice Genome
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Seq primer: TAATACGACTCACTATAGGG
            Class: BAC ends
            High quality sequence stop: 408.
FEATURES             Location/Qualifiers
     source          1. .855
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="genomic DNA"
                     /cultivar="japonica"
                     /cultivar="Nipponbare"
                     /db_xref="taxon:39947"
                     /clone="nbxb0083O17f"
                     /tissue_type="Leaf"
                     /lab_host="E. coli DH10B"
                     /clone_lib="CUGI Rice BAC Library"
                     /note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                     HindIII; Rice is one of two most popular grains in the
                     world. Half of the world  population especially those
                     inhabiting highly populated areas of the  humid tropics
                     and subtropics, rely on rice as their primary source of
                     carbohydrate. Monocotyledonous rice is a diploid plant
                     (2n=24) with a  haploid genome equivalent of 431 Mbp
                     (Arumuganathan and Earle, 1991).  The relatively small
                     genome of rice, three times larger than that of
                     Arabidopsis, makes it suitable for genomic studies. In
                     order to  facilitate positional cloning, physical mapping
                     and genome sequencing  of rice, we have constructed a BAC
                     library from Oryza sativa, Nipponbare  variety. The
                     library contains 36,864 clones with an average insert size
                     of 128.5 Kb providing 10.9 haploid genome equivalents. The
                     deep  coverage allows the isolation a particular sequence
                     with a probability  of 99.9 %. Two high density filters,
                     each containing 18,432 clones  (doubly spotted), represent
                     the whole library for colony screening."
ORIGIN

  Query Match             3.4%;  Score 20;  DB 11;  Length 855;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        488 AACCGGATTTTTATAAAACT 507
              ||||||||||||||||||||
Db        760 AACCGGATTTTTATAAAACT 779


RESULT 51
CL868149/c
LOCUS       CL868149                875 bp    DNA     linear   GSS 26-AUG-2004
DEFINITION  Gma_01_C05_T3 Soybean Genome Shotgun Sequences Glycine max genomic,
            genomic survey sequence.
ACCESSION   CL868149
VERSION     CL868149.1  GI:51562374
KEYWORDS    GSS.
SOURCE      Glycine max (soybean)
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
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            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 875)
  AUTHORS   Jackson,S.A., Walling,J.G. and SanMiguel,P.M.
  TITLE     Molecular and cytogenetic characterization of the heterochromatic,
            gene-poor centric regions of chromosomes of Glycine max L. Merr
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Scott A. Jackson
            Jackson Laboratory
            Purdue University
            915 W. State St., West Lafayette, IN 47907, USA
            Tel: 7654963621
            Fax: 7654967255
            Email: sjackson@purdue.edu
            Plate: 01  row: C  column: 05
            Seq primer: T3
            Class: shotgun
            High quality sequence stop: 875.
FEATURES             Location/Qualifiers
     source          1. .875
                     /organism="Glycine max"
                     /mol_type="genomic DNA"
                     /cultivar="Williams 82"
                     /db_xref="taxon:3847"
                     /sex="hermaphrodite"
                     /tissue_type="Leaf"
                     /dev_stage="seedling"
                     /clone_lib="Soybean Genome Shotgun Sequences"
                     /note="Organ: Leaf; Vector: Invitrogen ToPo vector;
                     Approximately 3-kb randomly sheared inserts"
ORIGIN

  Query Match             3.4%;  Score 20;  DB 13;  Length 875;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        495 TTTTTATAAAACTAAAATCA 514
              ||||||||||||||||||||
Db        770 TTTTTATAAAACTAAAATCA 751


RESULT 52
BF530961/c
LOCUS       BF530961                920 bp    mRNA    linear   EST 11-DEC-2000
DEFINITION  602072472F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4215425
            5', mRNA sequence.
ACCESSION   BF530961
VERSION     BF530961.1  GI:11618324
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 920)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9790  row: p  column: 18
            High quality sequence stop: 652.
FEATURES             Location/Qualifiers
     source          1. .920
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4215425"
                     /tissue_type="anaplastic oligodendroglioma with 1p/19q
                     loss"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Brn67"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 2.3 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match             3.4%;  Score 20;  DB 7;  Length 920;
  Best Local Similarity   100.0%;  Pred. No. 67;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        458 TGACTGTGCCACAGAACTCC 477
              ||||||||||||||||||||
Db        308 TGACTGTGCCACAGAACTCC 289


RESULT 53
CL465003
LOCUS       CL465003                959 bp    DNA     linear   GSS 31-MAR-2004
DEFINITION  SAIL_1232_C07.v1 SAIL Collection Arabidopsis thaliana genomic clone
            SAIL_1232_C07.v1, genomic survey sequence.
ACCESSION   CL465003
VERSION     CL465003.1  GI:45867908
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 959)
  AUTHORS   Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D.,
            Dietrich,B., Ho,P., Bacwaden,J., Ko,C., Clarke,J.D., Cotton,D.,
            Bullis,D., Snell,J., Miguel,T., Hutchison,D., Kimmerly,B.,
            Mitzel,T., Katagiri,F., Glazebrook,J., Law,M. and Goff,S.A.
  TITLE     A high-throughput Arabidopsis reverse genetics system
  JOURNAL   Plant Cell 14 (12), 2985-2994 (2002)
   PUBMED   12468722
COMMENT     Contact: Sessions A
            Applied Trait Genetics
            Syngenta Biotechnology Inc.
            3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
            Email: allen.sessions@syngenta.com
            ABRC Stock Number CS845125; T-DNA left border flanking sequences of
            Syngenta Arabidopsis Insertion Library (SAIL) lines are available
            through the Arabidopsis Biological Resource Center (ABRC).
            Sequences represent a pool of amplified genomic regions and not
            single contiguous sequences.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .959
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /ecotype="Columbia"
                     /db_xref="taxon:3702"
                     /clone="SAIL_1232_C07.v1"
                     /clone_lib="SAIL Collection"
                     /note="T-DNA left border sequences were isolated using a
                     modified TAIL-PCR strategy"
ORIGIN

  Query Match             3.4%;  Score 20;  DB 13;  Length 959;
  Best Local Similarity   100.0%;  Pred. No. 68;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         45 CCTCAACCACTCCCAAACCC 64
              ||||||||||||||||||||
Db        590 CCTCAACCACTCCCAAACCC 609
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RESULT 54
CNS01GIY
LOCUS       CNS01GIY               1035 bp    DNA     linear   GSS 01-JUN-2001
DEFINITION  Anopheles gambiae GSS T7 end of clone 06N18 of NotreDame1 library
            from strain PEST of Anopheles gambiae (African malaria mosquito),
            genomic survey sequence.
ACCESSION   AL143195
VERSION     AL143195.1  GI:7001313
KEYWORDS    GSS.
SOURCE      Anopheles gambiae (African malaria mosquito)
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Culicidae; Anophelinae; Anopheles.
REFERENCE   1  (bases 1 to 1035)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
REFERENCE   2  (bases 1 to 1035)
  AUTHORS   Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.
            Roux, Paris 75015, France
COMMENT     This clone is from an A. gambiae BAC library provided by F.H.
            Collins and sequenced by Genoscope in collaboration with the
            Laboratory of Biochem. and Biol. Molec. of Insects, Institut
            Pasteur.
FEATURES             Location/Qualifiers
     source          1. .1035
                     /organism="Anopheles gambiae"
                     /mol_type="genomic DNA"
                     /strain="PEST"
                     /db_xref="taxon:7165"
                     /clone="06N18"
                     /clone_lib="NotreDame1"
                     /note="end : T7"
ORIGIN

  Query Match             3.4%;  Score 20;  DB 14;  Length 1035;
  Best Local Similarity   100.0%;  Pred. No. 69;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        360 TGCAAAGCTGTTAATGGATC 379
              ||||||||||||||||||||
Db        308 TGCAAAGCTGTTAATGGATC 327


RESULT 55
DT990937
LOCUS       DT990937               1321 bp    mRNA    linear   EST 22-SEP-2005
DEFINITION  CNB152-F06.x1d-t SHGC-CNB Gasterosteus aculeatus cDNA clone
            CNB152-F06 3', mRNA sequence.
ACCESSION   DT990937
VERSION     DT990937.1  GI:76114747
KEYWORDS    EST.
SOURCE      Gasterosteus aculeatus (three spined stickleback)
  ORGANISM  Gasterosteus aculeatus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
            Gasterosteidae; Gasterosteus.
REFERENCE   1  (bases 1 to 1321)
  AUTHORS   Kingsley,D.M., Peichel,C., Balabahdra,S., Grimwood,J., Dickson,M.,
            Schmutz,J. and Myers,R.M.
  TITLE     Expressed sequence tags from Gasterosteus aculeatus
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Grimwood, Jane
            Stanford Human Genome Center
            Stanford University School of Medicine
            975 S California Ave, Palo Alto, CA 94304, USA
            Tel: 650 320 5917
            Fax: 650 320 5801
            Email: jane@shgc.stanford.edu
            Plate: 152
            High quality sequence start: 18
            High quality sequence stop: 787.
FEATURES             Location/Qualifiers
     source          1. .1321
                     /organism="Gasterosteus aculeatus"
                     /mol_type="mRNA"
                     /strain="Conner Creek sticklebacks, WA USA"
                     /db_xref="taxon:69293"
                     /clone="CNB152-F06"
                     /sex="mixed male and female"
                     /tissue_type="brain"
                     /dev_stage="adult"
                     /lab_host="DH10B (T1 phage resistant)"
                     /clone_lib="SHGC-CNB"
                     /note="Vector: Express 1; Total and poly A+ RNA was
                     isolated from the indicated stickleback tissue, and a cDNA
                     library was constructed in the Express 1 plasmid vector by
                     Open Biosystems. First strand cDNA synthesis was primed
                     with an 54 bp linker primer containing an oligodT sequence
                     preceeded by a synthetic NotI site (first strand primer:
                     5'-GACTAGTTCTAGATCGCGAGCGGCCGCCC(T)25-3'). Following
                     second strand synthesis, cDNAs were made blunt at the end
                     corresponding to the original 5 prime end of mRNA, and
                     cloned directionally into the NotI and EcoRV sites of
                     Express 1. Note that the EcoRV site is typically destroyed
                     in the blunt end cloning, leaving a junction of the form
                     'xxxATC' (where is ATC is the second half of the EcoRV
                     site, and xxx is derived from the cDNA sequence). A map of
                     the Express 1 vector is available at:
                     http://www.openbiosystems.com/cdna_library_construction_fa
                     q.php#8 The primary library was transformed and amplified
                     in DH10B (T1 phage resistant) bacteria. Clones available
                     from Open Biosystems:
                     http://www.openbiosystems.com/stickleback"
ORIGIN

  Query Match             3.4%;  Score 20;  DB 10;  Length 1321;
  Best Local Similarity   100.0%;  Pred. No. 72;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        130 TCCGAAGAGATTGATCATGA 149
              ||||||||||||||||||||
Db        941 TCCGAAGAGATTGATCATGA 960


RESULT 56
CN094503
LOCUS       CN094503               167 bp    mRNA    linear   EST 31-MAR-2004
DEFINITION  EC2BBA9DE06.b1 Xenopus tropicalis xtbs plasmid library Xenopus
            tropicalis cDNA clone xtbs09J12 3', mRNA sequence.
ACCESSION   CN094503
VERSION     CN094503.1  GI:45887199
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 167)
  AUTHORS   Thuret,R., Fierro,A.C., Coen,L., Perron,M., Demeneix,B., Wegnez,M.,
            Gyapay,G., Weissenbach,J., Wincker,P., Mazabraud,A. and Pollet,N.
  TITLE     Exploring the nervous system transcriptome in the model Xenopus
            tropicalis using EST analysis
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Pollet N
            Transgenese et Genetique des Amphibiens
            CNRS UMR 8080
            IBAIC bat 447, Universite Paris Sud, Orsay, F-91405, France
            Tel: +33 169157272
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            Fax: +33 169156816
            Email: Nicolas.Pollet@ibaic.u-psud.fr.
FEATURES             Location/Qualifiers
     source          1. .167
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /strain="Ivory Coast"
                     /db_xref="taxon:8364"
                     /clone="xtbs09J12"
                     /tissue_type="pool of brains and spinal cords from
                     tadpoles at stages 51-52 and 61-62"
                     /dev_stage="stage 51-52 and 61-62"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Xenopus tropicalis xtbs plasmid library"
                     /note="Vector: pCMVSPORT6_xtbs; Site_1: SfiI; Site_2:
                     SfiI; Xenopus tropicalis polyA+ RNA was obtained from
                     brain and spinal cord of tadpoles at stages 51-52 and
                     61-62. cDNAs were synthesized using the SMART system of
                     CLONTECH and directionally cloned into pCMVSPORT6_xtbs, a
                     modified version of pCMVSPORT6 allowing directional
                     cloning using asymetric SfiI sites. For antisense RNA
                     synthesis, use T7 promoter and for sense RNA use SP6
                     promoter. Library constructed by Dr. L. Coen and Prof. B.
                     Demeneix (Museum National d'Histoire Naturelle and CNRS
                     UMR 5166, Paris, France)."
ORIGIN

  Query Match             3.2%;  Score 19;  DB 8;  Length 167;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        495 TTTTTATAAAACTAAAATC 513
              |||||||||||||||||||
Db         89 TTTTTATAAAACTAAAATC 107


RESULT 57
DY151937
LOCUS       DY151937                196 bp    mRNA    linear   EST 01-FEB-2006
DEFINITION  000923BEMN018313HT BEMN Bos taurus cDNA, mRNA sequence.
ACCESSION   DY151937
VERSION     DY151937.1  GI:86346112
KEYWORDS    EST.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 196)
  AUTHORS   McCulloch,A., Wilson,T., Molenaar,A., Grigor,M., Davis,S.,
            Glenn,M., Havukkala,I., Watson,J., Crawford,A., Wheeler,T.,
            Hagemann,L., Lee,R., Hein,W., Johnstone,P., Maqbool,N., McMahon,C.,
            McCracken,J., Stelwagen,K., Farr,V., Singh,K., Whitley,J.,
            Nicholas,K., Savin,K., Mather,A., McPartlan,H., Whitley,J.,
            Wells,M., Bowman,P., Goddard,M., Langford,C., McEwan,J. and
            Atkinson,P.
  TITLE     AgResearch, Genesis and Primary Industry Victoria Bovine EST
            project
  JOURNAL   Unpublished (2006)
COMMENT     Contact: Maqbool N
            AgResearch Ltd.
            Invermay Agricultural Centre, Puddle Alley, Private Bag 50034,
            Mosgiel, New Zealand
            Email: nauman.maqbool@agresearch.co.nz.
FEATURES             Location/Qualifiers
     source          1. .196
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="Life Tech Normalised library"
                     /clone_lib="BEMN"
                     /note="Vector: pCMV-Sport6; Life Tech Normalised library"
ORIGIN

  Query Match             3.2%;  Score 19;  DB 10;  Length 196;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        329 AGATGTACCAGGTGGAGTT 347
              |||||||||||||||||||
Db        103 AGATGTACCAGGTGGAGTT 121


RESULT 58
CB438594
LOCUS       CB438594                199 bp    mRNA    linear   EST 25-MAR-2003
DEFINITION  687245 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   CB438594
VERSION     CB438594.1  GI:29222764
KEYWORDS    EST.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 199)
  AUTHORS   Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
            Wray,J.E. and Keele,J.W.
  TITLE     A second set of bovine ESTs from pooled-tissue normalized libraries
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Plate: FQY8043  row: N  column: 24
            Seq primer: GTAATACGACTCACTATAGGG.
FEATURES             Location/Qualifiers
     source          1. .199
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 6BOV"
                     /note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
                     Library made with RNA pooled from multiple tissues
                     including liver, lung, hypothalamus, pituitary, and
                     placenta/endometrium."
ORIGIN

  Query Match             3.2%;  Score 19;  DB 4;  Length 199;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         51 CCACTCCCAAACCCTGCTG 69
              |||||||||||||||||||
Db         19 CCACTCCCAAACCCTGCTG 37


RESULT 59
CR583097
LOCUS       CR583097                219 bp    mRNA    linear   EST 26-JUL-2004
DEFINITION  CR583097 XGC-tailbud-head Xenopus tropicalis cDNA clone THdA028d23
            5', mRNA sequence.
ACCESSION   CR583097
VERSION     CR583097.1  GI:50583097
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 219)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Garrett,N. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (2004)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Croning MDR
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
             TROPICALIS_SEQUENCE_ID: THdA028d23.p1kbSP6
             This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Nigel Garrett.
            Seq primer: SP6.
FEATURES             Location/Qualifiers
     source          1. .219
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="THdA028d23"
                     /dev_stage="tailbud head (stage 28-30)"
                     /lab_host="Escherichia coli DH10B."
                     /clone_lib="XGC-tailbud-head"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from tailbud
                     head. EcoRI-NotI cut cDNA was then ligated into pCS107
                     with EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

  Query Match             3.2%;  Score 19;  DB 8;  Length 219;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        495 TTTTTATAAAACTAAAATC 513
              |||||||||||||||||||
Db        170 TTTTTATAAAACTAAAATC 188


RESULT 60
AL864786/c
LOCUS       AL864786                229 bp    mRNA    linear   EST 03-DEC-2003
DEFINITION  AL864786 XGC-egg Xenopus tropicalis cDNA clone TEgg132g06 5', mRNA
            sequence.
ACCESSION   AL864786
VERSION     AL864786.2  GI:38659459
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 229)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     On Sep 15, 2002 this sequence version replaced gi:22885051.
            Contact: Taylor R
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TEgg132g06.p1kSP6
            Sequencing primer: SP6
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from egg.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
            5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli XL1-blue.
FEATURES             Location/Qualifiers
     source          1. .229
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TEgg132g06"
                     /dev_stage="egg"
                     /lab_host="Escherichia coli XL1-blue"
                     /clone_lib="XGC-egg"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from egg.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end"
ORIGIN

  Query Match             3.2%;  Score 19;  DB 1;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GGAACCTCCCCACACCCAC 20
              ||||||||||||||||||||
Db         66 GGAACCTCCCCACACCCAC 48


RESULT 61
BB391337
LOCUS       BB391337                237 bp    mRNA    linear   EST 13-JUL-2000
DEFINITION  BB391337 RIKEN full-length enriched, 0 day neonate cerebellum Mus
            musculus cDNA clone C230074B09 3' similar to AB014577 Homo sapiens
            mRNA for KIAA0677 protein, mRNA sequence.
ACCESSION   BB391337
VERSION     BB391337.1  GI:9114288
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 237)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T.,
            Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
            Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
            Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
            Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C.,
            Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H.,
            Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K.,
            Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A.,
            Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watahiki,A.,
            Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A.,
            Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,
            Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length
            cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
            Okazaki,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
             Please visit our web site (http://genome.rtc.riken.go.jp) for
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          further details.
FEATURES             Location/Qualifiers
     source          1. .237
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="C230074B09"
                     /tissue_type="cerebellum"
                     /dev_stage="0 day neonate"
                     /lab_host="DH10B"
                     /clone_lib="RIKEN full-length enriched, 0 day neonate
                     cerebellum"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 20.0 and subtraction to Rot = 479.0. Second
                     strand cDNA was prepared with the primer adapter of
                     sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC
                     3']. cDNA was cleaved with XhoI and BamHI. Vector: a
                     modified pBluescript KS(+) after bulk excision from Lambda
                     FLC I."
ORIGIN

  Query Match             3.2%;  Score 19;  DB 7;  Length 237;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        329 AGATGTACCAGGTGGAGTT 347
              |||||||||||||||||||
Db         83 AGATGTACCAGGTGGAGTT 101


RESULT 62
CN094504/c
LOCUS       CN094504                242 bp    mRNA    linear   EST 31-MAR-2004
DEFINITION  EC2BBA9DE06.g1 Xenopus tropicalis xtbs plasmid library Xenopus
            tropicalis cDNA clone xtbs09J12 5', mRNA sequence.
ACCESSION   CN094504
VERSION     CN094504.1  GI:45887200
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 242)
  AUTHORS   Thuret,R., Pierro,A.C., Coen,L., Perron,M., Demeneix,B., Wegnez,M.,
            Gyapay,G., Weissenbach,J., Wincker,P., Mazabraud,A. and Pollet,N.
  TITLE     Exploring the nervous system transcriptome in the model Xenopus
            tropicalis using EST analysis
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Pollet N
            Transgenese et Genetique des Amphibiens
            CNRS UMR 8080
            IBAIC bat 447, Universite Paris Sud, Orsay, F-91405, France
            Tel: +33 169157272
            Fax: +33 169156816
            Email: Nicolas.Pollet@ibaic.u-psud.fr.
FEATURES             Location/Qualifiers
     source          1. .242
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /strain="Ivory Coast"
                     /db_xref="taxon:8364"
                     /clone="xtbs09J12"
                     /tissue_type="pool of brains and spinal cords from
                     tadpoles at stages 51-52 and 61-62"
                     /dev_stage="stage 51-52 and 61-62"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Xenopus tropicalis xtbs plasmid library"
                     /note="Vector: pCMVSPORT6_xtbs; Site_1: SfiI; Site_2:
                     SfiI; Xenopus tropicalis polyA+ RNA was obtained from
                     brain and spinal cord of tadpoles at stages 51-52 and
                     61-62. cDNAs were synthesized using the SMART system of
                     CLONTECH and directionally cloned into pCMVSPORT6_xtbs, a
                     modified version of pCMVSPORT6 allowing directional
                     cloning using asymetric SfiI sites. For antisense RNA
                     synthesis, use T7 promoter and for sense RNA use SP6
                     promoter. Library constructed by Dr. L. Coen and Prof. B.
                     Demeneix (Museum National d'Histoire Naturelle and CNRS
                     UMR 5166, Paris, France)."
ORIGIN

  Query Match             3.2%;  Score 19;  DB 8;  Length 242;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        495 TTTTTATAAAACTAAAATC 513
              |||||||||||||||||||
Db         78 TTTTTATAAAACTAAAATC 60


RESULT 63
AL640225/c
LOCUS       AL640225                247 bp    mRNA    linear   EST 07-NOV-2003
DEFINITION  AL640225 XGC-neurula Xenopus tropicalis cDNA clone TNeu002k23 5',
            mRNA sequence.
ACCESSION   AL640225
VERSION     AL640225.2  GI:38219389
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 247)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     On Nov 7, 2001 this sequence version replaced gi:16792356.
            Contact: Huckle E
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
            5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli DH10B
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TNeu002k23.p1kSP6
            Sequencing primer: SP6.
FEATURES             Location/Qualifiers
     source          1. .247
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TNeu002k23"
                     /dev_stage="neurula"
                     /lab_host="Escherichia coli DH10B"
                     /clone_lib="XGC-neurula"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from neurula.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end."
ORIGIN
```

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  Query Match             3.2%;  Score 19;  DB 1;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        495 TTTTTATAAAACTAAAATC 513
              |||||||||||||||||||
Db        101 TTTTTATAAAACTAAAATC 83


RESULT 64
BX668635
LOCUS       BX668635                247 bp    mRNA    linear   EST 07-MAY-2004
DEFINITION  BX668635 Sus Scrofa library (scac) Sus scrofa cDNA clone
            scac0028i.i.24 3prim, mRNA sequence.
ACCESSION   BX668635
VERSION     BX668635.1  GI:37977384
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 247)
  AUTHORS   Bonnet,A., Tosser-Klopp,G., Benne,F., Cabau,C., Villeger,S.,
            Soares,M., Bonaldo,F. and Hatey,F.
  TITLE     A Pig Normalised Multi-Tissue cDNA Library
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Tosser-Klopp G
            Genetique Animale
            Institut National de la Recherche Agronomique
            Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
            cedex, FRANCE
            Tel: 33 (0) 5.61.28.51.14
            Fax: 33 (0) 5.61.28.53.08
            Email: tosser@toulouse.inra.fr
            Sequence cleaned of vector, adaptator and repetitions. Contact us
            at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
            sequence.
            Plate: 0028  row: i  column: 24.
FEATURES             Location/Qualifiers
     source          1. .247
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /clone="scac0028i.i.24"
                     /tissue_type="mixed"
                     /clone_lib="Sus Scrofa library (scac)"
                     /note="Vector: pT7T3D-PacI; tissues: adipose tissue,
                     brain, kidney, liver, muscle, ovary, testis,  heart,
                     hypothalamus, pancreas, skin, spleen, thymus, placenta,
                     pituitary  gland, seminal vesicle, small intestine,
                     uterus, adrenals, bulbo uretral  gland, cerebral trunk,
                     epididymis, female gonad, gall-bladder,  hippocampus,
                     large intestine, male gonad, melanocytes, stomach, udder"
ORIGIN

  Query Match             3.2%;  Score 19;  DB 4;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        209 TGAATGAGAGTTGCCTGGC 227
              |||||||||||||||||||
Db        162 TGAATGAGAGTTGCCTGGC 180


RESULT 65
BB425487/c
LOCUS       BB425487                247 bp    mRNA    linear   EST 18-JUL-2000
DEFINITION  BB425487 RIKEN full-length enriched, 12 days embryo spinal cord Mus
            musculus cDNA clone C530046M16 3', mRNA sequence.
ACCESSION   BB425487
VERSION     BB425487.1  GI:9265214
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 247)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T.,
            Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
            Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
            Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
            Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C.,
            Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H.,
            Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K.,
            Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A.,
            Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watahiki,A.,
            Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A.,
            Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,
            Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length
            cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
            Okazaki,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
             Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .247
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="C530046M16"
                     /tissue_type="spinal cord"
                     /dev_stage="12 days embryo"
                     /lab_host="DH10B"
                     /clone_lib="RIKEN full-length enriched, 12 days embryo
                     spinal cord"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. Second strand cDNA was prepared with the
                     primer adapter of sequence [5'
                     GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA
                     was cleaved with XhoI and BamHI. Vector: a modified
                     pBluescript KS(+) after bulk excision from Lambda FLC I."
ORIGIN
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  Query Match             3.2%;  Score 19;  DB 7;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        503 AAACTAAAATCAAGCTCTG 521
              |||||||||||||||||||
Db        104 AAACTAAAATCAAGCTCTG 86


RESULT 66
BX714043/c
LOCUS       BX714043                255 bp    mRNA    linear   EST 18-NOV-2003
DEFINITION  BX714043 XGC-tadpole Xenopus tropicalis cDNA clone TTpA016l03 5',
            mRNA sequence.
ACCESSION   BX714043
VERSION     BX714043.1  GI:38385449
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 255)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Croning MDR
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TTpA016l03.p1kSP6
            Sequencing primer: SP6
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Nigel Garrett.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from tadpole
            embryos. EcoRI-NotI cut cDNA was then ligated into pCS107 with
            EcoRI at the 5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli DH10B.
FEATURES             Location/Qualifiers
     source          1. .255
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TTpA016l03"
                     /dev_stage="tadpole (stage 35-40)"
                     /lab_host="E. coli DH10B"
                     /clone_lib="XGC-tadpole"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from tadpole
                     embryos. EcoRI-NotI cut cDNA was then ligated into pCS107
                     with EcoRI at the 5' end and NotI at the 3' end"
ORIGIN

  Query Match             3.2%;  Score 19;  DB 4;  Length 255;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        495 TTTTTATAAAACTAAAATC 513
              |||||||||||||||||||
Db        243 TTTTTATAAAACTAAAATC 225


RESULT 67
BI703350
LOCUS       BI703350                265 bp    mRNA    linear   EST 18-SEP-2001
DEFINITION  fs85e10.x1 Zebrafish neuronal Danio rerio cDNA clone IMAGE:5076571
            3', mRNA sequence.
ACCESSION   BI703350
VERSION     BI703350.1  GI:15665979
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 265)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
            Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library constructed by S. Lin DNA Sequencing by: Washington
            University Genome Sequencing Center Clone distribution: the
            I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
            Seq primer: T7 from Gibco.
FEATURES             Location/Qualifiers
     source          1. .265
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:5076571"
                     /sex="mixed"
                     /dev_stage="adult"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="Zebrafish neuronal"
                     /note="Organ: brain; Vector: pBluescript (modified);
                     Site_1: DraIII(Y); Site_2: DRAIII(X); Library is cloned
                     directionally between the DraIII(X) and DraIII(Y) sites
                     and has been amplified. Library constructed by S. Lin. "
ORIGIN

  Query Match             3.2%;  Score 19;  DB 2;  Length 265;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        442 CTGAATGTCAACAGTGTGA 460
              |||||||||||||||||||
Db        104 CTGAATGTCAACAGTGTGA 122


RESULT 68
AV338007
LOCUS       AV338007                267 bp    mRNA    linear   EST 11-NOV-1999
DEFINITION  AV338007 RIKEN full-length enriched, adult male olfactory bulb Mus
            musculus cDNA clone 6430407D11 3', mRNA sequence.
ACCESSION   AV338007
VERSION     AV338007.1  GI:6378059
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 267)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T.,
            Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F.,
            Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I.,
            Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M.,
            Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
            Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K.,
            Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y.,
            Suzuki,H., Suzuki,H., Takahashi,F., Tateno,M., Tominaga,N.,
            Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A.,
            Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al. 1999)
```

```
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
            Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
            Hayashizaki,Y.
             Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
            Okazaki,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
             Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .267
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="6430407D11"
                     /sex="male"
                     /tissue_type="olfactory brain"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="RIKEN full-length enriched, adult male
                     olfactory bulb"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 10.0 and subtraction to Rot = 100.0. Second
                     strand cDNA was prepared with the primer adapter of
                     sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC
                     3']. cDNA was cloned into the XhoI and BamHI sites.
                     Vector: a modified pBluescript KS(+) after bulk excision
                     from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
                     BamHI"
ORIGIN

  Query Match             3.2%;  Score 19;  DB 1;  Length 267;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        337 CAGGTGGAGTTCAAGGCCA 355
              ||||||||||||||||||||
Db        187 CAGGTGGAGTTCAAGGCCA 205


RESULT 69
H95006/c
LOCUS       H95006                   275 bp    mRNA    linear   EST 25-NOV-1996
DEFINITION  yw57d05.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA
            clone IMAGE:256329 5', mRNA sequence.
ACCESSION   H95006
VERSION     H95006.1  GI:1102639
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 275)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 137
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 939   Std Error: 0.00
            Seq primer: M13RP1.
FEATURES             Location/Qualifiers
     source          1. .275
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:3885939"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:256329"
                     /dev_stage="two placentae: one from 8 weeks and another
                     from 9 weeks post conception"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares_placenta_8to9weeks_2NbHP8to9W"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo."
ORIGIN

  Query Match             3.2%;  Score 19;  DB 10;  Length 275;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        469 CAGAACTCCTCCTTGGAAG 487
              ||||||||||||||||||||
Db        275 CAGAACTCCTCCTTGGAAG 257


RESULT 70
AL777805/c
LOCUS       AL777805                 276 bp    mRNA    linear   EST 12-NOV-2003
DEFINITION  AL777805 XGC-neurula Xenopus tropicalis cDNA clone TNeu077l17 5',
            mRNA sequence.
ACCESSION   AL777805
VERSION     AL777805.2  GI:38281824
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 276)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
```

```
  JOURNAL   Unpublished (2003)
COMMENT     On Jun 25, 2002 this sequence version replaced gi:21563509.
            Contact: Taylor R
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
            5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli DH10B
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TNeu077l17.p1cSP6
            Sequencing primer: SP6.
FEATURES             Location/Qualifiers
     source          1. .276
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TNeu077l17"
                     /dev_stage="neurula"
                     /lab_host="Escherichia coli DH10B"
                     /clone_lib="XGC-neurula"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from neurula.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

  Query Match             3.2%;  Score 19;  DB 1;  Length 276;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        495 TTTTTATAAAACTAAAATC 513
              |||||||||||||||||||
Db        117 TTTTTATAAAACTAAAATC 99


RESULT 71
BX683343
LOCUS       BX683343                280 bp    mRNA    linear   EST 14-NOV-2003
DEFINITION  BX683343 XGC-neurula Xenopus tropicalis cDNA clone TNeu077l17, mRNA
            sequence.
ACCESSION   BX683343
VERSION     BX683343.1  GI:38332463
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 280)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Croning MDR
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TNeu077l17.q1kT7
            Sequencing primer: T7
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
            5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli DH10B.
FEATURES             Location/Qualifiers
     source          1. .280
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TNeu077l17"
                     /dev_stage="neurula"
                     /lab_host="Escherichia coli DH10B"
                     /clone_lib="XGC-neurula"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from neurula.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

  Query Match             3.2%;  Score 19;  DB 4;  Length 280;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        495 TTTTTATAAAACTAAAATC 513
              |||||||||||||||||||
Db        174 TTTTTATAAAACTAAAATC 192


RESULT 72
AZ406693
LOCUS       AZ406693                283 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0176H05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0176H05 F, genomic survey sequence.
ACCESSION   AZ406693
VERSION     AZ406693.1  GI:10530706
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 283)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0176  row: H  column: 05
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 283.
FEATURES             Location/Qualifiers
     source          1. .283
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0176H05"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
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polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 3.2%; Score 19; DB 11; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 337 CAGGTGGAGTTCAAGGCCA 355
||||||||||||||||||||
Db 179 CAGGTGGAGTTCAAGGCCA 197

RESULT 73
BQ392367
LOCUS BQ392367 286 bp mRNA linear EST 22-MAY-2002
DEFINITION NISC_mq24a11.x1 NICHD_XGC_Emb5 Xenopus tropicalis cDNA clone IMAGE:5309109 3', mRNA sequence.
ACCESSION BQ392367
VERSION BQ392367.1 GI:21080054
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 286)
AUTHORS NIH-XCG http://image.llnl.gov/image/html/xenopuslib_info.shtml.
TITLE National Institute of Child Health and Human Development, National Cancer Insitute, Xenopus Gene Collection
JOURNAL Unpublished (2002)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation:
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Plate: LLAM11783 row: B column: 22
Seq primer: -21M13 forward primer (ABI).
FEATURES Location/Qualifiers
source 1. .286
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE:5309109"
/tissue_type="gastrula"
/dev_stage="embryo, stages 10-13"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHD_XGC_Emb5"
/note="Vector: pCMV-SPORT6.1; Site_1: NotI; Site_2: EcoRV; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.0 kb. Constructed by Invitrogen. Note: This is a Xenopus Gene Collection (XGC) library."
ORIGIN

Query Match 3.2%; Score 19; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 495 TTTTTATAAAACTAAAATC 513
||||||||||||||||||||
Db 210 TTTTTATAAAACTAAAATC 228

RESULT 74
AL643008
LOCUS AL643008 287 bp mRNA linear EST 07-NOV-2003
DEFINITION AL643008 XGC-neurula Xenopus tropicalis cDNA clone TNeu016b16 5', mRNA sequence.
ACCESSION AL643008
VERSION AL643008.2 GI:38221579
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 287)
AUTHORS Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
TITLE Sanger Xenopus tropicalis EST project 2001 (11_2003)
JOURNAL Unpublished (2003)
COMMENT On Nov 7, 2001 this sequence version replaced gi:16795133.
Contact: Huckle E
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.
EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end.
Vector: pCS107; Site_1: EcoRI; Site_2: NotI
Host: Escherichia coli DH10B
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TNeu016b16.p1kSP6
Sequencing primer: SP6.
FEATURES Location/Qualifiers
source 1. .287
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TNeu016b16"
/dev_stage="neurula"
/lab_host="Escherichia coli DH10B"
/clone_lib="XGC-neurula"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

Query Match 3.2%; Score 19; DB 1; Length 287;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 495 TTTTTATAAAACTAAAATC 513
||||||||||||||||||||
Db 219 TTTTTATAAAACTAAAATC 237

RESULT 75
BI703351/c
LOCUS BI703351 290 bp mRNA linear EST 18-SEP-2001
DEFINITION fs85e10.y1 Zebrafish neuronal Danio rerio cDNA clone IMAGE:5076571 5', mRNA sequence.
ACCESSION BI703351
VERSION BI703351.1 GI:15665980
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

```
REFERENCE   1  (bases 1 to 290)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
            Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Other_ESTs: fs85e10.x1
            Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library constructed by S. Lin DNA Sequencing by: Washington
            University Genome Sequencing Center Clone distribution: the
            I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
            Seq primer: T3 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .290
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:5076571"
                     /sex="mixed"
                     /dev_stage="adult"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="Zebrafish neuronal"
                     /note="Organ: brain; Vector: pBluescript (modified);
                     Site_1: DraIII(Y); Site_2: DRAIII(X); Library is cloned
                     directionally between the DraIII(X) and DraIII(Y) sites
                     and has been amplified. Library constructed by S. Lin. "
ORIGIN

  Query Match             3.2%;  Score 19;  DB 2;  Length 290;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        442 CTGAATGTCAACAGTGTGA 460
              ||||||||||||||||||
Db        172 CTGAATGTCAACAGTGTGA 154


RESULT 76
BB460815/c
LOCUS       BB460815                307 bp    mRNA    linear   EST 21-JUL-2000
DEFINITION  BB460815 RIKEN full-length enriched, 12 days embryo spinal ganglion
            Mus musculus cDNA clone D130068N23 3', mRNA sequence.
ACCESSION   BB460815
VERSION     BB460815.1  GI:9356308
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 307)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T.,
            Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
            Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
            Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
            Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C.,
            Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H.,
            Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K.,
            Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A.,
            Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watahiki,A.,
            Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A.,
            Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,
            Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length
            cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
            Okazaki,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
             Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .307
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="D130068N23"
                     /tissue_type="spinal ganglion"
                     /dev_stage="12 days embryo"
                     /lab_host="DH10B"
                     /clone_lib="RIKEN full-length enriched, 12 days embryo
                     spinal ganglion"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. Second strand cDNA was prepared with the
                     primer adapter of sequence [5'
                     GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA
                     was cleaved with BamHI and XhoI. Vector: a modified
                     pBluescript KS(+) after bulk excision from Lambda FLC I."
ORIGIN

  Query Match             3.2%;  Score 19;  DB 7;  Length 307;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        256 GGGAGTTGCCTGGCCTCCA 274
              ||||||||||||||||||
Db         52 GGGAGTTGCCTGGCCTCCA 34


RESULT 77
BQ392345
LOCUS       BQ392345                317 bp    mRNA    linear   EST 22-MAY-2002
DEFINITION  NISC_mq23h11.x1 NICHD_XGC_Emb5 Xenopus tropicalis cDNA clone
            IMAGE:5309444 3', mRNA sequence.
ACCESSION   BQ392345
VERSION     BQ392345.1  GI:21080032
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 317)
  AUTHORS   NIH-XCG http://image.llnl.gov/image/html/xenopuslib_info.shtml.
  TITLE     National Institute of Child Health and Human Development, National
            Cancer Insitute, Xenopus Gene Collection
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation:
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
             DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC)
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            info@image.llnl.gov
            Plate: LLAM11783  row: P  column: 21
            Seq primer: -21M13 forward primer (ABI).
FEATURES             Location/Qualifiers
     source          1. .317
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="IMAGE:5309444"
                     /tissue_type="gastrula"
                     /dev_stage="embryo, stages 10-13"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NICHD_XGC_Emb5"
                     /note="Vector: pCMV-SPORT6.1; Site_1: NotI; Site_2: EcoRV;
                     Cloned unidirectionally. Primer: Oligo dT. Average insert
                     size 2.0 kb. Constructed by Invitrogen. Note: This is a
                     Xenopus Gene Collection (XGC) library."
ORIGIN

  Query Match             3.2%;  Score 19;  DB 3;  Length 317;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        495 TTTTTATAAAACTAAAATC 513
              |||||||||||||||||||
Db        207 TTTTTATAAAACTAAAATC 225


RESULT 78
AG255889/c
LOCUS       AG255889                330 bp    DNA     linear   GSS 19-JUL-2003
DEFINITION  Lotus corniculatus var. japonicus DNA, clone:LjT40h03_sfi, genomic
            survey sequence.
ACCESSION   AG255889
VERSION     AG255889.1  GI:26655726
KEYWORDS    GSS.
SOURCE      Lotus corniculatus var. japonicus (Lotus japonicus)
  ORGANISM  Lotus corniculatus var. japonicus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
            Lotus.
REFERENCE   1
  AUTHORS   Sato,S., Nakamura,Y. and Tabata,S.
  TITLE     Lotus japonicus TAC End sequences
  JOURNAL   Published Only in Database (2002)
REFERENCE   2  (bases 1 to 330)
  AUTHORS   Sato,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute,
            The First Laboratory for Plant Gene Research; 2-6-7
            Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan
            (E-mail:ssato@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/,
            Tel:81-438-52-3935(ex.2336), Fax:81-438-52-3934)
FEATURES             Location/Qualifiers
     source          1. .330
                     /organism="Lotus corniculatus var. japonicus"
                     /mol_type="genomic DNA"
                     /strain="Miyakojima MG-20"
                     /variety="japonicus"
                     /db_xref="taxon:34305"
                     /clone="LjT40h03_sfi"
                     /clone_lib="genomic TAC library"
                     /note="VECTOR:pYLTAC7
                     synonym: Lotus japonicus"
ORIGIN

  Query Match             3.2%;  Score 19;  DB 14;  Length 330;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        494 ATTTTTATAAAACTAAAAT 512
              |||||||||||||||||||
Db        243 ATTTTTATAAAACTAAAAT 225


RESULT 79
BQ392422
LOCUS       BQ392422                334 bp    mRNA    linear   EST 22-MAY-2002
DEFINITION  NISC_mq24d03.x1 NICHD_XGC_Emb5 Xenopus tropicalis cDNA clone
            IMAGE:5309237 3', mRNA sequence.
ACCESSION   BQ392422
VERSION     BQ392422.1  GI:21080109
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 334)
  AUTHORS   NIH-XCG http://image.llnl.gov/image/html/xenopuslib_info.shtml.
  TITLE     National Institute of Child Health and Human Development, National
            Cancer Insitute, Xenopus Gene Collection
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation:
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
             DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC)
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            info@image.llnl.gov
            Plate: LLAM11783  row: H  column: 6
            Seq primer: -21M13 forward primer (ABI).
FEATURES             Location/Qualifiers
     source          1. .334
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="IMAGE:5309237"
                     /tissue_type="gastrula"
                     /dev_stage="embryo, stages 10-13"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NICHD_XGC_Emb5"
                     /note="Vector: pCMV-SPORT6.1; Site_1: NotI; Site_2: EcoRV;
                     Cloned unidirectionally. Primer: Oligo dT. Average insert
                     size 2.0 kb. Constructed by Invitrogen. Note: This is a
                     Xenopus Gene Collection (XGC) library."
ORIGIN

  Query Match             3.2%;  Score 19;  DB 3;  Length 334;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        495 TTTTTATAAAACTAAAATC 513
              |||||||||||||||||||
Db        171 TTTTTATAAAACTAAAATC 189


RESULT 80
AL849698/c
```

```
LOCUS       AL849698                335 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AL849698 XGC-egg Xenopus tropicalis cDNA clone TEgg003k15 5', mRNA
            sequence.
ACCESSION   AL849698
VERSION     AL849698.2  GI:38560935
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 335)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     On Sep 15, 2002 this sequence version replaced gi:22869920.
            Contact: Taylor R
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TEgg003k15.p1kSP6
            Sequencing primer: SP6
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from egg.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
            5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli XL1-blue.
FEATURES             Location/Qualifiers
     source          1. .335
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TEgg003k15"
                     /dev_stage="egg"
                     /lab_host="Escherichia coli XL1-blue"
                     /clone_lib="XGC-egg"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from egg.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end"
ORIGIN

  Query Match             3.2%;  Score 19;  DB 1;  Length 335;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        495 TTTTTATAAAACTAAAATC 513
              |||||||||||||||||||
Db        189 TTTTTATAAAACTAAAATC 171


RESULT 81
CX358439
LOCUS       CX358439                350 bp    mRNA    linear   EST 28-SEP-2005
DEFINITION  JGI_XZT28.rev NIH_XGC_tropTad5 Xenopus tropicalis cDNA clone XZT28
            3', mRNA sequence.
ACCESSION   CX358439
VERSION     CX358439.1  GI:57126998
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 350)
  AUTHORS   Richardson,P., Lucas,S., Rokhsar,D., Detter,J.C., Ng,D.C.,
            Brokstein,P. and Lindquist,E.A.
  TITLE     DOE Joint Genome Institute Xenopus tropicalis EST project
  JOURNAL   Unpublished (2004)
COMMENT     Other_ESTs: JGI_XZT28.fwd
            Contact: Lindquist,E.A., Richardson,P.
            DOE Joint Genome Institute
            2800 Mitchell Drive, Walnut Creek, CA 94598, USA
            Tel: 925 296 5600
            Fax: 925 296 5710
            Email: cdna@jgi-psf.org
            Tissue Procurement: Richard M. Harland Laboratory, University of
            California, Berkeley: http://tropicalis.berkeley.edu/home
            cDNA Library Preparation: Richard M. Harland Laboratory, University
            of California, Berkeley
            cDNA Library Arrayed by: DOE Joint Genome Institute:
            http://www.jgi.doe.gov
            DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
            Clone Unavailable: The master plate for this cDNA clone no longer
            exists.
            Naming Conventions: EST name is generated by the concatenation of
            the JGI Clone Id and the direction of sequencing. The suffix '.rev'
            indicates a reverse sequencing read of the insert. It does not
            necessarily reflect the orientation of the insert.
            Poly-A: Based upon the presence of a run of 14 or more T residues
            at the beginning of the sequence, this clone was polyadenylated.
            The resulting Poly-T sequence has been removed.
            Small Insert: Based upon one or more sequencing reads of this clone
            where vector sequence was present at both ends, this clone has been
            determined to contain a cDNA insert on the order of 600-1000 bases.
            Plate: XZT 0001  row: g  column: 7
            High quality sequence stop: 171
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .350
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="XZT28"
                     /tissue_type="whole embryo"
                     /dev_stage="Tadpole (st. 36-41)"
                     /lab_host="E. coli XL1-Blue derivative, Stratagene
                     ElectroTen-Blue"
                     /clone_lib="NIH_XGC_tropTad5"
                     /note="Vector: pCS108; Site_1: SalI; Site_2: NotI; Tadpole
                     library constructed by Russell B. Fletcher in R. Harland's
                     lab using poly A RNA and oligo dT primers (Invitrogen
                     SuperScript Plasmid System for cDNA Synthesis and
                     Cloning). SalI (5' end) -NotI (3' end) cDNA was inserted
                     into vector pCS108
                     (http://mcb.berkeley.edu/labs/harland/pages/plasmids.html)
                     ."
ORIGIN

  Query Match             3.2%;  Score 19;  DB 9;  Length 350;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        495 TTTTTATAAAACTAAAATC 513
              |||||||||||||||||||
Db         11 TTTTTATAAAACTAAAATC 29


RESULT 82
BX708129
LOCUS       BX708129                351 bp    mRNA    linear   EST 17-NOV-2003
DEFINITION  BX708129 XGC-tadpole Xenopus tropicalis cDNA clone TTpA002b09 3',
            mRNA sequence.
ACCESSION   BX708129
VERSION     BX708129.1  GI:38370336
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 351)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
```

```
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Croning MDR
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TTpA002b09.q1kT7
            Sequencing primer: T7
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Nigel Garrett.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from tadpole
            embryos. EcoRI-NotI cut cDNA was then ligated into pCS107 with
            EcoRI at the 5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli DH10B.
FEATURES             Location/Qualifiers
     source          1. .351
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TTpA002b09"
                     /dev_stage="tadpole (stage 35-40)"
                     /lab_host="E. coli DH10B"
                     /clone_lib="XGC-tadpole"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from tadpole
                     embryos. EcoRI-NotI cut cDNA was then ligated into pCS107
                     with EcoRI at the 5' end and NotI at the 3' end"
ORIGIN

  Query Match             3.2%;  Score 19;  DB 4;  Length 351;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        495 TTTTTATAAAACTAAAATC 513
              |||||||||||||||||||
Db        181 TTTTTATAAAACTAAAATC 199


RESULT 83
CN106168
LOCUS       CN106168                354 bp    mRNA    linear   EST 31-MAR-2004
DEFINITION  EC2CAA29AC03.b1 Xenopus tropicalis xthr plasmid library Xenopus
            tropicalis cDNA clone xthr29E05 3', mRNA sequence.
ACCESSION   CN106168
VERSION     CN106168.1  GI:45898864
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 354)
  AUTHORS   Thuret,R., Fierro,A.C., Coen,L., Perron,M., Demeneix,B., Wegnez,M.,
            Gyapay,G., Weissenbach,J., Wincker,P., Mazabraud,A. and Pollet,N.
  TITLE     Exploring the nervous system transcriptome in the model Xenopus
            tropicalis using EST analysis
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Pollet N
            Transgenese et Genetique des Amphibiens
            CNRS UMR 8080
            IBAIC bat 447, Universite Paris Sud, Orsay, F-91405, France
            Tel: +33 169157272
            Fax: +33 169156816
            Email: Nicolas.Pollet@ibaic.u-psud.fr.
FEATURES             Location/Qualifiers
     source          1. .354
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /strain="Ivory Coast"
                     /db_xref="taxon:8364"
                     /clone="xthr29E05"
                     /tissue_type="pool of heads and retinas from tailbud
                     stages 25-35"
                     /dev_stage="stage 25-35"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Xenopus tropicalis xthr plasmid library"
                     /note="Vector: pCMVSPORT6_xthr; Site_1: SfiI; Site_2:
                     SfiI; Xenopus tropicalis polyA+ RNA was obtained from pool
                     of heads and retinas from tailbud stages 25-35 cDNAs were
                     synthesized using the SMART system of CLONTECH and
                     directionally cloned into pCMVSPORT6_xthr, a modified
                     version of pCMVSPORT6 allowing directional cloning using
                     asymetric SfiI sites. For antisense RNA synthesis, use T7
                     promoter and for sense RNA use SP6 promoter. Library
                     constructed by Drs. N. Pollet, M. Perron, M. Wegnez, A.
                     Mazabraud (CNRS UMR 8080, Universite Paris Sud, Orsay,
                     France)."
ORIGIN

  Query Match             3.2%;  Score 19;  DB 8;  Length 354;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        495 TTTTTATAAAACTAAAATC 513
              |||||||||||||||||||
Db         87 TTTTTATAAAACTAAAATC 105


RESULT 84
AL855295
LOCUS       AL855295                361 bp    mRNA    linear   EST 02-DEC-2003
DEFINITION  AL855295 XGC-egg Xenopus tropicalis cDNA clone TEgg003k15 3', mRNA
            sequence.
ACCESSION   AL855295
VERSION     AL855295.2  GI:38630704
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 361)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     On Sep 15, 2002 this sequence version replaced gi:22875514.
            Contact: Taylor R
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TEgg003k15.q1kT7
            Sequencing primer: T7
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from egg.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
            5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli XL1-blue.
FEATURES             Location/Qualifiers
     source          1. .361
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TEgg003k15"
                     /dev_stage="egg"
                     /lab_host="Escherichia coli XL1-blue"
                     /clone_lib="XGC-egg"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from egg.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end"
ORIGIN
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  Query Match             3.2%;  Score 19;  DB 1;  Length 361;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        495 TTTTTATAAAACTAAAATC 513
              |||||||||||||||||||
Db        173 TTTTTATAAAACTAAAATC 191


RESULT 85
DR612001/c
LOCUS       DR612001                365 bp    mRNA    linear   EST 11-JUL-2005
DEFINITION  EST1002129 FvH Gibberella moniliformis cDNA clone FVHAA26, mRNA
            sequence.
ACCESSION   DR612001
VERSION     DR612001.1  GI:70686649
KEYWORDS    EST.
SOURCE      Gibberella moniliformis
  ORGANISM  Gibberella moniliformis
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE   1  (bases 1 to 365)
  AUTHORS   Brown,D.W., Cheung,F., Proctor,R.H., Butchko,A.E., Zheng,L, Lee,Y.,
            Utterback,T., Smith,S., Feldblyum,T., Glenn,A.E., Plattner,R.D.,
            Kendra,D.F., Town,C.D. and Whitelaw,C.A.
  TITLE     Comparative analysis of 87,000 expressed sequence tags from the
            fumonisin-producing fungus Fusarium verticillioides
  JOURNAL   Fungal Genet. Biol. 42 (10), 848-861 (2005)
   PUBMED   16099185
COMMENT     Contact: Brown, D.W.
            USDA/ARS/NCAUR
            USDA
            1815 N. University St, Peoria, IL 61604, USA
            Tel: 309 681 6230
            Fax: 309 681 6689
            Email: browndw@ncaur.usda.gov
            TIGR sequence name: FVHAA26TH
            Seq primer: AAT TAA CCC TCA CTA AAG GG.
FEATURES             Location/Qualifiers
     source          1. .365
                     /organism="Gibberella moniliformis"
                     /mol_type="mRNA"
                     /strain="m3125"
                     /db_xref="taxon:117187"
                     /clone="FVHAA26"
                     /tissue_type="mycelia"
                     /clone_lib="FvH"
                     /note="Vector: pBlueScript II SK(+) XR; Site_1: EcoRI;
                     Site_2: XhoI; anamorph: Fusarium verticillioides. Library
                     FvH was prepared from germinating conidia in an aqueous
                     extract of maize seedlings. The aqueous extract was
                     obtained by germinating surface-sterilized maize seeds for
                     four days on 1% water agar supplemented with 100 ug/ml
                     streptomycin sulfate. Under sterile conditions, 70 g of
                     excised roots and shoots from the resulting seedlings was
                     blended with 250 ml water, filtered once through Miracloth
                     (Calbiochem) and then again through #1 Whatman filter
                     paper. The extracts were inoculated to a spore
                     concentration of 5 x 106 conidia per ml and then incubated
                     for 10 hours at 30C with shaking at 200 RPM. Cultures were
                     vacuum filtered and the mycelial mats were frozen in
                     liquid nitrogen, ground to a powder, and then added to
                     TRIzol Reagent (Invitrogen, Carlsbad CA) at approximately
                     1 g mycelia per 10 ml TRIzol. The cDNA was directionally
                     ligated into the pBlueScript II SK(+) XR vector (cDNA
                     Synthesis Kit; Stratagene)."
ORIGIN

  Query Match             3.2%;  Score 19;  DB 10;  Length 365;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        126 CACTTCCGAAGAGATTGAT 144
              |||||||||||||||||||
Db        181 CACTTCCGAAGAGATTGAT 163


RESULT 86
DN068916
LOCUS       DN068916                366 bp    mRNA    linear   EST 14-SEP-2005
DEFINITION  JGI_CABD5093.rev NIH_XGC_tropLun1 Xenopus tropicalis cDNA clone
            CABD5093 3', mRNA sequence.
ACCESSION   DN068916
VERSION     DN068916.1  GI:59657884
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 366)
  AUTHORS   Richardson,P., Lucas,S., Rokhsar,D., Detter,J.C., Ng,D.C.,
            Brokstein,P. and Lindquist,E.A.
  TITLE     DOE Joint Genome Institute Xenopus tropicalis EST project
  JOURNAL   Unpublished (2004)
COMMENT     Other_ESTs: JGI_CABD5093.fwd
            Contact: Lindquist,E.A., Richardson,P.
            DOE Joint Genome Institute
            2800 Mitchell Drive, Walnut Creek, CA 94598, USA
            Tel: 925 296 5600
            Fax: 925 296 5710
            Email: cdna@jgi-psf.org
            Tissue Procurement: Robert M. Grainger
            cDNA Library Preparation: Bruce Blumberg Laboratory, University of
            California, Irvine
            cDNA Library Arrayed by: DOE Joint Genome Institute:
            http://www.jgi.doe.gov
            DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
            Clone Unavailable: The master plate for this cDNA clone no longer
            exists.
            Naming Conventions: EST name is generated by the concatenation of
            the JGI Clone Id and the direction of sequencing. The suffix '.rev'
            indicates a reverse sequencing read of the insert. It does not
            necessarily reflect the orientation of the insert.
            Poly-A: Based upon the presence of a run of 14 or more T residues
            at the beginning of the sequence, this clone was polyadenylated.
            The resulting Poly-T sequence has been removed.
            Plate: CABD 0053  row: j  column: 1
            High quality sequence stop: 334
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .366
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /strain="N6 (Nigerian 6th generation inbred)"
                     /db_xref="taxon:8364"
                     /clone="CABD5093"
                     /tissue_type="Lung"
                     /dev_stage="Adult"
                     /lab_host="ElectroMAX DH10B T1 Phage Resistant cells"
                     /clone_lib="NIH_XGC_tropLun1"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: XhoI; The
                     library was prepared from 5 ug of poly A+ RNA by oligo-dT
                     priming
                     (5'-ACTAGTGCGGCCGCCTAGGCCTCGAGTTTTTTTTTTTTTTTTV-3') and
                     Stratascript reverse transcriptase. After ligation of
                     EcoRI adapters (5'-AATTCGGCACGAGG-3') followed by kinasing
                     adapters and by XhoI digestion, the cDNA was size selected
                     by chromatography on Sepharose CL-2B columns and fractions
                     containing cDNAs larger than 1000 bp were ligated into
                     EcoRI/XhoI-digested pCS107. Reference for library
                     construction: Current Genomics 4, 635-644. Library
                     constructed by Michelle Tabb and Bruce Blumberg (Dept of
                     Developmental and Cell Biology, University of California,
                     Irvine)."
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ORIGIN

  Query Match             3.2%;  Score 19;  DB 9;  Length 366;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        495 TTTTTATAAAACTAAAATC 513
              |||||||||||||||||||
Db        147 TTTTTATAAAACTAAAATC 165


RESULT 87
CF879856
LOCUS       CF879856                376 bp    mRNA    linear   EST 31-OCT-2003
DEFINITION  tric081xk20.b1 T.reesei mycelial culture, Version 6 October 2003
            Hypocrea jecorina cDNA clone tric081xk20, mRNA sequence.
ACCESSION   CF879856
VERSION     CF879856.1  GI:38134538
KEYWORDS    EST.
SOURCE      Hypocrea jecorina (anamorph: Trichoderma reesei)
  ORGANISM  Hypocrea jecorina
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
REFERENCE   1  (bases 1 to 376)
  AUTHORS   Diener,S.E., Dunn-Coleman,N., Foreman,P., Houfek,T.D.,
            Teunissen,P.J.M., van Solingen,P., Dankmeyer,L., Mitchell,T.K.,
            Ward,M. and Dean,R.A.
  TITLE     Characterization of the protein processing and secretion pathways
            in a comprehensive set of expressed sequence tags from Trichoderma
            reesei
  JOURNAL   FEMS Microbiol. Lett. 230 (2), 275-282 (2004)
   PUBMED   14757250
COMMENT     Contact: Ralph A. Dean
            Fungal Genomics Laboratory
            North Carolina State University
            Campus Box 7251, Raleigh, NC 27695, USA
            Tel: 919-513-0020
            Fax: 919-513-0024
            Email: ralph_dean@ncsu.edu
            Seq primer: LT-F1 primer.
FEATURES             Location/Qualifiers
     source          1. .376
                     /organism="Hypocrea jecorina"
                     /mol_type="mRNA"
                     /strain="QM6a"
                     /db_xref="taxon:51453"
                     /clone="tric081xk20"
                     /dev_stage="mycelia"
                     /clone_lib="T.reesei mycelial culture, Version 6 October
                     2003"
                     /note="Vector: pREP3Y; Site_1: Not I/Sal I; Mycelial
                     culture grown from 24 hrs to 6 days with varying Carbon
                     and Nitrogen sources and concentrations."
ORIGIN

  Query Match             3.2%;  Score 19;  DB 5;  Length 376;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 CCTCCCCACACCCACACCA 24
              |||||||||||||||||||
Db        342 CCTCCCCACACCCACACCA 360


RESULT 88
CR437136/c
LOCUS       CR437136                379 bp    mRNA    linear   EST 19-JUN-2004
DEFINITION  CR437136 XGC-tailbud Xenopus tropicalis cDNA clone TTbA069f05 5',
            mRNA sequence.
ACCESSION   CR437136
VERSION     CR437136.1  GI:48962723
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 379)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Garrett,N. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (2004)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Croning MDR
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
             TROPICALIS_SEQUENCE_ID: TTbA069f05.p1kSP6
             This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Nigel Garrett.
            Seq primer: SP6.
FEATURES             Location/Qualifiers
     source          1. .379
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TTbA069f05"
                     /dev_stage="tailbud (stage 28-30)"
                     /lab_host="Escherichia coli DH10B."
                     /clone_lib="XGC-tailbud"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from tailbud.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

  Query Match             3.2%;  Score 19;  DB 8;  Length 379;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        495 TTTTTATAAAACTAAAATC 513
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Db        233 TTTTTATAAAACTAAAATC 215


RESULT 89
CR560333
LOCUS       CR560333                386 bp    mRNA    linear   EST 19-JUL-2004
DEFINITION  CR560333 XGC-tailbud-head Xenopus tropicalis cDNA clone THdA003h06
            3', mRNA sequence.
ACCESSION   CR560333
VERSION     CR560333.1  GI:50390410
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Garrett,N. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (2004)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Croning MDR
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
             TROPICALIS_SEQUENCE_ID: THdA003h06.q1kT7
             This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Nigel Garrett.
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .386
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="THdA003h06"
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                     /dev_stage="tailbud head (stage 28-30)"
                     /lab_host="Escherichia coli DH10B."
                     /clone_lib="XGC-tailbud-head"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from tailbud
                     head. EcoRI-NotI cut cDNA was then ligated into pCS107
                     with EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

  Query Match             3.2%;  Score 19;  DB 8;  Length 386;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        495 TTTTTATAAAACTAAAATC 513
              |||||||||||||||||||
Db        170 TTTTTATAAAACTAAAATC 188


RESULT 90
CR437137
LOCUS       CR437137                410 bp    mRNA    linear   EST 19-JUN-2004
DEFINITION  CR437137 XGC-tailbud Xenopus tropicalis cDNA clone TTbA069f05 3',
            mRNA sequence.
ACCESSION   CR437137
VERSION     CR437137.1  GI:48962724
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 410)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Garrett,N. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (2004)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Croning MDR
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
             TROPICALIS_SEQUENCE_ID: TTbA069f05.q1kT7
             This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Nigel Garrett.
            Seq primer: T7.
FEATURES             Location/Qualifiers
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                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TTbA069f05"
                     /dev_stage="tailbud (stage 28-30)"
                     /lab_host="Escherichia coli DH10B."
                     /clone_lib="XGC-tailbud"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from tailbud.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

  Query Match             3.2%;  Score 19;  DB 8;  Length 410;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        495 TTTTTATAAAACTAAAATC 513
              |||||||||||||||||||
Db        178 TTTTTATAAAACTAAAATC 196


RESULT 91
BY675748/c
LOCUS       BY675748                415 bp    mRNA    linear   EST 16-DEC-2002
DEFINITION  BY675748 RIKEN full-length enriched, 12.5 days embryo Rathke's
            pouches Mus musculus cDNA clone K920003L19 3', mRNA sequence.
ACCESSION   BY675748
VERSION     BY675748.1  GI:27061773
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 415)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
            Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
            Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
            Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
            Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
            Hayashizaki,Y. Direct Submission
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
             cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
             Tissues were provided by Michelle Brinkmeier and Sally Camper (
            Dept. Human Genetics University of Michigan Medical School 4301
            MSRB 3 1500 W. Medical Center Dr. Ann Arbor,MI 48109-0638 USA )
```

whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
FEATURES Location/Qualifiers
source 1. .415
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CD-1"
/db_xref="taxon:10090"
/clone="K920003L19"
/tissue_type="Rathke's pouches"
/dev_stage="12.5 days embryo"
/clone_lib="RIKEN full-length enriched, 12.5 days embryo Rathke's pouches"
ORIGIN

Query Match 3.2%; Score 19; DB 4; Length 415;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AACCTCCCCACACCCACAC 22
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Db 159 AACCTCCCCACACCCACAC 141

RESULT 92
BQ394236
LOCUS BQ394236 421 bp mRNA linear EST 22-MAY-2002
DEFINITION NISC_ng08a11.x1 NICHD_XGC_Emb6 Xenopus tropicalis cDNA clone IMAGE:5382453 3', mRNA sequence.
ACCESSION BQ394236
VERSION BQ394236.1 GI:21081923
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 421)
AUTHORS NIH-XCG http://image.llnl.gov/image/html/xenopuslib_info.shtml.
TITLE National Institute of Child Health and Human Development, National Cancer Insitute, Xenopus Gene Collection
JOURNAL Unpublished (2002)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation:
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Plate: LLAM11974 row: B column: 22
Seq primer: -21M13 forward primer (ABI).
FEATURES Location/Qualifiers
source 1. .421
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE:5382453"
/tissue_type="neurula"
/dev_stage="embryo, stages 14-19"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHD_XGC_Emb6"
/note="Vector: pCMV-SPORT6.1; Site_1: NotI; Site_2: EcoRV; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb. Constructed by Invitrogen. Note: This is a Xenopus Gene Collection (XGC) library."
ORIGIN

Query Match 3.2%; Score 19; DB 3; Length 421;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 495 TTTTTATAAAACTAAAATC 513
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Db 214 TTTTTATAAAACTAAAATC 232

RESULT 93
BY448508/c
LOCUS BY448508 423 bp mRNA linear EST 13-DEC-2002
DEFINITION BY448508 RIKEN full-length enriched, 15 days pregnant adult female amnion Mus musculus cDNA clone K630030F20 3', mRNA sequence.
ACCESSION BY448508
VERSION BY448508.1 GI:26740129
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 423)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

```
FEATURES             Location/Qualifiers
     source          1. .423
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="K630030F20"
                     /sex="female"
                     /tissue_type="amnion"
                     /dev_stage="15 days pregnant adult"
                     /clone_lib="RIKEN full-length enriched, 15 days pregnant
                     adult female amnion"
ORIGIN

  Query Match             3.2%;  Score 19;  DB 4;  Length 423;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 AACCTCCCCACACCCACAC 22
              ||||||||||||||||||
Db        164 AACCTCCCCACACCCACAC 146


RESULT 94
CX311082
LOCUS       CX311082                431 bp    mRNA    linear   EST 29-SEP-2005
DEFINITION  JGI_XZT11080.rev NIH_XGC_tropTad5 Xenopus tropicalis cDNA clone
            XZT11080 3', mRNA sequence.
ACCESSION   CX311082
VERSION     CX311082.1  GI:57035687
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 431)
  AUTHORS   Richardson,P., Lucas,S., Rokhsar,D., Detter,J.C., Ng,D.C.,
            Brokstein,P. and Lindquist,E.A.
  TITLE     DOE Joint Genome Institute Xenopus tropicalis EST project
  JOURNAL   Unpublished (2004)
COMMENT     Other_ESTs: JGI_XZT11080.fwd
            Contact: Lindquist,E.A., Richardson,P.
            DOE Joint Genome Institute
            2800 Mitchell Drive, Walnut Creek, CA 94598, USA
            Tel: 925 296 5600
            Fax: 925 296 5710
            Email: cdna@jgi-psf.org
            Tissue Procurement: Richard M. Harland Laboratory, University of
            California, Berkeley: http://tropicalis.berkeley.edu/home
            cDNA Library Preparation: Richard M. Harland Laboratory, University
            of California, Berkeley
            cDNA Library Arrayed by: DOE Joint Genome Institute:
            http://www.jgi.doe.gov
            DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
            Clone Unavailable: The master plate for this cDNA clone no longer
            exists.
            Naming Conventions: EST name is generated by the concatenation of
            the JGI Clone Id and the direction of sequencing. The suffix '.rev'
            indicates a reverse sequencing read of the insert. It does not
            necessarily reflect the orientation of the insert.
            Plate: XZT 0113  row: p  column: 10
            High quality sequence stop: 386.
FEATURES             Location/Qualifiers
     source          1. .431
                     /organism="Xenopus tropicalis"
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                     /db_xref="taxon:8364"
                     /clone="XZT11080"
                     /tissue_type="whole embryo"
                     /dev_stage="Tadpole (st. 36-41)"
                     /lab_host="E. coli XL1-Blue derivative, Stratagene
                     ElectroTen-Blue"
                     /clone_lib="NIH_XGC_tropTad5"
                     /note="Vector: pCS108; Site_1: SalI; Site_2: NotI; Tadpole
                     library constructed by Russell B. Fletcher in R. Harland's
                     lab using poly A RNA and oligo dT primers (Invitrogen
                     SuperScript Plasmid System for cDNA Synthesis and
                     Cloning). SalI (5' end) -NotI (3' end) cDNA was inserted
                     into vector pCS108
                     (http://mcb.berkeley.edu/labs/harland/pages/plasmids.html)
                     ."
ORIGIN

  Query Match             3.2%;  Score 19;  DB 8;  Length 431;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        495 TTTTTATAAAACTAAAATC 513
              ||||||||||||||||||
Db         87 TTTTTATAAAACTAAAATC 105


RESULT 95
AL966626/c
LOCUS       AL966626                433 bp    mRNA    linear   EST 05-DEC-2003
DEFINITION  AL966626 XGC-gastrula Xenopus tropicalis cDNA clone TGas137b24 5',
            mRNA sequence.
ACCESSION   AL966626
VERSION     AL966626.2  GI:39021328
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 433)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     On Nov 27, 2002 this sequence version replaced gi:25790221.
            Contact: Taylor R
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TGas137b24.p1kSP6
            Sequencing primer: SP6
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from stages 10-13
            gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with
            EcoRI at the 5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli XL1- blue.
FEATURES             Location/Qualifiers
     source          1. .433
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TGas137b24"
                     /dev_stage="gastrula (stages 10.5-12 mixed)"
                     /lab_host="Escherichia coli XL1-blue"
                     /clone_lib="XGC-gastrula"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from stages
```

10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

Query Match 3.2%; Score 19; DB 1; Length 433;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 495 TTTTTATAAAACTAAAATC 513
||||||||||||||||||||
Db 205 TTTTTATAAAACTAAAATC 187

RESULT 96
CN106169/c
LOCUS CN106169 433 bp mRNA linear EST 31-MAR-2004
DEFINITION EC2CAA29AC03.g1 Xenopus tropicalis xthr plasmid library Xenopus tropicalis cDNA clone xthr29E05 5', mRNA sequence.
ACCESSION CN106169
VERSION CN106169.1 GI:45898865
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 433)
AUTHORS Thuret,R., Fierro,A.C., Coen,L., Perron,M., Demeneix,B., Wegnez,M., Gyapay,G., Weissenbach,J., Wincker,P., Mazabraud,A. and Pollet,N.
TITLE Exploring the nervous system transcriptome in the model Xenopus tropicalis using EST analysis
JOURNAL Unpublished (2004)
COMMENT Contact: Pollet N
Transgenese et Genetique des Amphibiens
CNRS UMR 8080
IBAIC bat 447, Universite Paris Sud, Orsay, F-91405, France
Tel: +33 169157272
Fax: +33 169156816
Email: Nicolas.Pollet@ibaic.u-psud.fr.
FEATURES Location/Qualifiers
source 1. .433
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/strain="Ivory Coast"
/db_xref="taxon:8364"
/clone="xthr29E05"
/tissue_type="pool of heads and retinas from tailbud stages 25-35"
/dev_stage="stage 25-35"
/lab_host="E.coli DH10B"
/clone_lib="Xenopus tropicalis xthr plasmid library"
/note="Vector: pCMVSPORT6_xthr; Site_1: SfiI; Site_2: SfiI; Xenopus tropicalis polyA+ RNA was obtained from pool of heads and retinas from tailbud stages 25-35 cDNAs were synthesized using the SMART system of CLONTECH and directionally cloned into pCMVSPORT6_xthr, a modified version of pCMVSPORT6 allowing directional cloning using asymetric SfiI sites. For antisense RNA synthesis, use T7 promoter and for sense RNA use SP6 promoter. Library constructed by Drs. N. Pollet, M. Perron, M. Wegnez, A. Mazabraud (CNRS UMR 8080, Universite Paris Sud, Orsay, France)."
ORIGIN

Query Match 3.2%; Score 19; DB 8; Length 433;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 495 TTTTTATAAAACTAAAATC 513
||||||||||||||||||||
Db 267 TTTTTATAAAACTAAAATC 249

RESULT 97
CK989220/c
LOCUS CK989220 434 bp mRNA linear EST 19-MAR-2004
DEFINITION BgHC-23.76 BgHC Biomphalaria glabrata cDNA 5', mRNA sequence.
ACCESSION CK989220
VERSION CK989220.1 GI:45596257
KEYWORDS EST.
SOURCE Biomphalaria glabrata
ORGANISM Biomphalaria glabrata
Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora; Lymnaeoidea; Planorbidae; Biomphalaria.
REFERENCE 1 (bases 1 to 434)
AUTHORS Mitta,G., Galinier,R., Tisseyre,P., Allienne,J.-F., Girerd-Chambaz,Y., Guillou,F., Bouchut,A. and Coustau,C.
TITLE Gene discovery and expression analysis of immune-relevant genes from Biomphalaria glabrata hemocytes
JOURNAL Dev. Comp. Immunol. 29 (5), 393-407 (2005)
PUBMED 15707661
COMMENT Contact: Mitta Guillaume
Parasitologie fonctionnelle et evolutive.
CNRS / Univ. Perpignan
52 Ave Paul Alduy, Universite, 66 860 Perpignan cedex, France
Tel: 33 3 68 66 21 88
Fax: 33 3 68 66 22 81
Email: mitta@univ-perp.fr
Seq primer: CGAAGTTATCTCGACG.
FEATURES Location/Qualifiers
source 1. .434
/organism="Biomphalaria glabrata"
/mol_type="mRNA"
/isolate="Bg.Bra strain"
/db_xref="taxon:6526"
/sex="hermaphrodite"
/cell_type="Circulating hemocytes"
/clone_lib="BgHC"
/note="Vector: pDNR-LIB; The library was designed with 500 ng of total RNA using the creator SMART cDNA library construction kit (Clontech)."
ORIGIN

Query Match 3.2%; Score 19; DB 8; Length 434;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 207 CATGAATGAGAGTTGCCTG 225
||||||||||||||||||||
Db 139 CATGAATGAGAGTTGCCTG 121

RESULT 98
AQ928052/c
LOCUS AQ928052 436 bp DNA linear GSS 21-DEC-1999
DEFINITION RPCI-23-258G4.TJ RPCI-23 Mus musculus genomic clone RPCI-23-258G4, genomic survey sequence.
ACCESSION AQ928052
VERSION AQ928052.1 GI:6617055
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 436)
AUTHORS Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. and Fraser,C.M.
TITLE Mouse BAC End Sequences from Library RPCI-23
JOURNAL Unpublished (1999)
COMMENT Other_GSSs: RPCI-23-258G4.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research

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            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-23. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
            or from Resea ch Genetics (info@resgen.com). BAC end page:
            http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 258  row: G  column: 4
            Seq primer: SP6
            Class: BAC ends.
FEATURES              Location/Qualifiers
     source           1. .436
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="RPCI-23-258G4"
                      /sex="Female"
                      /lab_host="DH10B"
                      /clone_lib="RPCI-23"
                      /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
                      EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
                      brain genomic DNA was isolated and  partially digested
                      with a combination of EcoRI and EcoRI Methylase.   Size
                      selected DNA was cloned into the pBACe3.6 vector at the
                      EcoRI  sites.  The ligation products were transformed into
                      DH10B  electrocompetent cells (BRL Life Technologies).   "
ORIGIN

  Query Match             3.2%;  Score 19;  DB 11;  Length 436;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        337 CAGGTGGAGTTCAAGGCCA 355
              ||||||||||||||||||||
Db         38 CAGGTGGAGTTCAAGGCCA 20


RESULT 99
CF940887
LOCUS       CF940887                439 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  NcESTqab73f07.y1 Nc-1 Tachyzoite cDNA Library 2 Neospora caninum
            cDNA 5', mRNA sequence.
ACCESSION   CF940887
VERSION     CF940887.1  GI:38441457
KEYWORDS    EST.
SOURCE      Neospora caninum
  ORGANISM  Neospora caninum
            Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
            Sarcocystidae; Neospora.
REFERENCE   1  (bases 1 to 439)
  AUTHORS   Cole,R., Fogarty,S., Tang,K., Howe,D.K., Sibley,L.D., Clifton,S.,
            Marra,M., Hillier,L., Pape,D., Martin,J., Wylie,T., Theising,B.,
            Bowers,Y., Gibbons,M., Ritter,E., Bennet,J., Ronko,I.,
            Tsagareishvili,R., Fedele,M., Belaygorod,L., Franklin,C.,
            Carr,L.M., Grow,A., Maguire,L., Wadkins,J., Richey,J., Waterston,R.
            and Wilson,R.
  TITLE     USDA-WashU Neospora EST Project
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Sandy Clifton, Ph.D. - Neospora
            USDA-WashU Neospora EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Contact David Sibley (toxoest@borcim.wustl.edu) for further
            information relating to organism, libraries, or clone availability.
            Putative full length read
            vector to vector length is
            Seq primer: -40RP from Gibco.
FEATURES              Location/Qualifiers
     source           1. .439
                      /organism="Neospora caninum"
                      /mol_type="mRNA"
                      /db_xref="taxon:29176"
                      /dev_stage="Tachyzoite"
                      /lab_host="GC10 Competent Cells(PGC)"
                      /clone_lib="Nc-1 Tachyzoite cDNA Library 2"
                      /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
                      XhoI; The cDNA library was constructed by Keliang Tang,
                      and Robert Cole at Washington University. cDNA was
                      synthesized from poly mRNA using an oligo-dT primer
                      containing a XhoI site. Following second strand synthesis,
                      EcoRI adapters were ligated to the cDNA, and products were
                      size-selected on sephacryl S500. The cDNA were
                      directionally cloned into the EcoRI/XhoI prepared
                      pBluescript II SK+ vector, and electroporated into GC10
                      Competent Cells(PGC). The library may contain a small
                      percentage of host or bacterial contaminants."
ORIGIN

  Query Match             3.2%;  Score 19;  DB 5;  Length 439;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        396 TCTGGATCAAAACATGCTG 414
              ||||||||||||||||||||
Db        226 TCTGGATCAAAACATGCTG 244


RESULT 100
CR441087/c
LOCUS       CR441087                442 bp    mRNA    linear   EST 19-JUN-2004
DEFINITION  CR441087 XGC-tailbud Xenopus tropicalis cDNA clone TTbA078g04 5',
            mRNA sequence.
ACCESSION   CR441087
VERSION     CR441087.1  GI:48966674
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 442)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Garrett,N. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (2004)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Croning MDR
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
             TROPICALIS_SEQUENCE_ID: TTbA078g04.p1kSP6
             This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Nigel Garrett.
            Seq primer: SP6.
FEATURES              Location/Qualifiers
     source           1. .442
                      /organism="Xenopus tropicalis"
                      /mol_type="mRNA"
                      /db_xref="taxon:8364"
                      /clone="TTbA078g04"
                      /dev_stage="tailbud (stage 28-30)"
                      /lab_host="Escherichia coli DH10B."
                      /clone_lib="XGC-tailbud"
                      /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                      was oligo dT primed from 5ug of poly A+ RNA from tailbud.
                      EcoRI-NotI cut cDNA was then ligated into pCS107 with
                      EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

  Query Match             3.2%;  Score 19;  DB 8;  Length 442;
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Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        495 TTTTTATAAAACTAAAATC 513
              |||||||||||||||||||
Db        296 TTTTTATAAAACTAAAATC 278
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2006, 22:44:33 ; Search time 134.358 Seconds
(without alignments)
8230.433 Million cell updates/sec

Title: US-10-821-670A-35
Perfect score: 591
Sequence: 1 aggaacctccccacacccac.....tgagctatctgaatgcttcc 591

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1403666 seqs, 935554401 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2806514

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 200 summaries

Database : Issued_Patents_NA:*
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3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
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9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	591	100.0	591	3	US-09-917-265A-35	Sequence 35, Appl
c	2	591	100.0	591	3	US-09-917-265A-37	Sequence 37, Appl
	3	558	94.4	1533	3	US-09-917-265A-43	Sequence 43, Appl
c	4	558	94.4	1533	3	US-09-917-265A-45	Sequence 45, Appl
	5	558	94.4	1599	3	US-09-917-265A-38	Sequence 38, Appl
c	6	558	94.4	1599	3	US-09-917-265A-40	Sequence 40, Appl
	7	540	91.4	666	3	US-09-917-265A-32	Sequence 32, Appl
c	8	540	91.4	666	3	US-09-917-265A-34	Sequence 34, Appl
	9	507	85.8	561	3	US-09-917-265A-101	Sequence 101, App
c	10	507	85.8	561	3	US-09-917-265A-103	Sequence 103, App
	11	480	81.2	591	3	US-09-011-143-9	Sequence 9, Appli
	12	480	81.2	591	3	US-09-302-495-9	Sequence 9, Appli
	13	480	81.2	591	3	US-10-079-616-9	Sequence 9, Appli
	14	480	81.2	1441	3	US-09-011-143-8	Sequence 8, Appli
	15	480	81.2	1441	3	US-09-302-495-8	Sequence 8, Appli
	16	480	81.2	1441	3	US-10-079-616-8	Sequence 8, Appli
	17	189	32.0	689	3	US-09-011-143-26	Sequence 26, Appl
	18	189	32.0	689	3	US-09-302-495-26	Sequence 26, Appl
	19	189	32.0	689	3	US-10-079-616-26	Sequence 26, Appl
	20	81	13.7	591	3	US-09-917-265A-49	Sequence 49, Appl
c	21	81	13.7	591	3	US-09-917-265A-51	Sequence 51, Appl
	22	81	13.7	666	3	US-09-917-265A-46	Sequence 46, Appl
c	23	81	13.7	666	3	US-09-917-265A-48	Sequence 48, Appl
	24	81	13.7	669	3	US-09-079-984A-2	Sequence 2, Appli
	25	81	13.7	669	3	US-09-079-984A-12	Sequence 12, Appl
	26	81	13.7	669	3	US-09-390-729-2	Sequence 2, Appli
	27	81	13.7	669	3	US-09-390-729-12	Sequence 12, Appl
	28	81	13.7	1455	3	US-09-917-265A-104	Sequence 104, App
c	29	81	13.7	1455	3	US-09-917-265A-106	Sequence 106, App
	30	81	13.7	1533	3	US-09-917-265A-66	Sequence 66, Appl
c	31	81	13.7	1533	3	US-09-917-265A-68	Sequence 68, Appl
	32	81	13.7	1599	3	US-09-917-265A-61	Sequence 61, Appl
c	33	81	13.7	1599	3	US-09-917-265A-63	Sequence 63, Appl
	34	65	11.0	601	3	US-09-949-016-20385	Sequence 20385, A
	35	65	11.0	601	3	US-09-949-016-87352	Sequence 87352, A
	36	65	11.0	660	2	US-08-186-529-3	Sequence 3, Appli
	37	65	11.0	660	2	US-08-640-386A-3	Sequence 3, Appli
	38	65	11.0	721	2	US-08-184-009-199	Sequence 199, App
	39	65	11.0	721	2	US-08-458-356-199	Sequence 199, App
	40	65	11.0	721	3	US-08-460-736-199	Sequence 199, App
	41	65	11.0	721	3	US-09-535-370-199	Sequence 199, App
	42	65	11.0	721	3	US-09-663-667-199	Sequence 199, App
	43	65	11.0	762	3	US-08-848-760B-21	Sequence 21, Appl
	44	65	11.0	762	3	US-09-826-025-21	Sequence 21, Appl
	45	65	11.0	762	5	US-09-543-679A-2890	Sequence 2890, Ap
	46	65	11.0	1019	3	US-09-949-016-2462	Sequence 2462, Ap
	47	65	11.0	1026	2	US-08-751-767A-1	Sequence 1, Appli
	48	65	11.0	1026	3	US-09-023-655-1041	Sequence 1041, Ap
	49	65	11.0	1026	3	US-09-949-016-130	Sequence 130, App
	50	65	11.0	1287	3	US-09-634-368-6	Sequence 6, Appli
	51	65	11.0	1316	2	US-08-684-687-3	Sequence 3, Appli
	52	65	11.0	1316	3	US-09-851-520-3	Sequence 3, Appli
	53	65	11.0	1364	2	US-08-265-087-3	Sequence 3, Appli
	54	65	11.0	1364	2	US-08-621-493-3	Sequence 3, Appli
	55	65	11.0	1364	2	US-08-965-688-3	Sequence 3, Appli
	56	65	11.0	1364	3	US-09-260-173-3	Sequence 3, Appli
	57	65	11.0	1395	3	US-09-924-703-5	Sequence 5, Appli
	58	65	11.0	1560	2	US-08-751-767A-11	Sequence 11, Appl
	59	65	11.0	1623	2	US-08-751-767A-9	Sequence 9, Appli
	60	65	11.0	1645	3	US-09-310-842-2	Sequence 2, Appli
	61	65	11.0	4521	5	US-09-543-679A-2893	Sequence 2893, Ap
	62	65	11.0	6139	2	US-08-751-767A-7	Sequence 7, Appli
	63	65	11.0	10764	3	US-09-949-016-11872	Sequence 11872, A
	64	65	11.0	10765	3	US-09-949-016-14204	Sequence 14204, A
	65	56	9.5	601	3	US-09-949-016-20381	Sequence 20381, A
	66	56	9.5	601	3	US-09-949-016-87348	Sequence 87348, A
	67	43	7.3	79	3	US-09-011-143-24	Sequence 24, Appl
	68	43	7.3	79	3	US-09-302-495-24	Sequence 24, Appl
	69	43	7.3	79	3	US-10-079-616-24	Sequence 24, Appl
	70	27	4.6	39	3	US-09-917-265A-91	Sequence 91, Appl
	71	27	4.6	582	3	US-09-634-368-1	Sequence 1, Appli
	72	27	4.6	713	2	US-08-385-335A-10	Sequence 10, Appl
	73	27	4.6	1278	3	US-09-634-368-5	Sequence 5, Appli
	74	27	4.6	1569	3	US-09-634-368-12	Sequence 12, Appl
	75	27	4.6	2013	3	US-09-634-368-11	Sequence 11, Appl
	76	27	4.6	2709	3	US-09-634-368-13	Sequence 13, Appl
	77	27	4.6	6295	2	US-08-659-206A-4	Sequence 4, Appli
	78	27	4.6	7287	2	US-08-659-206A-1	Sequence 1, Appli
c	79	24	4.1	27	3	US-09-917-265A-90	Sequence 90, Appl
c	80	24	4.1	36	3	US-09-011-143-25	Sequence 25, Appl
c	81	24	4.1	36	3	US-09-302-495-25	Sequence 25, Appl
c	82	24	4.1	36	3	US-10-079-616-25	Sequence 25, Appl
c	83	24	4.1	41	3	US-09-917-265A-92	Sequence 92, Appl
	84	21	3.6	32	2	US-08-859-998-383	Sequence 383, App
	85	21	3.6	32	3	US-09-225-928-383	Sequence 383, App
	86	21	3.6	32	3	US-09-225-201B-383	Sequence 383, App
	87	20	3.4	20	2	US-08-012-543-13	Sequence 13, Appl
	88	20	3.4	20	3	US-08-621-841-19	Sequence 19, Appl
c	89	20	3.4	20	3	US-08-621-841-52	Sequence 52, Appl
c	90	20	3.4	20	3	US-09-851-520-28	Sequence 28, Appl
c	91	20	3.4	20	3	US-09-851-520-31	Sequence 31, Appl
c	92	20	3.4	20	3	US-09-851-520-39	Sequence 39, Appl
c	93	20	3.4	20	3	US-09-851-520-40	Sequence 40, Appl
c	94	20	3.4	20	3	US-09-851-520-41	Sequence 41, Appl
c	95	20	3.4	20	3	US-09-851-520-42	Sequence 42, Appl
c	96	20	3.4	20	3	US-09-851-520-45	Sequence 45, Appl

c 97	20	3.4	20	3	US-09-851-520-57	Sequence 57, Appl
c 98	20	3.4	20	3	US-09-851-520-58	Sequence 58, Appl
c 99	19	3.2	20	3	US-09-851-520-59	Sequence 59, Appl
c 100	19	3.2	39	2	US-08-184-009-198	Sequence 198, App
c 101	19	3.2	39	2	US-08-458-356-198	Sequence 198, App
c 102	19	3.2	39	3	US-09-079-984A-6	Sequence 6, Appli
c 103	19	3.2	39	3	US-09-079-984A-10	Sequence 10, Appl
c 104	19	3.2	39	3	US-08-460-736-198	Sequence 198, App
c 105	19	3.2	39	3	US-09-535-370-198	Sequence 198, App
c 106	19	3.2	39	3	US-09-390-729-6	Sequence 6, Appli
c 107	19	3.2	39	3	US-09-390-729-10	Sequence 10, Appl
c 108	19	3.2	39	3	US-09-663-667-198	Sequence 198, App
c 109	19	3.2	601	3	US-09-949-016-199753	Sequence 199753,
c 110	19	3.2	601	3	US-09-949-016-199754	Sequence 199754,
c 111	19	3.2	601	3	US-09-949-016-199755	Sequence 199755,
c 112	19	3.2	601	3	US-09-949-016-199756	Sequence 199756,
c 113	19	3.2	672	3	US-09-328-352-1948	Sequence 1948, Ap
c 114	19	3.2	373182	3	US-09-949-016-17371	Sequence 17371, A
c 115	19	3.2	373694	3	US-09-949-016-12062	Sequence 12062, A
c 116	18	3.0	18	4	US-09-341-700A-1646	Sequence 1646, Ap
c 117	18	3.0	18	4	US-09-341-700A-1647	Sequence 1647, Ap
c 118	18	3.0	18	4	US-09-341-700A-1652	Sequence 1652, Ap
c 119	18	3.0	22	3	US-09-917-265A-94	Sequence 94, Appl
c 120	18	3.0	409	3	US-09-189-060B-13	Sequence 13, Appl
121	18	3.0	415	3	US-09-189-060B-15	Sequence 15, Appl
122	18	3.0	495	3	US-09-328-352-1301	Sequence 1301, Ap
c 123	18	3.0	1095	3	US-09-248-796A-894	Sequence 894, App
124	18	3.0	2925	4	US-10-094-749-256	Sequence 256, App
125	18	3.0	3327	4	US-09-880-107-3432	Sequence 3432, Ap
126	18	3.0	4456	3	US-09-095-443-1	Sequence 1, Appli
127	18	3.0	5200	5	US-10-433-794-21	Sequence 21, Appl
c 128	18	3.0	6711	3	US-09-949-016-16879	Sequence 16879, A
c 129	18	3.0	6752	3	US-09-949-016-14776	Sequence 14776, A
c 130	18	3.0	421491	3	US-09-949-016-12805	Sequence 12805, A
c 131	18	3.0	421494	3	US-09-949-016-14060	Sequence 14060, A
c 132	17	2.9	17	4	US-09-341-700A-1645	Sequence 1645, Ap
c 133	17	2.9	20	3	US-09-851-520-32	Sequence 32, Appl
c 134	17	2.9	29	3	US-08-848-760B-20	Sequence 20, Appl
c 135	17	2.9	29	3	US-09-826-025-20	Sequence 20, Appl
c 136	17	2.9	51	3	US-09-917-265A-96	Sequence 96, Appl
137	17	2.9	136	2	US-08-467-963C-13	Sequence 13, Appl
138	17	2.9	136	2	US-08-838-189D-13	Sequence 13, Appl
139	17	2.9	136	3	US-08-852-344D-13	Sequence 13, Appl
140	17	2.9	136	3	US-08-344-639E-13	Sequence 13, Appl
141	17	2.9	136	3	US-08-467-969A-13	Sequence 13, Appl
142	17	2.9	136	3	US-08-467-961A-13	Sequence 13, Appl
143	17	2.9	136	3	US-08-001-554A-13	Sequence 13, Appl
144	17	2.9	498	3	US-09-543-681A-2528	Sequence 2528, Ap
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146	17	2.9	548	3	US-09-270-767-21302	Sequence 21302, A
147	17	2.9	567	3	US-09-134-000C-1464	Sequence 1464, Ap
148	17	2.9	601	3	US-09-949-016-60002	Sequence 60002, A
c 149	17	2.9	601	3	US-09-949-016-72434	Sequence 72434, A
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155	17	2.9	601	3	US-09-949-016-115711	Sequence 115711,
156	17	2.9	601	3	US-09-949-016-115712	Sequence 115712,
157	17	2.9	601	3	US-09-949-016-115804	Sequence 115804,
158	17	2.9	601	3	US-09-949-016-115805	Sequence 115805,
159	17	2.9	601	3	US-09-949-016-115897	Sequence 115897,
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161	17	2.9	601	3	US-09-949-016-115990	Sequence 115990,
162	17	2.9	601	3	US-09-949-016-115991	Sequence 115991,
163	17	2.9	601	3	US-09-949-016-116083	Sequence 116083,
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165	17	2.9	601	3	US-09-949-016-116176	Sequence 116176,
166	17	2.9	601	3	US-09-949-016-116177	Sequence 116177,
167	17	2.9	601	3	US-09-949-016-116269	Sequence 116269,
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c 172	17	2.9	624	3	US-10-120-988-351	Sequence 351, App
173	17	2.9	645	3	US-09-248-796A-13889	Sequence 13889, A
174	17	2.9	666	3	US-09-949-016-4938	Sequence 4938, Ap
175	17	2.9	666	4	US-09-880-107-3375	Sequence 3375, Ap
176	17	2.9	696	3	US-09-107-532A-2085	Sequence 2085, Ap
c 177	17	2.9	826	2	US-08-631-200-10	Sequence 10, Appl
c 178	17	2.9	826	2	US-08-829-553-10	Sequence 10, Appl
c 179	17	2.9	826	2	US-08-922-267A-10	Sequence 10, Appl
c 180	17	2.9	826	2	US-08-936-707A-10	Sequence 10, Appl
c 181	17	2.9	826	2	US-08-936-706A-10	Sequence 10, Appl
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c 183	17	2.9	826	3	US-09-406-071-10	Sequence 10, Appl
c 184	17	2.9	826	3	US-09-814-986-10	Sequence 10, Appl
c 185	17	2.9	1097	3	US-09-976-594-115	Sequence 115, App
186	17	2.9	1176	3	US-09-543-681A-4120	Sequence 4120, Ap
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188	17	2.9	1617	2	US-08-467-963C-25	Sequence 25, Appl
189	17	2.9	1617	2	US-08-838-189D-25	Sequence 25, Appl
190	17	2.9	1617	3	US-08-852-344D-25	Sequence 25, Appl
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194	17	2.9	1844	2	US-08-838-189D-1	Sequence 1, Appli
195	17	2.9	1844	3	US-08-852-344D-1	Sequence 1, Appli
196	17	2.9	1844	3	US-08-344-639E-1	Sequence 1, Appli
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198	17	2.9	1844	3	US-08-467-961A-1	Sequence 1, Appli
199	17	2.9	1844	3	US-08-001-554A-1	Sequence 1, Appli
c 200	17	2.9	3247	3	US-08-718-388-4	Sequence 4, Appli

ALIGNMENTS

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RESULT 1
US-09-917-265A-35
; Sequence 35, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(591)
US-09-917-265A-35

  Query Match            100.0%;  Score 591;  DB 3;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-296;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
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Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
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Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
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Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
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Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
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Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
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Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

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Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
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Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

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Db        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
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RESULT 2
US-09-917-265A-37/c
; Sequence 37, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-37

  Query Match            100.0%;  Score 591;  DB 3;  Length 591;
  Best Local Similarity  100.0%;  Pred. No. 4.2e-296;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
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Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
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Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
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Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1


RESULT 3
US-09-917-265A-43
; Sequence 43, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-09-917-265A-43

  Query Match            94.4%;  Score 558;  DB 3;  Length 1533;
  Best Local Similarity  100.0%;  Pred. No. 5.3e-279;
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Db       1036 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 1095

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Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
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Db       1276 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 1335

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Db       1336 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 1395

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
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Db       1396 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 1455

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
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Db       1456 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 1515

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Db       1516 AGCTATCTGAATGCTTCC 1533
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RESULT 4
US-09-917-265A-45/c
; Sequence 45, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265A-45

Query Match 94.4%; Score 558; DB 3; Length 1533;
Best Local Similarity 100.0%; Pred. No. 5.3e-279;
Matches 558; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        574 AGCTATCTGAATGCTTCC 591
                ||||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1
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RESULT 5
US-09-917-265A-38
; Sequence 38, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1599)
US-09-917-265A-38

Query Match 94.4%; Score 558; DB 3; Length 1599;
Best Local Similarity 100.0%; Pred. No. 5.3e-279;
Matches 558; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1042 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 1101

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1102 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 1161

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1162 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 1221

Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1222 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 1281

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1282 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 1341

Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1342 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 1401

Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1402 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 1461

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1462 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 1521

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1522 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 1581

Qy        574 AGCTATCTGAATGCTTCC 591
              ||||||||||||||||||
Db       1582 AGCTATCTGAATGCTTCC 1599


RESULT 6
US-09-917-265A-40/c
; Sequence 40, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-40

  Query Match             94.4%;  Score 558;  DB 3;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 5.3e-279;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        574 AGCTATCTGAATGCTTCC 591
              ||||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1


RESULT 7
US-09-917-265A-32
; Sequence 32, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
US-09-917-265A-32

  Query Match             91.4%;  Score 540;  DB 3;  Length 666;
  Best Local Similarity   99.8%;  Pred. No. 1.1e-269;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615
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Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666
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RESULT 8
US-09-917-265A-34/c
; Sequence 34, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265A-34

Query Match 91.4%; Score 540; DB 3; Length 666;
Best Local Similarity 99.8%; Pred. No. 1.1e-269;
Matches 590; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
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RESULT 9
US-09-917-265A-101
; Sequence 101, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 101
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(561)
US-09-917-265A-101

Query Match 85.8%; Score 507; DB 3; Length 561;
Best Local Similarity 99.8%; Pred. No. 1.4e-252;
Matches 557; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183

Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303

Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363

Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543

Qy        574 AGCTATCTGAATGCTTCC 591
              ||||||||||||||||||
Db        544 AGCTATCTGAATGCTTCC 561
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RESULT 10
US-09-917-265A-103/c
; Sequence 103, Application US/09917265A

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; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 103
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-103

  Query Match             85.8%;  Score 507;  DB 3;  Length 561;
  Best Local Similarity   99.8%;  Pred. No. 1.4e-252;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        574 AGCTATCTGAATGCTTCC 591
              |||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1


RESULT 11
US-09-011-143-9
; Sequence 9, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  591 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-9

  Query Match             81.2%;  Score 480;  DB 3;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-238;
  Matches  480;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
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Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480


RESULT 12
US-09-302-495-9
; Sequence 9, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 591 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-302-495-9

  Query Match             81.2%;  Score 480;  DB 3;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-238;
  Matches  480;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480


RESULT 13
US-10-079-616-9
; Sequence 9, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 591 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-079-616-9
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  Query Match             81.2%;  Score 480;  DB 3;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-238;
  Matches  480;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480


RESULT 14
US-09-011-143-8
; Sequence 8, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1441 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-8

  Query Match             81.2%;  Score 480;  DB 3;  Length 1441;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-238;
  Matches  480;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 277

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 337

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 397

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 457

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 517

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 577

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        578 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 637

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        638 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 697


RESULT 15
US-09-302-495-8
; Sequence 8, Application US/09302495
; Patent No. 6518045
;  GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
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;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/302,495
;              FILING DATE: 30-Apr-1999
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: US/09/011,143
;              FILING DATE: 04-FEB-1998
;              APPLICATION NUMBER: PCT/JP97/01824
;              FILING DATE: 29-MAY-1997
;              APPLICATION NUMBER: JP 165249/1996
;              FILING DATE: 04-JUN-1996
;         ATTORNEY/AGENT INFORMATION:
;              NAME: BROWDY, Roger L.
;              REGISTRATION NUMBER: 25,618
;              REFERENCE/DOCKET NUMBER: IMAMURA=1
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: 202-628-5197
;              TELEFAX: 202-737-3528
;    INFORMATION FOR SEQ ID NO: 8:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 1441 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;         MOLECULE TYPE: cDNA
;         SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-302-495-8

  Query Match             81.2%;  Score 480;  DB 3;  Length 1441;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-238;
  Matches  480;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 277

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 337

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 397

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 457

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 517

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 577

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        578 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 637

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        638 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 697


RESULT 16
US-10-079-616-8
; Sequence 8, Application US/10079616
; Patent No. 6566097
;    GENERAL INFORMATION:
;         APPLICANT: IMAMURA, Takayuki
;                    MAEDA, Hiroaki
;                    FUJIYASU, Takeshi
;                    IMAGAWA, Yoshitaka
;                    TOKIYOSHI, Sachio
;         TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;         NUMBER OF SEQUENCES: 26
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: BROWDY AND NEIMARK
;              STREET: 419 Seventh Street, N.W., Suite 300
;              CITY: Washington
;              STATE: D.C.
;              COUNTRY: USA
;              ZIP: 20004
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/10/079,616
;              FILING DATE: 22-Feb-2002
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: 09/011,143
;              FILING DATE: 04-FEB-1998
;              APPLICATION NUMBER: PCT/JP97/01824
;              FILING DATE: 29-MAY-1997
;              APPLICATION NUMBER: JP 165249/1996
;              FILING DATE: 04-JUN-1996
;         ATTORNEY/AGENT INFORMATION:
;              NAME: BROWDY, Roger L.
;              REGISTRATION NUMBER: 25,618
;              REFERENCE/DOCKET NUMBER: IMAMURA=1
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: 202-628-5197
;              TELEFAX: 202-737-3528
;    INFORMATION FOR SEQ ID NO: 8:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 1441 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;         MOLECULE TYPE: cDNA
;         SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-079-616-8

  Query Match             81.2%;  Score 480;  DB 3;  Length 1441;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-238;
  Matches  480;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 277

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 337

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 397

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 457

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 517

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 577
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Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        578 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 637

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        638 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 697


RESULT 17
US-09-011-143-26
; Sequence 26, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  26:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  689 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-26

  Query Match             32.0%;  Score 189;  DB 3;  Length 689;
  Best Local Similarity   100.0%;  Pred. No. 9.3e-88;
  Matches  189;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 141

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 201

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 261

Qy        181 GAGGCCTGC 189
              |||||||||
Db        262 GAGGCCTGC 270


RESULT 18
US-09-302-495-26
; Sequence 26, Application US/09302495
; Patent No. 6518045
;  GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/302,495
;            FILING DATE: 30-Apr-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;  INFORMATION FOR SEQ ID NO: 26:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 689 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-302-495-26

  Query Match             32.0%;  Score 189;  DB 3;  Length 689;
  Best Local Similarity   100.0%;  Pred. No. 9.3e-88;
  Matches  189;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 141

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 201

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 261

Qy        181 GAGGCCTGC 189
              |||||||||
Db        262 GAGGCCTGC 270


RESULT 19
US-10-079-616-26
; Sequence 26, Application US/10079616
; Patent No. 6566097
;  GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;  INFORMATION FOR SEQ ID NO: 26:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 689 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-079-616-26

  Query Match            32.0%;  Score 189;  DB 3;  Length 689;
  Best Local Similarity   100.0%;  Pred. No. 9.3e-88;
  Matches  189;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 141

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 201

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 261

Qy        181 GAGGCCTGC 189
              |||||||||
Db        262 GAGGCCTGC 270


RESULT 20
US-09-917-265A-49
; Sequence 49, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(591)
US-09-917-265A-49

  Query Match            13.7%;  Score 81;  DB 3;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        223 CTGGCTTCCAGAGAGATCTCT 243


RESULT 21
US-09-917-265A-51/c
; Sequence 51, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-51

  Query Match            13.7%;  Score 81;  DB 3;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
                ||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 22
US-09-917-265A-46
; Sequence 46, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
US-09-917-265A-46

  Query Match           13.7%;  Score 81;  DB 3;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
                ||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 23
US-09-917-265A-48/c
; Sequence 48, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-48

  Query Match           13.7%;  Score 81;  DB 3;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
                ||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 24
US-09-079-984A-2
; Sequence 2, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,984A
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  669 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 666
;      IDENTIFICATION METHOD:  Similarity
US-09-079-984A-2

  Query Match           13.7%;  Score 81;  DB 3;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
                ||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 25
US-09-079-984A-12
; Sequence 12, Application US/09079984A
```

```
; Patent No. 6231850
; GENERAL INFORMATION:
;   APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;   APPLICANT:  Yamada, Katsushige
;   TITLE OF INVENTION:  Canine interleukin 12, a production method
;   TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;   TITLE OF INVENTION:  method using it
;   NUMBER OF SEQUENCES:  16
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Miller & Christenbury Intellectual Property
;     ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;     STREET:  1600 Market Street, 39th Floor
;     CITY:  Philadelphia
;     STATE:  PA
;     COUNTRY:  USA
;     ZIP:  19103
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy Disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  WordPerfect 5.1
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/079,984A
;     FILING DATE:  15-MAY-1998
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Austin R. Miller
;     REGISTRATION NUMBER:  16,602
;     REFERENCE/DOCKET NUMBER:  1051-98
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (215) 563-1810
;     TELEFAX:  (215) 568-6946
; INFORMATION FOR SEQ ID NO:  12:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  669 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  double
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  cDNA to mRNA
;   ORIGINAL SOURCE:
;     ORGANISM:  Canis familiaris
;   FEATURE:
;     NAME/KEY:  Canine IL12
;     LOCATION:  1 to 666
;     IDENTIFICATION METHOD:  Similarity
US-09-079-984A-12

  Query Match             13.7%;  Score 81;  DB 3;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 26
US-09-390-729-2
; Sequence 2, Application US/09390729
; Patent No. 6562334
; GENERAL INFORMATION:
;   APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;   APPLICANT:  Yamada, Katsushige
;   TITLE OF INVENTION:  Canine interleukin 12, a production method
;   TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;   TITLE OF INVENTION:  method using it
;   NUMBER OF SEQUENCES:  16
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Miller & Christenbury Intellectual Property
;     ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;     STREET:  1600 Market Street, 39th Floor
;     CITY:  Philadelphia
;     STATE:  PA
;     COUNTRY:  USA
;     ZIP:  19103
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy Disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  WordPerfect 5.1
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/390,729
;     FILING DATE:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  09/079,984
;     FILING DATE:  15-MAY-1998
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Austin R. Miller
;     REGISTRATION NUMBER:  16,602
;     REFERENCE/DOCKET NUMBER:  1051-98
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (215) 563-1810
;     TELEFAX:  (215) 568-6946
; INFORMATION FOR SEQ ID NO:  2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  669 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  double
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  cDNA to mRNA
;   ORIGINAL SOURCE:
;     ORGANISM:  Canis familiaris
;   FEATURE:
;     NAME/KEY:  Canine IL12
;     LOCATION:  1 to 666
;     IDENTIFICATION METHOD:  Similarity
US-09-390-729-2

  Query Match             13.7%;  Score 81;  DB 3;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 27
US-09-390-729-12
; Sequence 12, Application US/09390729
; Patent No. 6562334
; GENERAL INFORMATION:
;   APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;   APPLICANT:  Yamada, Katsushige
;   TITLE OF INVENTION:  Canine interleukin 12, a production method
;   TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;   TITLE OF INVENTION:  method using it
;   NUMBER OF SEQUENCES:  16
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Miller & Christenbury Intellectual Property
;     ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;     STREET:  1600 Market Street, 39th Floor
;     CITY:  Philadelphia
;     STATE:  PA
;     COUNTRY:  USA
;     ZIP:  19103
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy Disk
;     COMPUTER:  IBM PC compatible
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;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  WordPerfect 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/390,729
;       FILING DATE:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  09/079,984
;       FILING DATE:  15-MAY-1998
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Austin R. Miller
;       REGISTRATION NUMBER:  16,602
;       REFERENCE/DOCKET NUMBER:  1051-98
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (215) 563-1810
;       TELEFAX:  (215) 568-6946
;   INFORMATION FOR SEQ ID NO:  12:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  669 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA to mRNA
;     ORIGINAL SOURCE:
;       ORGANISM:  Canis familiaris
;     FEATURE:
;       NAME/KEY:  Canine IL12
;       LOCATION:  1 to 666
;       IDENTIFICATION METHOD:  Similarity
US-09-390-729-12

  Query Match             13.7%;  Score 81;  DB 3;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 28
US-09-917-265A-104
; Sequence 104, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 104
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (232)..(897)
US-09-917-265A-104

  Query Match             13.7%;  Score 81;  DB 3;  Length 1455;
  Best Local Similarity   100.0%;  Pred. No. 8.6e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 528

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        529 CTGGCTTCCAGAGAGATCTCT 549


RESULT 29
US-09-917-265A-106/c
; Sequence 106, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 106
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-106

  Query Match             13.7%;  Score 81;  DB 3;  Length 1455;
  Best Local Similarity   100.0%;  Pred. No. 8.6e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 928

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        927 CTGGCTTCCAGAGAGATCTCT 907


RESULT 30
US-09-917-265A-66
; Sequence 66, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-09-917-265A-66

  Query Match             13.7%;  Score 81;  DB 3;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 8.6e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
```

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1105 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1164

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
                ||||||||||||||||||||
Db       1165 CTGGCTTCCAGAGAGATCTCT 1185


RESULT 31
US-09-917-265A-68/c
; Sequence 68, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-68

  Query Match             13.7%;  Score 81;  DB 3;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 8.6e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
                ||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 32
US-09-917-265A-61
; Sequence 61, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-09-917-265A-61

  Query Match             13.7%;  Score 81;  DB 3;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 8.6e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1230

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
                ||||||||||||||||||||
Db       1231 CTGGCTTCCAGAGAGATCTCT 1251


RESULT 33
US-09-917-265A-63/c
; Sequence 63, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-63

  Query Match             13.7%;  Score 81;  DB 3;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 8.6e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
                ||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 34
US-09-949-016-20385
; Sequence 20385, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20385
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-20385

  Query Match             11.0%;  Score 65;  DB 3;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
```

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         100 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 159

Qy         544 ATTCG 548
               |||||
Db         160 ATTCG 164


RESULT 35
US-09-949-016-87352
; Sequence 87352, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 87352
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-87352

  Query Match             11.0%;  Score 65;  DB 3;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         100 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 159

Qy         544 ATTCG 548
               |||||
Db         160 ATTCG 164


RESULT 36
US-08-186-529-3
; Sequence 3, Application US/08186529
; Patent No. 5573764
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,529
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McDaniels, Patricia A.
;      REGISTRATION NUMBER:  33,194
;      REFERENCE/DOCKET NUMBER:  GI 5225
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8401
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  660 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Lymphoblast
;      CELL LINE:  RPMI 8866
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..660
US-08-186-529-3

  Query Match             11.0%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy         544 ATTCG 548
               |||||
Db         610 ATTCG 614


RESULT 37
US-08-640-386A-3
; Sequence 3, Application US/08640386A
; Patent No. 5756085
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/640,386A
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;      REFERENCE/DOCKET NUMBER:  GI 5225A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8224
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  660 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
```

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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Lymphoblast
;      CELL LINE:  RPMI 8866
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..660
US-08-640-386A-3

  Query Match             11.0%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        544 ATTCG 548
              |||||
Db        610 ATTCG 614


RESULT 38
US-08-184-009-199
; Sequence 199, Application US/08184009
; Patent No. 5833975
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/184,009
;      FILING DATE:  19-JAN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  199:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  721 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-184-009-199

  Query Match             11.0%;  Score 65;  DB 2;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy        544 ATTCG 548
              |||||
Db        671 ATTCG 675


RESULT 39
US-08-458-356-199
; Sequence 199, Application US/08458356
; Patent No. 5942235
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,356
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  199:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  721 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-458-356-199

  Query Match             11.0%;  Score 65;  DB 2;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy        544 ATTCG 548
              |||||
Db        671 ATTCG 675


RESULT 40
US-08-460-736-199
; Sequence 199, Application US/08460736
; Patent No. 6265189
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
```

```
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,736
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  199:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  721 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-460-736-199

  Query Match             11.0%;  Score 65;  DB 3;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy        544 ATTCG 548
              |||||
Db        671 ATTCG 675


RESULT 41
US-09-535-370-199
; Sequence 199, Application US/09535370
; Patent No. 6537594
;   GENERAL INFORMATION:
;        APPLICANT: Paoletti, Enzo
;                   Tartaglia, James
;                   Cox, William I.
;        TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
;        NUMBER OF SEQUENCES: 217
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Curtis, Morris & Safford
;             STREET: 530 Fifth Avenue
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10036
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/535,370
;             FILING DATE: 24-Mar-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/460,736
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Frommer, William S.
;             REGISTRATION NUMBER: 25,506
;             REFERENCE/DOCKET NUMBER: 454310-2530
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 840-3333
;             TELEFAX: (212) 840-0712
;             TELEX: 425066CURTMS
;    INFORMATION FOR SEQ ID NO: 199:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 721 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 199:
US-09-535-370-199

  Query Match             11.0%;  Score 65;  DB 3;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy        544 ATTCG 548
              |||||
Db        671 ATTCG 675


RESULT 42
US-09-663-667-199
; Sequence 199, Application US/09663667
; Patent No. 6780407
;   GENERAL INFORMATION:
;        APPLICANT: Paoletti, Enzo
;                   Tartaglia, James
;                   Cox, William I.
;        TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
;        NUMBER OF SEQUENCES: 217
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Curtis, Morris & Safford
;             STREET: 530 Fifth Avenue
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10036
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/663,667
;             FILING DATE: 15-Sep-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/184,009
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Frommer, William S.
;             REGISTRATION NUMBER: 25,506
;             REFERENCE/DOCKET NUMBER: 454310-2530
;        TELECOMMUNICATION INFORMATION:
```

```
;             TELEPHONE: (212) 840-3333
;             TELEFAX: (212) 840-0712
;             TELEX: 425066CURTMS
;   INFORMATION FOR SEQ ID NO: 199:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 721 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 199:
US-09-663-667-199

  Query Match             11.0%;  Score 65;  DB 3;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy        544 ATTCG 548
              |||||
Db        671 ATTCG 675


RESULT 43
US-08-848-760B-21
; Sequence 21, Application US/08848760B
; Patent No. 6248721
;   GENERAL INFORMATION:
;        APPLICANT: Chang, Lung-Ji
;        TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
;        NUMBER OF SEQUENCES: 33
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
;             STREET: 2421 N.W. 41st Street, Suite A-1
;             CITY: Gainesville
;             STATE: Florida
;             COUNTRY: United States of America
;             ZIP: 32606
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/848,760B
;             FILING DATE: 25-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/838,702
;             FILING DATE: 09-APR-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: PACE, DORAN R.
;             REGISTRATION NUMBER: 38,261
;             REFERENCE/DOCKET NUMBER: CNG-100C1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (352) 375-8100
;             TELEFAX: (352) 372-5800
;   INFORMATION FOR SEQ ID NO: 21:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 762 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: other nucleic acid
;             DESCRIPTION: /desc = "DNA"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-08-848-760B-21

  Query Match             11.0%;  Score 65;  DB 3;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        544 ATTCG 548
              |||||
Db        712 ATTCG 716


RESULT 44
US-09-826-025-21
; Sequence 21, Application US/09826025
; Patent No. 6730512
;   GENERAL INFORMATION:
;        APPLICANT: Chang, Lung-Ji
;        TITLE OF INVENTION: Combination Immunogene Therapy
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Medlen & Carroll, LLP
;             STREET: 220 Montgomery Street, Suite 2200
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: United States of America
;             ZIP: 94104
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/826,025
;             FILING DATE: 04-Apr-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/838,702
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ingolia, Diane E.
;             REGISTRATION NUMBER: 40,027
;             REFERENCE/DOCKET NUMBER: CHANG-02687
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 705-8410
;             TELEFAX: (415) 397-8338
;   INFORMATION FOR SEQ ID NO: 21:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 762 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: other nucleic acid
;             DESCRIPTION: /desc = "DNA"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-826-025-21

  Query Match             11.0%;  Score 65;  DB 3;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        544 ATTCG 548
              |||||
Db        712 ATTCG 716


RESULT 45
US-09-543-679A-2890
; Sequence 2890, Application US/09543679A
; Patent No. 7034007
```

```
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
;        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                            OF AIRWAY DISORDERS ASSOCIATED WITH
;                            BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;        NUMBER OF SEQUENCES: 3111
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 Clarke Drive
;             CITY: Cranbury
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: N/A
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/543,679A
;             FILING DATE: 13-Apr-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/127,958
;             FILING DATE: 1998-08-03
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-0067191b
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2890:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 762 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2890:
US-09-543-679A-2890

  Query Match             11.0%;  Score 65;  DB 5;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        544 ATTCG 548
              |||||
Db        712 ATTCG 716


RESULT 46
US-09-949-016-2462
; Sequence 2462, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2462
;   LENGTH: 1019
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-2462

  Query Match             11.0%;  Score 65;  DB 3;  Length 1019;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        712 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 771

Qy        544 ATTCG 548
              |||||
Db        772 ATTCG 776


RESULT 47
US-08-751-767A-1
; Sequence 1, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1026 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  170..826
US-08-751-767A-1

  Query Match             11.0%;  Score 65;  DB 2;  Length 1026;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 778
```

```
Qy        544 ATTCG 548
              |||||
Db        779 ATTCG 783


RESULT 48
US-09-023-655-1041
; Sequence 1041, Application US/09023655
; Patent No. 6607879
;  GENERAL INFORMATION:
;    APPLICANT:  Cocks, Benjamin G.
;    APPLICANT:  Susan G. Stuart
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1508
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/023,655
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0001 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  1041:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1026 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GENBANK
;      CLONE:  g180623
US-09-023-655-1041

  Query Match             11.0%;  Score 65;  DB 3;  Length 1026;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 778

Qy        544 ATTCG 548
              |||||
Db        779 ATTCG 783


RESULT 49
US-09-949-016-130
; Sequence 130, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 130
;   LENGTH: 1026
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-130

  Query Match             11.0%;  Score 65;  DB 3;  Length 1026;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 778

Qy        544 ATTCG 548
              |||||
Db        779 ATTCG 783


RESULT 50
US-09-634-368-6
; Sequence 6, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 1287
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: human Fc-p35
;   OTHER INFORMATION: fusion protein coding sequence
US-09-634-368-6

  Query Match             11.0%;  Score 65;  DB 3;  Length 1287;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1177 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1236

Qy        544 ATTCG 548
              |||||
Db       1237 ATTCG 1241


RESULT 51
US-08-684-687-3
; Sequence 3, Application US/08684687
```

```
; Patent No. 5830451
;  GENERAL INFORMATION:
;    APPLICANT:  KIEFF, ELLIOTT D.
;    APPLICANT:  DEVERGNE, ODILE
;    TITLE OF INVENTION:  A NOVEL HAEMATOPOIETIC CYTOKINE AND USES
;    TITLE OF INVENTION:  THEREFOR
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  WOLF, GREENFIELD & SACKS, P.C.
;      STREET:  600 ATLANTIC AVENUE
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/684,687
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,092
;      FILING DATE:  11-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  GATES, EDWARD R.
;      REGISTRATION NUMBER:  31,616
;      REFERENCE/DOCKET NUMBER:  B0801/7051
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1316 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  HOMO SAPIENS
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  102..863
US-08-684-687-3

  Query Match             11.0%;  Score 65;  DB 2;  Length 1316;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 812

Qy        544 ATTCG 548
              |||||
Db        813 ATTCG 817


RESULT 52
US-09-851-520-3
; Sequence 3, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
;   LENGTH: 1316
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (102)...(863)
US-09-851-520-3

  Query Match             11.0%;  Score 65;  DB 3;  Length 1316;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 812

Qy        544 ATTCG 548
              |||||
Db        813 ATTCG 817


RESULT 53
US-08-265-087-3
; Sequence 3, Application US/08265087
; Patent No. 5571515
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/265,087
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1364 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  101..859
US-08-265-087-3

  Query Match             11.0%;  Score 65;  DB 2;  Length 1364;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-23;
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  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 811

Qy        544 ATTCG 548
              |||||
Db        812 ATTCG 816


RESULT 54
US-08-621-493-3
; Sequence 3, Application US/08621493
; Patent No. 5723127
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/621,493
;      FILING DATE:  25-MAR-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1364 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  101..859
US-08-621-493-3

  Query Match             11.0%;  Score 65;  DB 2;  Length 1364;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 811

Qy        544 ATTCG 548
              |||||
Db        812 ATTCG 816


RESULT 55
US-08-965-688-3
; Sequence 3, Application US/08965688
; Patent No. 5976539
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/965,688
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/621,493
;      FILING DATE:  25-MAR-1996
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1364 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  101..859
US-08-965-688-3

  Query Match             11.0%;  Score 65;  DB 2;  Length 1364;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 811

Qy        544 ATTCG 548
              |||||
Db        812 ATTCG 816


RESULT 56
US-09-260-173-3
; Sequence 3, Application US/09260173
; Patent No. 6168923
;   GENERAL INFORMATION:
;        APPLICANT: Scott, Phillip
;                   Trinchieri, Giorgio
```

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;       TITLE OF INVENTION: Compositions and Methods for Use of
;                           IL-12 as an Adjuvant
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Howson and Howson
;            STREET: Spring House Corporate Center, PO Box 457
;            CITY: Spring House
;            STATE: Pennsylvania
;            COUNTRY: USA
;            ZIP: 19477
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/260,173
;            FILING DATE: 01-Mar-1999
;            CLASSIFICATION: <Unknown>
;                            17-JUN-1994
;                            18-APR-1994
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/965,688
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: 08/265,087
;            FILING DATE: 17-JUN-1994
;            APPLICATION NUMBER: US 08/229,282
;            FILING DATE: 18-APR-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Bak, Mary E.
;            REGISTRATION NUMBER: 31,215
;            REFERENCE/DOCKET NUMBER: WST51AUSA
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 215-540-9206
;            TELEFAX: 215-540-5818
;   INFORMATION FOR SEQ ID NO: 3:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1364 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: unknown
;       MOLECULE TYPE: cDNA
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  101..859
;       SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-260-173-3

  Query Match             11.0%;  Score 65;  DB 3;  Length 1364;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 811

Qy        544 ATTCG 548
              |||||
Db        812 ATTCG 816


RESULT 57
US-09-924-703-5
; Sequence 5, Application US/09924703
; Patent No. 6555658
; GENERAL INFORMATION:
;  APPLICANT: TRINCHIERI, GIORGIO
;  APPLICANT:  PERUSSIA, BICE
;  APPLICANT:  CLARK, STEVEN C.
;  APPLICANT:  WONG, GORDON G.
;  APPLICANT:  HEWICK, RODNEY
;  APPLICANT:  KOBAYASHI, MICHIKO
;  TITLE OF INVENTION: ANTIBODIES TO NATURAL KILLER STIMULATORY FACTOR
;  FILE REFERENCE: 01142.0142.0100
;  CURRENT APPLICATION NUMBER: US/09/924,703
;  CURRENT FILING DATE:  2001-08-09
;  PRIOR APPLICATION NUMBER: 09/325,958
;  PRIOR FILING DATE: 1999-06-04
;  PRIOR APPLICATION NUMBER: 08/858,000
;  PRIOR FILING DATE: 1997-05-16
;  PRIOR APPLICATION NUMBER: 08/403,013
;  PRIOR FILING DATE: 1995-03-13
;  PRIOR APPLICATION NUMBER: 07/584,941
;  PRIOR FILING DATE: 1990-09-18
;  PRIOR APPLICATION NUMBER: 07/307,817
;  PRIOR FILING DATE: 1989-02-07
;  PRIOR APPLICATION NUMBER: 07/269,945
;  PRIOR FILING DATE: 1988-11-10
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 1395
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
;   OTHER INFORMATION: sequence of the 30 kD subunit of NKSF
;   NAME/KEY: CDS
;   LOCATION: (114)..(872)
US-09-924-703-5

  Query Match             11.0%;  Score 65;  DB 3;  Length 1395;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        765 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 824

Qy        544 ATTCG 548
              |||||
Db        825 ATTCG 829


RESULT 58
US-08-751-767A-11
; Sequence 11, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
```

```
;       TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:  1560 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..1557
US-08-751-767A-11

  Query Match             11.0%;  Score 65;  DB 2;  Length 1560;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1450 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1509

Qy        544 ATTCG 548
              |||||
Db       1510 ATTCG 1514


RESULT 59
US-08-751-767A-9
; Sequence 9, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  NIXON & VANDERHYE P.C.
;       STREET:  1100 NORTH GLEBE ROAD
;       CITY:  ARLINGTON
;       STATE:  VA
;       COUNTRY:  USA
;       ZIP:  22201
;    COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/751,767A
;       FILING DATE:  08-NOV-1996
;       CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;       NAME:  SADOFF, B.J.
;       REGISTRATION NUMBER:  36,663
;       REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  7038164091
;       TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:  1623 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..1620
US-08-751-767A-9

  Query Match             11.0%;  Score 65;  DB 2;  Length 1623;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1513 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1572

Qy        544 ATTCG 548
              |||||
Db       1573 ATTCG 1577


RESULT 60
US-09-310-842-2
; Sequence 2, Application US/09310842A
; Patent No. 6451593
; GENERAL INFORMATION:
;  APPLICANT: Wittig, Prof. Burghardt
;  APPLICANT: Junghans, Claas
;  TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
;  TITLE OF INVENTION: Therapy
;  FILE REFERENCE: XI 597/99
;  CURRENT APPLICATION NUMBER: US/09/310,842A
;  CURRENT FILING DATE: 1999-05-12
;  EARLIER APPLICATION NUMBER: DE 196 48 625.4
;  EARLIER FILING DATE: 1996-11-13
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 1645
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (1)..(1645)
;   OTHER INFORMATION: Interleukin-12 (IL-12, p35-subunit); Oligo DNA
;   OTHER INFORMATION: Dumbbell
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1)..(2)
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at
;   OTHER INFORMATION: position 1 to 2  can be modified with amino or caroxy
;   OTHER INFORMATION: features
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1644)..(1645)
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1644
;   OTHER INFORMATION: to 1645  can be modified with amino or caroxy features
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Strandness: both;  nucleic
;   OTHER INFORMATION: acid (linear),  hypothetical: No. 6451593 anti-sense: No
US-09-310-842-2

  Query Match             11.0%;  Score 65;  DB 3;  Length 1645;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1284 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1343

Qy        544 ATTCG 548
              |||||
Db       1344 ATTCG 1348


RESULT 61
US-09-543-679A-2893
; Sequence 2893, Application US/09543679A
; Patent No. 7034007
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
;        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
```

```
;                          OF AIRWAY DISORDERS ASSOCIATED WITH
;                          BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;       NUMBER OF SEQUENCES: 3111
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;            STREET: 7 Clarke Drive
;            CITY: Cranbury
;            STATE: NJ
;            COUNTRY: USA
;            ZIP: 08512
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD-R
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: N/A
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/543,679A
;            FILING DATE: 13-Apr-2000
;            CLASSIFICATION: UNKNOWN
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/127,958
;            FILING DATE: 1998-08-03
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Amzel, Viviana
;            REGISTRATION NUMBER: 30,930
;            REFERENCE/DOCKET NUMBER: EPI-0067191b
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 609-409-3035
;            TELEFAX: 413-254-9245
;            TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2893:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 4521 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2893:
US-09-543-679A-2893

  Query Match            11.0%;  Score 65;  DB 5;  Length 4521;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        544 ATTCG 548
              |||||
Db        712 ATTCG 716


RESULT 62
US-08-751-767A-7
; Sequence 7, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6139 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3222..4841
US-08-751-767A-7

  Query Match            11.0%;  Score 65;  DB 2;  Length 6139;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4734 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 4793

Qy        544 ATTCG 548
              |||||
Db       4794 ATTCG 4798


RESULT 63
US-09-949-016-11872
; Sequence 11872, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11872
;   LENGTH: 10764
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-11872

  Query Match            11.0%;  Score 65;  DB 3;  Length 10764;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8457 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 8516

Qy        544 ATTCG 548
              |||||
Db       8517 ATTCG 8521
```

```
RESULT 64
US-09-949-016-14204
; Sequence 14204, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14204
;   LENGTH: 10765
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-14204

  Query Match             11.0%;  Score 65;  DB 3;  Length 10765;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8457 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 8516

Qy        544 ATTCG 548
              |||||
Db       8517 ATTCG 8521


RESULT 65
US-09-949-016-20381
; Sequence 20381, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20381
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-20381

  Query Match              9.5%;  Score 56;  DB 3;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-19;
  Matches   56;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 199


RESULT 66
US-09-949-016-87348
; Sequence 87348, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 87348
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-87348

  Query Match              9.5%;  Score 56;  DB 3;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-19;
  Matches   56;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        133 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 199


RESULT 67
US-09-011-143-24
; Sequence 24, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
```

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  79 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-24

  Query Match             7.3%;  Score 43;  DB 3;  Length 79;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-12;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        147 TGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGC 189
              |||||||||||||||||||||||||||||||||||||||||||
Db          1 TGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGC 43


RESULT 68
US-09-302-495-24
; Sequence 24, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 24:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 79 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-302-495-24

  Query Match             7.3%;  Score 43;  DB 3;  Length 79;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-12;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        147 TGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGC 189
              |||||||||||||||||||||||||||||||||||||||||||
Db          1 TGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGC 43


RESULT 69
US-10-079-616-24
; Sequence 24, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 24:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 79 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-079-616-24

  Query Match             7.3%;  Score 43;  DB 3;  Length 79;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-12;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        147 TGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGC 189
              |||||||||||||||||||||||||||||||||||||||||||
Db          1 TGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGC 43


RESULT 70
US-09-917-265A-91
; Sequence 91, Application US/09917265A
```

```
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91
;   LENGTH: 39
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-917-265A-91

  Query Match             4.6%;  Score 27;  DB 3;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 0.00089;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAA 60
              |||||||||||||||||||||||||||
Db         13 ATGTTCCAGTGCCTCAACCACTCCCAA 39


RESULT 71
US-09-634-368-1
; Sequence 1, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 582
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine p35
;   OTHER INFORMATION: coding sequence for mature protein
US-09-634-368-1

  Query Match             4.6%;  Score 27;  DB 3;  Length 582;
  Best Local Similarity   100.0%;  Pred. No. 0.00084;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        313 ATCTATGAGGACTTGAAGATGTACCAG 339
              |||||||||||||||||||||||||||
Db        301 ATCTATGAGGACTTGAAGATGTACCAG 327


RESULT 72
US-08-385-335A-10
; Sequence 10, Application US/08385335A
; Patent No. 5891680
;  GENERAL INFORMATION:
;    APPLICANT:  Lieschke, Graham J.
;    APPLICANT:  Mulligan, Richard C.
;    TITLE OF INVENTION:  Bioactive Fusion Proteins
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/385,335A
;      FILING DATE:  08-FEB-1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  WHI95-01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-861-6240
;      TELEFAX:  617-861-9540
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  713 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-08-385-335A-10

  Query Match             4.6%;  Score 27;  DB 2;  Length 713;
  Best Local Similarity   100.0%;  Pred. No. 0.00084;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        313 ATCTATGAGGACTTGAAGATGTACCAG 339
              |||||||||||||||||||||||||||
Db        413 ATCTATGAGGACTTGAAGATGTACCAG 439


RESULT 73
US-09-634-368-5
; Sequence 5, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 1278
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: Fc-p35 fusion protein coding sequence
US-09-634-368-5

  Query Match             4.6%;  Score 27;  DB 3;  Length 1278;
  Best Local Similarity   100.0%;  Pred. No. 0.00083;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        313 ATCTATGAGGACTTGAAGATGTACCAG 339
              |||||||||||||||||||||||||||
Db        997 ATCTATGAGGACTTGAAGATGTACCAG 1023
```

```
RESULT 74
US-09-634-368-12
; Sequence 12, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 1569
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p35-linker-p40 fusion protein coding sequence
US-09-634-368-12

  Query Match             4.6%;  Score 27;  DB 3;  Length 1569;
  Best Local Similarity   100.0%;  Pred. No. 0.00083;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        313 ATCTATGAGGACTTGAAGATGTACCAG 339
              |||||||||||||||||||||||||||
Db        301 ATCTATGAGGACTTGAAGATGTACCAG 327


RESULT 75
US-09-634-368-11
; Sequence 11, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 2013
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p35-linker-p40-IL-2 fusion protein coding sequence
US-09-634-368-11

  Query Match             4.6%;  Score 27;  DB 3;  Length 2013;
  Best Local Similarity   100.0%;  Pred. No. 0.00082;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        313 ATCTATGAGGACTTGAAGATGTACCAG 339
              |||||||||||||||||||||||||||
Db        301 ATCTATGAGGACTTGAAGATGTACCAG 327


RESULT 76
US-09-634-368-13
; Sequence 13, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 13
;   LENGTH: 2709
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: Fc-p35-linker-p40-IL-2 fusion protein coding
;   OTHER INFORMATION: sequence
US-09-634-368-13

  Query Match             4.6%;  Score 27;  DB 3;  Length 2709;
  Best Local Similarity   100.0%;  Pred. No. 0.00082;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        313 ATCTATGAGGACTTGAAGATGTACCAG 339
              |||||||||||||||||||||||||||
Db        997 ATCTATGAGGACTTGAAGATGTACCAG 1023


RESULT 77
US-08-659-206A-4
; Sequence 4, Application US/08659206A
; Patent No. 5922685
;  GENERAL INFORMATION:
;    APPLICANT:  Rakhmilevich, Alexander
;    TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/659,206A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  110229.91144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6295 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "plasmid pWRG3196"
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(955..1260, 1334..1675)
;      OTHER INFORMATION:  /product= "p35 gene product"
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2377..3384
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;      OTHER INFORMATION:  /product= "p40 gene product"
US-08-659-206A-4

  Query Match             4.6%;  Score 27;  DB 2;  Length 6295;
  Best Local Similarity   100.0%;  Pred. No. 0.00081;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        313 ATCTATGAGGACTTGAAGATGTACCAG 339
              |||||||||||||||||||||||||||
Db       1394 ATCTATGAGGACTTGAAGATGTACCAG 1420


RESULT 78
US-08-659-206A-1
; Sequence 1, Application US/08659206A
; Patent No. 5922685
;  GENERAL INFORMATION:
;    APPLICANT:  Rakhmilevich, Alexander
;    TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/659,206A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  110229.91144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7287 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Plasmid DNA"
;    IMMEDIATE SOURCE:
;      CLONE:  pWRG3169
;    FEATURE:
;      NAME/KEY:  promoter
;      LOCATION:  1..628
;    FEATURE:
;      NAME/KEY:  iDNA
;      LOCATION:  629..810
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(953..1258, 1332..1673)
;      OTHER INFORMATION:  /product= "p35 gene product"
;    FEATURE:
;      NAME/KEY:  polyA_site
;      LOCATION:  1797..2024
;    FEATURE:
;      NAME/KEY:  promoter
;      LOCATION:  2110..2737
;    FEATURE:
;      NAME/KEY:  iDNA
;      LOCATION:  2738..2919
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2983..3990
;      OTHER INFORMATION:  /product= "p40 gene product"
;    FEATURE:
;      NAME/KEY:  polyA_site
;      LOCATION:  4075..4306
US-08-659-206A-1

  Query Match             4.6%;  Score 27;  DB 2;  Length 7287;
  Best Local Similarity   100.0%;  Pred. No. 0.00081;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        313 ATCTATGAGGACTTGAAGATGTACCAG 339
              |||||||||||||||||||||||||||
Db       1392 ATCTATGAGGACTTGAAGATGTACCAG 1418


RESULT 79
US-09-917-265A-90/c
; Sequence 90, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90
;   LENGTH: 27
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-917-265A-90

  Query Match             4.1%;  Score 24;  DB 3;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.032;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        568 ATGATGAGCTATCTGAATGCTTCC 591
              ||||||||||||||||||||||||
Db         27 ATGATGAGCTATCTGAATGCTTCC 4


RESULT 80
US-09-011-143-25/c
; Sequence 25, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
```

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;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/011,143
;       FILING DATE:  04-FEB-1998
;       CLASSIFICATION:  536
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/JP97/01824
;       FILING DATE:  29-MAY-1997
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 165249/1996
;       FILING DATE:  04-JUN-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  BROWDY, Roger L.
;       REGISTRATION NUMBER:  25,618
;       REFERENCE/DOCKET NUMBER:  IMAMURA=1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-628-5197
;       TELEFAX:  202-737-3528
;   INFORMATION FOR SEQ ID NO:  25:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  36 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-09-011-143-25

  Query Match             4.1%;  Score 24;  DB 3;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 0.032;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        346 TTCAAGGCCATGAATGCAAAGCTG 369
              ||||||||||||||||||||||||
Db         36 TTCAAGGCCATGAATGCAAAGCTG 13


RESULT 81
US-09-302-495-25/c
; Sequence 25, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/302,495
;            FILING DATE: 30-Apr-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 25:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 36 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-302-495-25

  Query Match             4.1%;  Score 24;  DB 3;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 0.032;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        346 TTCAAGGCCATGAATGCAAAGCTG 369
              ||||||||||||||||||||||||
Db         36 TTCAAGGCCATGAATGCAAAGCTG 13


RESULT 82
US-10-079-616-25/c
; Sequence 25, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 25:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 36 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
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```
;       SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-10-079-616-25

  Query Match             4.1%;  Score 24;  DB 3;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 0.032;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        346 TTCAAGGCCATGAATGCAAAGCTG 369
              ||||||||||||||||||||||||
Db         36 TTCAAGGCCATGAATGCAAAGCTG 13


RESULT 83
US-09-917-265A-92/c
; Sequence 92, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92
;   LENGTH: 41
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-917-265A-92

  Query Match             4.1%;  Score 24;  DB 3;  Length 41;
  Best Local Similarity   100.0%;  Pred. No. 0.032;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        568 ATGATGAGCTATCTGAATGCTTCC 591
              ||||||||||||||||||||||||
Db         41 ATGATGAGCTATCTGAATGCTTCC 18


RESULT 84
US-08-859-998-383
; Sequence 383, Application US/08859998
; Patent No. 5994076
;  GENERAL INFORMATION:
;    APPLICANT:  Chenchik, Alex
;    APPLICANT:  Jokhadze, George
;    APPLICANT:  Bibilashvilli, Robert
;    TITLE OF INVENTION:  METHOD OF ASSAYING DIFFERENTIAL
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1375
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  2200 Sand Hill Road, Suite 100
;      CITY:  Menlo Park
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,998
;      FILING DATE:  21-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Field, Bret E.
;      REGISTRATION NUMBER:  37,620
;      REFERENCE/DOCKET NUMBER:  09096/002001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-322-5070
;      TELEFAX:  415-854-0875
;  INFORMATION FOR SEQ ID NO:  383:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      OTHER INFORMATION:  oligonucleotide primer
US-08-859-998-383

  Query Match             3.6%;  Score 21;  DB 2;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        331 ATGTACCAGGTGGAGTTCAAG 351
              |||||||||||||||||||||
Db          1 ATGTACCAGGTGGAGTTCAAG 21


RESULT 85
US-09-225-928-383
; Sequence 383, Application US/09225928
; Patent No. 6352829
;   GENERAL INFORMATION:
;        APPLICANT: Chenchik, Alex
;                   Jokhadze, George
;                   Bibilashvilli, Robert
;        TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
;                            EXPRESSION
;        NUMBER OF SEQUENCES: 1375
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Fish & Richardson, P.C.
;             STREET: 2200 Sand Hill Road, Suite 100
;             CITY: Menlo Park
;             STATE: CA
;             COUNTRY: US
;             ZIP: 94025
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: Windows95
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/225,928
;             FILING DATE: 05-Jan-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/859,998
;             FILING DATE: 21-MAY-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Field, Bret E.
;             REGISTRATION NUMBER: 37,620
;             REFERENCE/DOCKET NUMBER: 09096/002001
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415-322-5070
;             TELEFAX: 415-854-0875
;   INFORMATION FOR SEQ ID NO: 383:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 32 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
```

```
;        FEATURE:
;             OTHER INFORMATION:  oligonucleotide primer
;        SEQUENCE DESCRIPTION: SEQ ID NO: 383:
US-09-225-928-383

  Query Match             3.6%;  Score 21;  DB 3;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        331 ATGTACCAGGTGGAGTTCAAG 351
              |||||||||||||||||||||
Db          1 ATGTACCAGGTGGAGTTCAAG 21


RESULT 86
US-09-225-201B-383
; Sequence 383, Application US/09225201B
; Patent No. 6489455
;  GENERAL INFORMATION:
;       APPLICANT: Chenchik, Alex
;                  Jokhadze, George
;                  Bibilashvilli, Robert
;       TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
;                           EXPRESSION
;       NUMBER OF SEQUENCES: 1375
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Fish & Richardson, P.C.
;            STREET: 2200 Sand Hill Road, Suite 100
;            CITY: Menlo Park
;            STATE: CA
;            COUNTRY: US
;            ZIP: 94025
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: Windows95
;            SOFTWARE: FastSEQ for Windows Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/225,201B
;            FILING DATE: 05-Jan-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/859,998
;            FILING DATE: 21-MAY-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Field, Bret E.
;            REGISTRATION NUMBER: 37,620
;            REFERENCE/DOCKET NUMBER: 09096/002001
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 415-322-5070
;            TELEFAX: 415-854-0875
;  INFORMATION FOR SEQ ID NO: 383:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 32 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       FEATURE:
;            OTHER INFORMATION:  oligonucleotide primer
;       SEQUENCE DESCRIPTION: SEQ ID NO: 383:
US-09-225-201B-383

  Query Match             3.6%;  Score 21;  DB 3;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        331 ATGTACCAGGTGGAGTTCAAG 351
              |||||||||||||||||||||
Db          1 ATGTACCAGGTGGAGTTCAAG 21


RESULT 87
US-08-012-543-13
; Sequence 13, Application US/08012543
; Patent No. 5596072
;  GENERAL INFORMATION:
;    APPLICANT:  Culpepper, Janice
;    APPLICANT:  McKenzie, Andrew
;    APPLICANT:  Dang, Warren
;    APPLICANT:  de Waal Malefyt, Rene
;    APPLICANT:  Heath, Andrew
;    APPLICANT:  Aversa, Gregorio
;    APPLICANT:  Briere, Francine
;    APPLICANT:  Banchereau, Jacques
;    APPLICANT:  de Vries, Jan
;    APPLICANT:  Zurawski, Gerard
;    TITLE OF INVENTION:  Human Interleukin-13
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DNAX Research Institute
;      STREET:  901 California Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/012,543
;      FILING DATE:  01-FEB-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/933,416
;      FILING DATE:  21-AUG-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  DX0302K1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-852-9196
;      TELEFAX:  415-496-1200
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-012-543-13

  Query Match             3.4%;  Score 20;  DB 2;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.8;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        253 AATGGGAGTTGCCTGGCCTC 272
              ||||||||||||||||||||
Db          1 AATGGGAGTTGCCTGGCCTC 20


RESULT 88
US-08-621-841-19
; Sequence 19, Application US/08621841
; Patent No. 6096869
;  GENERAL INFORMATION:
;    APPLICANT:  Stanley, Margaret A.
;    APPLICANT:  Scarpini, Cinzia G.
;    TITLE OF INVENTION:  TREATMENT OF PAPILLOMAVIRUS-ASSOCIATED
;    TITLE OF INVENTION:  LESIONS
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
```

```
;       CITY:  San Francisco
;       STATE:  California
;       COUNTRY:  United States
;       ZIP:  94111
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/621,841
;       FILING DATE:  22-MAR-1996
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 9505784.0
;       FILING DATE:  22-MAR-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Dreger, Walter H.
;       REGISTRATION NUMBER:  24,190
;       REFERENCE/DOCKET NUMBER:  A-63316
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 781-1989
;       TELEFAX:  (415) 398-3249
;   INFORMATION FOR SEQ ID NO:  19:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  20 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
US-08-621-841-19

  Query Match             3.4%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.8;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        249 AACTAATGGGAGTTGCCTGG 268
              ||||||||||||||||||||
Db          1 AACTAATGGGAGTTGCCTGG 20


RESULT 89
US-08-621-841-52/c
; Sequence 52, Application US/08621841
; Patent No. 6096869
;  GENERAL INFORMATION:
;     APPLICANT:  Stanley, Margaret A.
;     APPLICANT:  Scarpini, Cinzia G.
;     TITLE OF INVENTION:  TREATMENT OF PAPILLOMAVIRUS-ASSOCIATED
;     TITLE OF INVENTION:  LESIONS
;     NUMBER OF SEQUENCES:  58
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;       STREET:  Four Embarcadero Center, Suite 3400
;       CITY:  San Francisco
;       STATE:  California
;       COUNTRY:  United States
;       ZIP:  94111
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/621,841
;       FILING DATE:  22-MAR-1996
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 9505784.0
;       FILING DATE:  22-MAR-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Dreger, Walter H.
;       REGISTRATION NUMBER:  24,190
;       REFERENCE/DOCKET NUMBER:  A-63316
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 781-1989
;       TELEFAX:  (415) 398-3249
;   INFORMATION FOR SEQ ID NO:  52:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  20 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
US-08-621-841-52

  Query Match             3.4%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.8;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        513 CAAGCTCTGCATACTTCTTC 532
              ||||||||||||||||||||
Db         20 CAAGCTCTGCATACTTCTTC 1


RESULT 90
US-09-851-520-28/c
; Sequence 28, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 28
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-520-28

  Query Match             3.4%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.8;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         93 GAAGGCCAGACAAACTCTAG 112
              ||||||||||||||||||||
Db         20 GAAGGCCAGACAAACTCTAG 1


RESULT 91
US-09-851-520-31/c
; Sequence 31, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 31
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-520-31
```

```
  Query Match             3.4%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.8;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        166 AAAACCAGCACAGTGGAGGC 185
              ||||||||||||||||||||
Db         20 AAAACCAGCACAGTGGAGGC 1


RESULT 92
US-09-851-520-39/c
; Sequence 39, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 39
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-520-39

  Query Match             3.4%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.8;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        253 AATGGGAGTTGCCTGGCCTC 272
              ||||||||||||||||||||
Db         20 AATGGGAGTTGCCTGGCCTC 1


RESULT 93
US-09-851-520-40/c
; Sequence 40, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 40
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-520-40

  Query Match             3.4%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.8;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        260 GTTGCCTGGCCTCCAGAAAG 279
              ||||||||||||||||||||
Db         20 GTTGCCTGGCCTCCAGAAAG 1


RESULT 94
US-09-851-520-41/c
; Sequence 41, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 41
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-520-41

  Query Match             3.4%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.8;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        266 TGGCCTCCAGAAAGACCTCT 285
              ||||||||||||||||||||
Db         20 TGGCCTCCAGAAAGACCTCT 1


RESULT 95
US-09-851-520-42/c
; Sequence 42, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 42
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-520-42

  Query Match             3.4%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.8;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        271 TCCAGAAAGACCTCTTTTAT 290
              ||||||||||||||||||||
Db         20 TCCAGAAAGACCTCTTTTAT 1


RESULT 96
US-09-851-520-45/c
; Sequence 45, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 45
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-520-45

  Query Match             3.4%;  Score 20;  DB 3;  Length 20;
```

```
  Best Local Similarity   100.0%;  Pred. No. 3.8;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        329 AGATGTACCAGGTGGAGTTC 348
              ||||||||||||||||||||
Db         20 AGATGTACCAGGTGGAGTTC 1


RESULT 97
US-09-851-520-57/c
; Sequence 57, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 57
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-520-57

  Query Match             3.4%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.8;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        488 AACCGGATTTTTATAAAACT 507
              ||||||||||||||||||||
Db         20 AACCGGATTTTTATAAAACT 1


RESULT 98
US-09-851-520-58/c
; Sequence 58, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 58
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-520-58

  Query Match             3.4%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.8;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        521 GCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||
Db         20 GCATACTTCTTCATGCTTTC 1


RESULT 99
US-09-851-520-59/c
; Sequence 59, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 59
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-520-59

  Query Match             3.2%;  Score 19;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        530 TTCATGCTTTCAGAATTCG 548
              ||||||||||||||||||||
Db         20 TTCATGCTTTCAGAATTCG 2


RESULT 100
US-08-184-009-198/c
; Sequence 198, Application US/08184009
; Patent No. 5833975
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/184,009
;      FILING DATE:  19-JAN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  198:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  39 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-184-009-198

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Db         34 GAGCTATCTGAATGCTTCC 16
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2006, 23:31:05 ; Search time 993.447 Seconds
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Gapop 60.0 , Gapext 60.0

Searched: 18892170 seqs, 6143817638 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
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; ORGANISM: Felis catus
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; NAME/KEY: CDS
; LOCATION: (1)..(591)
; OTHER INFORMATION:
US-09-917-265-35

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Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591


RESULT 2
US-09-917-265-37/c
; Sequence 37, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-37

  Query Match            100.0%;  Score 591;  DB 3;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-307;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1


RESULT 3
US-10-821-670-35
; Sequence 35, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(591)
US-10-821-670-35

  Query Match            100.0%;  Score 591;  DB 9;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-307;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
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Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591


RESULT 4
US-10-821-670-37/c
; Sequence 37, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-37

  Query Match            100.0%;  Score 591;  DB 9;  Length 591;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-307;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1


RESULT 5
US-09-917-265-43
; Sequence 43, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
;   OTHER INFORMATION:
US-09-917-265-43

  Query Match            94.4%;  Score 558;  DB 3;  Length 1533;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-289;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        976 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 1035

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1036 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 1095

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1096 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 1155

Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1156 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 1215

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1216 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 1275

Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
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Db       1276 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 1335

Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1336 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 1395

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1396 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 1455

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1456 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 1515

Qy        574 AGCTATCTGAATGCTTCC 591
                 ||||||||||||||||||
Db       1516 AGCTATCTGAATGCTTCC 1533


RESULT 6
US-09-917-265-45/c
; Sequence 45, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-45

  Query Match             94.4%;  Score 558;  DB 3;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-289;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        574 AGCTATCTGAATGCTTCC 591
                 ||||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1


RESULT 7
US-10-821-670-43
; Sequence 43, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-10-821-670-43

  Query Match             94.4%;  Score 558;  DB 9;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-289;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        976 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 1035

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1036 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 1095

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
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Db       1096 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 1155

Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1156 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 1215

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1216 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 1275

Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1276 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 1335

Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
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Db       1336 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 1395

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1396 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 1455
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Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1456 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 1515

Qy        574 AGCTATCTGAATGCTTCC 591
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Db       1516 AGCTATCTGAATGCTTCC 1533
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RESULT 8
US-10-821-670-45/c
; Sequence 45, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
US-10-821-670-45

Query Match 94.4%; Score 558; DB 9; Length 1533;
Best Local Similarity 100.0%; Pred. No. 1.7e-289;
Matches 558; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        574 AGCTATCTGAATGCTTCC 591
              ||||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1
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RESULT 9
US-09-917-265-38
; Sequence 38, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1599)
; OTHER INFORMATION:
US-09-917-265-38

Query Match 94.4%; Score 558; DB 3; Length 1599;
Best Local Similarity 100.0%; Pred. No. 1.7e-289;
Matches 558; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1042 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 1101

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1102 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 1161

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1162 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 1221

Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1222 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 1281

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1282 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 1341

Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1342 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 1401

Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1402 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 1461

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
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Db       1462 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 1521

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1522 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 1581

Qy        574 AGCTATCTGAATGCTTCC 591
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Db       1582 AGCTATCTGAATGCTTCC 1599
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RESULT 10
US-09-917-265-40/c
; Sequence 40, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-40

  Query Match             94.4%;  Score 558;  DB 3;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-289;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        574 AGCTATCTGAATGCTTCC 591
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Db         18 AGCTATCTGAATGCTTCC 1


RESULT 11
US-10-821-670-38
; Sequence 38, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-10-821-670-38

  Query Match             94.4%;  Score 558;  DB 9;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-289;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1042 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 1101

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1102 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 1161

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1162 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 1221

Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1222 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 1281

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1282 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 1341

Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1342 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 1401

Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1402 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 1461

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1462 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 1521

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1522 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 1581

Qy        574 AGCTATCTGAATGCTTCC 591
              ||||||||||||||||||
Db       1582 AGCTATCTGAATGCTTCC 1599


RESULT 12
US-10-821-670-40/c
; Sequence 40, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
```

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;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-40

  Query Match             94.4%;  Score 558;  DB 9;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-289;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy          94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy         154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy         214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy         274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy         334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy         394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy         454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         138 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy         514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy         574 AGCTATCTGAATGCTTCC 591
               ||||||||||||||||||
Db          18 AGCTATCTGAATGCTTCC 1


RESULT 13
US-09-917-265-32
; Sequence 32, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
;   OTHER INFORMATION:
US-09-917-265-32

  Query Match             91.4%;  Score 540;  DB 3;  Length 666;
  Best Local Similarity   99.8%;  Pred. No. 8.2e-280;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy          61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy         121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy         181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy         241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy         301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy         361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy         421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy         481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy         541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666


RESULT 14
US-09-917-265-34/c
; Sequence 34, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
;   LENGTH: 666
;   TYPE: DNA
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;   ORGANISM: Felis catus
US-09-917-265-34

  Query Match             91.4%;  Score 540;  DB 3;  Length 666;
  Best Local Similarity   99.8%;  Pred. No. 8.2e-280;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1


RESULT 15
US-10-821-670-32
; Sequence 32, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
US-10-821-670-32

  Query Match             91.4%;  Score 540;  DB 9;  Length 666;
  Best Local Similarity   99.8%;  Pred. No. 8.2e-280;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666


RESULT 16
US-10-821-670-34/c
; Sequence 34, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-34

  Query Match             91.4%;  Score 540;  DB 9;  Length 666;
  Best Local Similarity   99.8%;  Pred. No. 8.2e-280;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1


RESULT 17
US-09-917-265-101
; Sequence 101, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(561)
;   OTHER INFORMATION:
US-09-917-265-101

  Query Match            85.8%;  Score 507;  DB 3;  Length 561;
  Best Local Similarity   99.8%;  Pred. No. 5e-262;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183

Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303

Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363

Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543

Qy        574 AGCTATCTGAATGCTTCC 591
              |||||||||||||||||
Db        544 AGCTATCTGAATGCTTCC 561


RESULT 18
US-09-917-265-103/c
; Sequence 103, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 103
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-103

  Query Match            85.8%;  Score 507;  DB 3;  Length 561;
  Best Local Similarity   99.8%;  Pred. No. 5e-262;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379
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Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        574 AGCTATCTGAATGCTTCC 591
              ||||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1
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RESULT 19
US-10-821-670-101
; Sequence 101, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 101
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(561)
US-10-821-670-101

Query Match 85.8%; Score 507; DB 9; Length 561;
Best Local Similarity 99.8%; Pred. No. 5e-262;
Matches 557; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183

Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303

Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363

Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543

Qy        574 AGCTATCTGAATGCTTCC 591
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Db        544 AGCTATCTGAATGCTTCC 561
```

RESULT 20
US-10-821-670-103/c
; Sequence 103, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 103
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Felis catus
US-10-821-670-103

Query Match 85.8%; Score 507; DB 9; Length 561;
Best Local Similarity 99.8%; Pred. No. 5e-262;
Matches 557; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy         34 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 93
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy         94 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        154 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        214 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        274 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        334 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 393
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        394 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        454 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 513
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        514 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        574 AGCTATCTGAATGCTTCC 591
              ||||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1


RESULT 21
US-10-079-616-9
; Sequence 9, Application US/10079616
; Publication No. US20020107366A1
;  GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 591 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-079-616-9

  Query Match             81.2%;  Score 480;  DB 6;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-247;
  Matches  480;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480


RESULT 22
US-10-079-616-8
; Sequence 8, Application US/10079616
; Publication No. US20020107366A1
;  GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
```

```
;              REGISTRATION NUMBER: 25,618
;              REFERENCE/DOCKET NUMBER: IMAMURA=1
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: 202-628-5197
;              TELEFAX: 202-737-3528
;    INFORMATION FOR SEQ ID NO: 8:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 1441 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;         MOLECULE TYPE: cDNA
;         SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-079-616-8

  Query Match             81.2%;  Score 480;  DB 6;  Length 1441;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-247;
  Matches  480;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 277

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 337

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 397

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 457

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 517

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 577

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        578 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 637

Qy        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        638 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 697


RESULT 23
US-10-041-672C-2
; Sequence 2, Application US/10041672C
; Publication No. US20030157059A1
; GENERAL INFORMATION:
;  APPLICANT: Mologen Forschungs-, Entwicklungs- und Vetriebs GmbH
;  APPLICANT:  Universitat Zurich
;  TITLE OF INVENTION: FELINE INTERLEUKIN-12 AS IMMUNOSTIMULANT
;  FILE REFERENCE: NHL-NP-36
;  CURRENT APPLICATION NUMBER: US/10/041,672C
;  CURRENT FILING DATE:  2002-01-08
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 669
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: feline IL-12 p35
US-10-041-672C-2

  Query Match             38.6%;  Score 228;  DB 7;  Length 669;
  Best Local Similarity   99.1%;  Pred. No. 1.2e-111;
  Matches  428;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATTGATGAGCTG 432
              ||||||||||||
Db        496 ATTGATGAGCTG 507


RESULT 24
US-10-079-616-26
; Sequence 26, Application US/10079616
; Publication No. US20020107366A1
;  GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
```

```
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 26:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 689 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-079-616-26

  Query Match             32.0%;  Score 189;  DB 6;  Length 689;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-90;
  Matches  189;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 141

Qy         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 201

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 261

Qy        181 GAGGCCTGC 189
              |||||||||
Db        262 GAGGCCTGC 270


RESULT 25
US-09-917-265-49
; Sequence 49, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(591)
;   OTHER INFORMATION:
US-09-917-265-49

  Query Match             13.7%;  Score 81;  DB 3;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        223 CTGGCTTCCAGAGAGATCTCT 243


RESULT 26
US-09-917-265-51/c
; Sequence 51, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-51

  Query Match             13.7%;  Score 81;  DB 3;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 27
US-10-821-670-49
; Sequence 49, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(591)
US-10-821-670-49

  Query Match             13.7%;  Score 81;  DB 9;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        223 CTGGCTTCCAGAGAGATCTCT 243
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RESULT 28
US-10-821-670-51/c
; Sequence 51, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-51

  Query Match             13.7%;  Score 81;  DB 9;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 29
US-09-917-265-46
; Sequence 46, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
;   OTHER INFORMATION:
US-09-917-265-46

  Query Match             13.7%;  Score 81;  DB 3;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 30
US-09-917-265-48/c
; Sequence 48, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-48

  Query Match             13.7%;  Score 81;  DB 3;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 31
US-10-821-670-46
; Sequence 46, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
US-10-821-670-46

  Query Match             13.7%;  Score 81;  DB 9;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318
```

```
RESULT 32
US-10-821-670-48/c
; Sequence 48, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-48

  Query Match             13.7%;  Score 81;  DB 9;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 33
US-09-917-265-104
; Sequence 104, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (232)..(897)
;   OTHER INFORMATION:
US-09-917-265-104

  Query Match             13.7%;  Score 81;  DB 3;  Length 1455;
  Best Local Similarity   100.0%;  Pred. No. 2e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 528

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        529 CTGGCTTCCAGAGAGATCTCT 549


RESULT 34
US-09-917-265-106/c
; Sequence 106, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 106
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-106

  Query Match             13.7%;  Score 81;  DB 3;  Length 1455;
  Best Local Similarity   100.0%;  Pred. No. 2e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 928

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        927 CTGGCTTCCAGAGAGATCTCT 907


RESULT 35
US-10-821-670-104
; Sequence 104, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 104
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (232)..(897)
US-10-821-670-104

  Query Match             13.7%;  Score 81;  DB 9;  Length 1455;
  Best Local Similarity   100.0%;  Pred. No. 2e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 528

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        529 CTGGCTTCCAGAGAGATCTCT 549


RESULT 36
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US-10-821-670-106/c
; Sequence 106, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 106
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-106

  Query Match             13.7%;  Score 81;  DB 9;  Length 1455;
  Best Local Similarity   100.0%;  Pred. No. 2e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 928

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        927 CTGGCTTCCAGAGAGATCTCT 907


RESULT 37
US-09-917-265-66
; Sequence 66, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
;   OTHER INFORMATION:
US-09-917-265-66

  Query Match             13.7%;  Score 81;  DB 3;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 2e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1105 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1164

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db       1165 CTGGCTTCCAGAGAGATCTCT 1185


RESULT 38
```

```
US-09-917-265-68/c
; Sequence 68, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-68

  Query Match             13.7%;  Score 81;  DB 3;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 2e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 39
US-10-821-670-66
; Sequence 66, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-10-821-670-66

  Query Match             13.7%;  Score 81;  DB 9;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 2e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1105 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1164

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db       1165 CTGGCTTCCAGAGAGATCTCT 1185


RESULT 40
US-10-821-670-68/c
```

```
; Sequence 68, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-68

  Query Match             13.7%;  Score 81;  DB 9;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 2e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 41
US-09-917-265-61
; Sequence 61, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
US-09-917-265-61

  Query Match             13.7%;  Score 81;  DB 3;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 2e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1230

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db       1231 CTGGCTTCCAGAGAGATCTCT 1251


RESULT 42
US-09-917-265-63/c
; Sequence 63, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-63

  Query Match             13.7%;  Score 81;  DB 3;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 2e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 43
US-10-821-670-61
; Sequence 61, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-10-821-670-61

  Query Match             13.7%;  Score 81;  DB 9;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 2e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1230

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db       1231 CTGGCTTCCAGAGAGATCTCT 1251


RESULT 44
US-10-821-670-63/c
; Sequence 63, Application US/10821670
```

```
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-63

  Query Match             13.7%;  Score 81;  DB 9;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 2e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 45
US-10-041-672C-8
; Sequence 8, Application US/10041672C
; Publication No. US20030157059A1
; GENERAL INFORMATION:
;  APPLICANT: Mologen Forschungs-, Entwicklungs- und Vetriebs GmbH
;  APPLICANT:  Universitat Zurich
;  TITLE OF INVENTION: FELINE INTERLEUKIN-12 AS IMMUNOSTIMULANT
;  FILE REFERENCE: NHL-NP-36
;  CURRENT APPLICATION NUMBER: US/10/041,672C
;  CURRENT FILING DATE:  2002-01-08
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 71
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer f12p35-1-lang
US-10-041-672C-8

  Query Match             12.0%;  Score 71;  DB 7;  Length 71;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-27;
  Matches   71;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        410 TGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCAC 469
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCAC 60

Qy        470 AGAACTCCTCC 480
              ||||||||||||
Db         61 AGAACTCCTCC 71


RESULT 46
US-10-741-601-946
; Sequence 946, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 946
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-946

  Query Match             11.0%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 72

Qy        544 ATTCG 548
              |||||
Db         73 ATTCG 77


RESULT 47
US-10-741-601-947
; Sequence 947, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 947
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-947

  Query Match             11.0%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 80

Qy        544 ATTCG 548
              |||||
Db         81 ATTCG 85


RESULT 48
US-10-741-601-951
; Sequence 951, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 951
;   LENGTH: 201
;   TYPE: DNA
```

```
;   ORGANISM: Homo sapiens
US-10-741-601-951

  Query Match             11.0%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 181

Qy        544 ATTCG 548
              |||||
Db        182 ATTCG 186


RESULT 49
US-10-741-601-955
; Sequence 955, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 955
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-955

  Query Match             11.0%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 72

Qy        544 ATTCG 548
              |||||
Db         73 ATTCG 77


RESULT 50
US-10-741-601-957
; Sequence 957, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 957
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-957

  Query Match             11.0%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 80

Qy        544 ATTCG 548
              |||||
Db         81 ATTCG 85


RESULT 51
US-10-741-601-960
; Sequence 960, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 960
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-960

  Query Match             11.0%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 181

Qy        544 ATTCG 548
              |||||
Db        182 ATTCG 186


RESULT 52
US-10-741-601-7417
; Sequence 7417, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7417
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-7417

  Query Match             11.0%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 72

Qy        544 ATTCG 548
              |||||
Db         73 ATTCG 77


RESULT 53
US-10-741-601-7418
```

```
; Sequence 7418, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7418
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-7418

  Query Match             11.0%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 80

Qy        544 ATTCG 548
              |||||
Db         81 ATTCG 85


RESULT 54
US-10-741-601-7431
; Sequence 7431, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7431
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-7431

  Query Match             11.0%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 181

Qy        544 ATTCG 548
              |||||
Db        182 ATTCG 186


RESULT 55
US-10-741-601-11370/c
; Sequence 11370, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11370
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-11370

  Query Match             11.0%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 130

Qy        544 ATTCG 548
              |||||
Db        129 ATTCG 125


RESULT 56
US-10-741-601-11372/c
; Sequence 11372, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11372
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-11372

  Query Match             11.0%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 122

Qy        544 ATTCG 548
              |||||
Db        121 ATTCG 117


RESULT 57
US-10-741-601-11417/c
; Sequence 11417, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11417
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-11417

  Query Match             11.0%;  Score 65;  DB 8;  Length 201;
```

```
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 21

Qy        544 ATTCG 548
              |||||
Db         20 ATTCG 16


RESULT 58
US-10-741-600-3487
; Sequence 3487, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3487
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-3487

  Query Match             11.0%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 72

Qy        544 ATTCG 548
              |||||
Db         73 ATTCG 77


RESULT 59
US-10-741-600-3488
; Sequence 3488, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3488
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-3488

  Query Match             11.0%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 80

Qy        544 ATTCG 548
              |||||
Db         81 ATTCG 85


RESULT 60
US-10-741-600-3492
; Sequence 3492, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3492
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-3492

  Query Match             11.0%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 181

Qy        544 ATTCG 548
              |||||
Db        182 ATTCG 186


RESULT 61
US-10-741-600-3496
; Sequence 3496, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3496
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-3496

  Query Match             11.0%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 72

Qy        544 ATTCG 548
              |||||
Db         73 ATTCG 77


RESULT 62
US-10-741-600-3498
; Sequence 3498, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
```

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;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3498
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-3498

  Query Match             11.0%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 80

Qy        544 ATTCG 548
              |||||
Db         81 ATTCG 85


RESULT 63
US-10-741-600-3501
; Sequence 3501, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3501
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-3501

  Query Match             11.0%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 181

Qy        544 ATTCG 548
              |||||
Db        182 ATTCG 186


RESULT 64
US-10-741-600-20963
; Sequence 20963, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20963
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-20963

  Query Match             11.0%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 72

Qy        544 ATTCG 548
              |||||
Db         73 ATTCG 77


RESULT 65
US-10-741-600-20964
; Sequence 20964, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20964
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-20964

  Query Match             11.0%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 80

Qy        544 ATTCG 548
              |||||
Db         81 ATTCG 85


RESULT 66
US-10-741-600-20992
; Sequence 20992, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20992
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-20992

  Query Match             11.0%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 181

Qy        544 ATTCG 548
              |||||
Db        182 ATTCG 186


RESULT 67
US-10-741-600-28831/c
; Sequence 28831, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28831
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-28831

  Query Match             11.0%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 130

Qy        544 ATTCG 548
              |||||
Db        129 ATTCG 125


RESULT 68
US-10-741-600-28833/c
; Sequence 28833, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28833
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-28833

  Query Match             11.0%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 122

Qy        544 ATTCG 548
              |||||
Db        121 ATTCG 117


RESULT 69
US-10-741-600-28877/c
; Sequence 28877, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28877
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-28877

  Query Match             11.0%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 21

Qy        544 ATTCG 548
              |||||
Db         20 ATTCG 16


RESULT 70
US-10-995-561-1976
; Sequence 1976, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1976
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-1976

  Query Match             11.0%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 72

Qy        544 ATTCG 548
              |||||
Db         73 ATTCG 77


RESULT 71
US-10-995-561-1977
; Sequence 1977, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
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;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1977
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-1977

  Query Match             11.0%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 80

Qy        544 ATTCG 548
              |||||
Db         81 ATTCG 85


RESULT 72
US-10-995-561-1981
; Sequence 1981, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1981
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-1981

  Query Match             11.0%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 181

Qy        544 ATTCG 548
              |||||
Db        182 ATTCG 186


RESULT 73
US-10-995-561-1986
; Sequence 1986, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1986
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-1986

  Query Match             11.0%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 72

Qy        544 ATTCG 548
              |||||
Db         73 ATTCG 77


RESULT 74
US-10-995-561-1988
; Sequence 1988, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1988
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-1988

  Query Match             11.0%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 80

Qy        544 ATTCG 548
              |||||
Db         81 ATTCG 85


RESULT 75
US-10-995-561-1991
; Sequence 1991, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1991
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-1991

  Query Match             11.0%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 181

Qy        544 ATTCG 548
              |||||
Db        182 ATTCG 186


RESULT 76
US-10-995-561-18302
; Sequence 18302, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18302
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-18302

  Query Match             11.0%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 72

Qy        544 ATTCG 548
              |||||
Db         73 ATTCG 77


RESULT 77
US-10-995-561-18303
; Sequence 18303, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18303
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-18303

  Query Match             11.0%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 80

Qy        544 ATTCG 548
              |||||
Db         81 ATTCG 85


RESULT 78
US-10-995-561-18335
; Sequence 18335, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18335
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-18335

  Query Match             11.0%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 181

Qy        544 ATTCG 548
              |||||
Db        182 ATTCG 186


RESULT 79
US-10-995-561-26362/c
; Sequence 26362, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26362
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-26362

  Query Match             11.0%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 21

Qy        544 ATTCG 548
              |||||
Db         20 ATTCG 16


RESULT 80
US-10-995-561-26545/c
; Sequence 26545, Application US/10995561
; Publication No. US20050272054A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26545
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-26545

  Query Match             11.0%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 130

Qy        544 ATTCG 548
              |||||
Db        129 ATTCG 125


RESULT 81
US-10-995-561-26548/c
; Sequence 26548, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26548
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-26548

  Query Match             11.0%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 122

Qy        544 ATTCG 548
              |||||
Db        121 ATTCG 117


RESULT 82
US-10-995-561-73346/c
; Sequence 73346, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73346
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-73346

  Query Match             11.0%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 130

Qy        544 ATTCG 548
              |||||
Db        129 ATTCG 125


RESULT 83
US-10-995-561-73349/c
; Sequence 73349, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73349
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-73349

  Query Match             11.0%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 122

Qy        544 ATTCG 548
              |||||
Db        121 ATTCG 117


RESULT 84
US-10-995-561-73383/c
; Sequence 73383, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73383
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
```

```
US-10-995-561-73383

  Query Match             11.0%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 21

Qy        544 ATTCG 548
              |||||
Db         20 ATTCG 16


RESULT 85
US-09-754-014-6
; Sequence 6, Application US/09754014
; Patent No. US20020119940A1
;   GENERAL INFORMATION:
;        APPLICANT: Jeff No. US20020119940A1dstrom
;                   Bruce Freimark
;                   Deepa Deshpande
;        TITLE OF INVENTION: GENE EXPRESSION AND DELIVERY SYTEMS
;                            AND USES
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                     Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 90071-2066
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                          storage
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: IBM P.C. DOS 5.0
;             SOFTWARE: FastSEQ for Windows 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/754,014
;             FILING DATE: 03-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/948,958
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Berkman, Charles S.
;             REGISTRATION NUMBER: 38,077
;             REFERENCE/DOCKET NUMBER: 226/284
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 660 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-754-014-6

  Query Match             11.0%;  Score 65;  DB 3;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        544 ATTCG 548
              |||||
Db        610 ATTCG 614


RESULT 86
US-09-836-866-4
; Sequence 4, Application US/09836866
; Patent No. US20020123473A1
;   GENERAL INFORMATION:
;        APPLICANT: No. US20020123473A1dstrom, Jeff
;                   Freimark, Bruce
;                   Deshpande, Deepa
;        TITLE OF INVENTION: IL-12 GENE EXPRESSION AND
;                            DELIVERY SYTEMS AND USES
;        NUMBER OF SEQUENCES: 8
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                     Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 90071-2066
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                          storage
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: IBM P.C. DOS 5.0
;             SOFTWARE: FastSEQ for Windows 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/836,866
;             FILING DATE: 16-Apr-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/949,160
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Warburg, Richard J.
;             REGISTRATION NUMBER: 32,327
;             REFERENCE/DOCKET NUMBER: 226/285
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 660 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-836-866-4

  Query Match             11.0%;  Score 65;  DB 3;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        544 ATTCG 548
              |||||
Db        610 ATTCG 614


RESULT 87
US-10-267-384-199
; Sequence 199, Application US/10267384
; Publication No. US20030198623A1
;   GENERAL INFORMATION:
;        APPLICANT: Paoletti, Enzo
;                   Tartaglia, James
```

```
;                Cox, William I.
;       TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
;       NUMBER OF SEQUENCES: 217
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Curtis, Morris & Safford
;            STREET: 530 Fifth Avenue
;            CITY: New York
;            STATE: NY
;            COUNTRY: USA
;            ZIP: 10036
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/267,384
;            FILING DATE: 09-Oct-2002
;            CLASSIFICATION: 435
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Frommer, William S.
;            REGISTRATION NUMBER: 25,506
;            REFERENCE/DOCKET NUMBER: 454310-2530
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 840-3333
;            TELEFAX: (212) 840-0712
;            TELEX: 425066CURTMS
;   INFORMATION FOR SEQ ID NO: 199:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 721 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 199:
US-10-267-384-199

  Query Match            11.0%;  Score 65;  DB 7;  Length 721;
  Best Local Similarity  100.0%;  Pred. No. 8.2e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy        544 ATTCG 548
              |||||
Db        671 ATTCG 675


RESULT 88
US-09-826-025-21
; Sequence 21, Application US/09826025
; Patent No. US20020162123A1
;   GENERAL INFORMATION:
;       APPLICANT: Chang, Lung-Ji
;       TITLE OF INVENTION: Combination Immunogene Therapy
;       NUMBER OF SEQUENCES: 25
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Medlen & Carroll, LLP
;            STREET: 220 Montgomery Street, Suite 2200
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: United States of America
;            ZIP: 94104
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/826,025
;            FILING DATE: 04-Apr-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/838,702
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Ingolia, Diane E.
;            REGISTRATION NUMBER: 40,027
;            REFERENCE/DOCKET NUMBER: CHANG-02687
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 705-8410
;            TELEFAX: (415) 397-8338
;   INFORMATION FOR SEQ ID NO: 21:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 762 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: other nucleic acid
;            DESCRIPTION: /desc = "DNA"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-826-025-21

  Query Match            11.0%;  Score 65;  DB 3;  Length 762;
  Best Local Similarity  100.0%;  Pred. No. 8.2e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        544 ATTCG 548
              |||||
Db        712 ATTCG 716


RESULT 89
US-10-785-577-21
; Sequence 21, Application US/10785577
; Publication No. US20040237129A1
;   GENERAL INFORMATION:
;       APPLICANT: Chang, Lung-Ji
;       TITLE OF INVENTION: Combination Immunogene Therapy
;       NUMBER OF SEQUENCES: 25
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Medlen & Carroll, LLP
;            STREET: 220 Montgomery Street, Suite 2200
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: United States of America
;            ZIP: 94104
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/785,577
;            FILING DATE: 23-Feb-2004
;            CLASSIFICATION: 424
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/838,702
;            FILING DATE: 9-Apr-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Ingolia, Diane E.
;            REGISTRATION NUMBER: 40,027
;            REFERENCE/DOCKET NUMBER: CHANG-02687
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 705-8410
;            TELEFAX: (415) 397-8338
;   INFORMATION FOR SEQ ID NO: 21:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 762 base pairs
;            TYPE: nucleic acid
```

```
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: other nucleic acid
;             DESCRIPTION: /desc = "DNA"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-10-785-577-21

  Query Match             11.0%;  Score 65;  DB 9;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        544 ATTCG 548
              |||||
Db        712 ATTCG 716


RESULT 90
US-10-688-845-57
; Sequence 57, Application US/10688845
; Publication No. US20040247578A1
; GENERAL INFORMATION:
;  APPLICANT: Lotze, Michael T
;  APPLICANT:  Tahara, Hideaki
;  TITLE OF INVENTION: Methods And Reagents For Inducing Immunity
;  FILE REFERENCE: UPT-004
;  CURRENT APPLICATION NUMBER: US/10/688,845
;  CURRENT FILING DATE:  2003-10-15
;  PRIOR APPLICATION NUMBER: 60/418,865
;  PRIOR FILING DATE: 2002-10-15
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
;   LENGTH: 762
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-688-845-57

  Query Match             11.0%;  Score 65;  DB 9;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        544 ATTCG 548
              |||||
Db        712 ATTCG 716


RESULT 91
US-10-373-456-19
; Sequence 19, Application US/10373456
; Publication No. US20040009146A1
; GENERAL INFORMATION:
;  APPLICANT: Podhajcer, Osvaldo
;  TITLE OF INVENTION: Anti-Tumor Vaccine and Method
;  FILE REFERENCE: 1423P-US/101141-14
;  CURRENT APPLICATION NUMBER: US/10/373,456
;  CURRENT FILING DATE:  2003-02-25
;  PRIOR APPLICATION NUMBER: US 60/359,836
;  PRIOR FILING DATE: 2002-02-26
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 811
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-373-456-19

  Query Match             11.0%;  Score 65;  DB 7;  Length 811;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
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Db        498 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 557

Qy        544 ATTCG 548
              |||||
Db        558 ATTCG 562


RESULT 92
US-10-349-507-4
; Sequence 4, Application US/10349507
; Publication No. US20030199002A1
; GENERAL INFORMATION:
;  APPLICANT: Hekimi , Siegfried
;  APPLICANT:  Jiang , Ning
;  APPLICANT:  Benard, Claire
;  APPLICANT:  Kebir , Hania
;  APPLICANT:  McCright, Brenton
;  APPLICANT:  Lakowski , Bernard
;  TITLE OF INVENTION: CLK-2 NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
;  FILE REFERENCE: 11202-006-999
;  CURRENT APPLICATION NUMBER: US/10/349,507
;  CURRENT FILING DATE:  2003-01-22
;  PRIOR APPLICATION NUMBER: 10/312,187
;  PRIOR FILING DATE: 2002-12-20
;  PRIOR APPLICATION NUMBER: PCT/CA01/00913
;  PRIOR FILING DATE: 2001-06-20
;  PRIOR APPLICATION NUMBER: 60/213,174
;  PRIOR FILING DATE: 2000-06-22
;  PRIOR APPLICATION NUMBER: 60/254,932
;  PRIOR FILING DATE: 2000-12-13
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 856
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (170)...(826)
US-10-349-507-4

  Query Match             11.0%;  Score 65;  DB 7;  Length 856;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 778

Qy        544 ATTCG 548
              |||||
Db        779 ATTCG 783


RESULT 93
US-10-267-565-4
; Sequence 4, Application US/10267565
; Publication No. US20030204059A1
; GENERAL INFORMATION:
;  APPLICANT: Gately, Maurice
;  APPLICANT:  Gubler, Ulrich
;  APPLICANT:  Hulmes, Jeffery
;  APPLICANT:  Podlaski, Frank
;  APPLICANT:  Stern, Alvin
;  TITLE OF INVENTION: PURIFICATION AND CHARACTERIZATION OF CYTOTOXIC
;  TITLE OF INVENTION:  LYMPHOCYTE MATURATION FACTOR AND MONOCLONAL
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;  TITLE OF INVENTION:  ANTIBODIES THERETO
;  FILE REFERENCE: 11126-005
;  CURRENT APPLICATION NUMBER: US/10/267,565
;  CURRENT FILING DATE:  2003-01-23
;  PRIOR APPLICATION NUMBER: 09/401,839
;  PRIOR FILING DATE: 1999-09-22
;  PRIOR APPLICATION NUMBER: 08/459,151
;  PRIOR FILING DATE: 1995-06-02
;  PRIOR APPLICATION NUMBER: 08/205,011
;  PRIOR FILING DATE: 1994-03-02
;  PRIOR APPLICATION NUMBER: 07/857,023
;  PRIOR FILING DATE: 1992-03-24
;  PRIOR APPLICATION NUMBER: 07/572,284
;  PRIOR FILING DATE: 1990-08-27
;  PRIOR APPLICATION NUMBER: 07/520,935
;  PRIOR FILING DATE: 1990-05-09
;  PRIOR APPLICATION NUMBER: 07/455,708
;  PRIOR FILING DATE: 1989-12-22
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 856
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (170)...(826)
US-10-267-565-4

  Query Match             11.0%;  Score 65;  DB 7;  Length 856;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 778

Qy        544 ATTCG 548
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Db        779 ATTCG 783


RESULT 94
US-10-373-456-17
; Sequence 17, Application US/10373456
; Publication No. US20040009146A1
; GENERAL INFORMATION:
;  APPLICANT: Podhajcer, Osvaldo
;  TITLE OF INVENTION: Anti-Tumor Vaccine and Method
;  FILE REFERENCE: 1423P-US/101141-14
;  CURRENT APPLICATION NUMBER: US/10/373,456
;  CURRENT FILING DATE:  2003-02-25
;  PRIOR APPLICATION NUMBER: US 60/359,836
;  PRIOR FILING DATE: 2002-02-26
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
;   LENGTH: 868
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-373-456-17

  Query Match             11.0%;  Score 65;  DB 7;  Length 868;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 620

Qy        544 ATTCG 548
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Db        621 ATTCG 625


RESULT 95
US-10-172-399-5
; Sequence 5, Application US/10172399
; Publication No. US20030045495A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Chuan-Yuan
;  APPLICANT:  Dewhirst, Mark
;  APPLICANT:  Huang, Qian
;  TITLE OF INVENTION: A METHOD FOR SELECTIVE EXPRESSION OF THERAPEUTIC GENES BY HYPERTHE
;  FILE REFERENCE: 180-129
;  CURRENT APPLICATION NUMBER: US/10/172,399
;  CURRENT FILING DATE:  2002-06-14
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 1026
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (170)..(829)
US-10-172-399-5

  Query Match             11.0%;  Score 65;  DB 6;  Length 1026;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
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Db        719 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 778

Qy        544 ATTCG 548
              |||||
Db        779 ATTCG 783


RESULT 96
US-10-641-643-1041
; Sequence 1041, Application US/10641643
; Publication No. US20040077003A1
;   GENERAL INFORMATION:
;        APPLICANT: Cocks, Benjamin G.
;                   Susan G. Stuart
;                   Jeffrey J. Seilhamer
;        TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
;                            GENE EXPRESSION
;        NUMBER OF SEQUENCES: 1508
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
;             STREET: 3174 PORTER DRIVE
;             CITY: PALO ALTO
;             STATE: CALIFORNIA
;             COUNTRY: USA
;             ZIP: 94304
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/641,643
;             FILING DATE: 14-Aug-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: <Unknown>
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Zeller, Karen J.
;             REGISTRATION NUMBER: 37,071
;             REFERENCE/DOCKET NUMBER: PA-0001 US
;        TELECOMMUNICATION INFORMATION:
```

```
;             TELEPHONE: (650) 855-0555
;             TELEFAX: (650) 845-4166
;   INFORMATION FOR SEQ ID NO: 1041:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1026 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        IMMEDIATE SOURCE:
;             LIBRARY: GENBANK
;             CLONE: g180623
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1041 :
US-10-641-643-1041

  Query Match             11.0%;  Score 65;  DB 8;  Length 1026;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
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Db        719 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 778

Qy        544 ATTCG 548
              |||||
Db        779 ATTCG 783


RESULT 97
US-10-603-064-6
; Sequence 6, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
;  APPLICANT: Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION: Multiple Cytokine Protein Complexes
;  FILE REFERENCE: LEX-010
;  CURRENT APPLICATION NUMBER: US/10/603,064
;  CURRENT FILING DATE:  2003-06-24
;  PRIOR APPLICATION NUMBER: US/09/634,368
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: 60/147,924
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 1287
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: human Fc-p35
;   OTHER INFORMATION: fusion protein coding sequence
US-10-603-064-6

  Query Match             11.0%;  Score 65;  DB 8;  Length 1287;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1177 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1236

Qy        544 ATTCG 548
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Db       1237 ATTCG 1241


RESULT 98
US-10-476-960-3
; Sequence 3, Application US/10476960
; Publication No. US20040248828A1
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Isis Pharmaceuticals, Inc.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTSP-0392
;  CURRENT APPLICATION NUMBER: US/10/476,960
;  CURRENT FILING DATE:  2003-11-05
;  PRIOR APPLICATION NUMBER: 09/851,520
;  PRIOR FILING DATE: 2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
;   LENGTH: 1316
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (102)...(863)
US-10-476-960-3

  Query Match             11.0%;  Score 65;  DB 9;  Length 1316;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
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Db        753 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 812

Qy        544 ATTCG 548
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Db        813 ATTCG 817


RESULT 99
US-11-089-191-3
; Sequence 3, Application US/11089191
; Publication No. US20050261228A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Susan Gregory
;  APPLICANT:  Ronnie C. Hanecak
;  APPLICANT:  Kevin P. Anderson
;  APPLICANT:  Ming-Yi Chiang
;  APPLICANT:  Vickie Brown-Driver
;  APPLICANT:  David J. Ecker
;  APPLICANT:  Timothy Vickers
;  APPLICANT:  Jacqueline Wyatt
;  APPLICANT:  Eric G. Marcusson
;  APPLICANT:  Nicholas M. Dean
;  APPLICANT:  Sanjay Bhanot
;  APPLICANT:  Elizabeth J. Ackermann
;  APPLICANT:  Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: BNDL-0021US.P1
;  CURRENT APPLICATION NUMBER: US/11/089,191
;  CURRENT FILING DATE:  2005-03-23
;  PRIOR APPLICATION NUMBER: 10/476,960
;  PRIOR FILING DATE: 2003-11-07
;  PRIOR APPLICATION NUMBER: PCT/US02/13871
;  PRIOR FILING DATE: 2002-05-01
;  PRIOR APPLICATION NUMBER: 09/851,520
;  PRIOR FILING DATE: 2001-05-07
;  PRIOR APPLICATION NUMBER: 10/67,236
;  PRIOR FILING DATE: 2003-09-17
;  PRIOR APPLICATION NUMBER: 10/038,335
;  PRIOR FILING DATE: 2002-01-02
;  PRIOR APPLICATION NUMBER: 09/299,058
;  PRIOR FILING DATE: 1999-04-23
;  PRIOR APPLICATION NUMBER: 08/403,888
;  PRIOR FILING DATE: 1995-06-12
;  PRIOR APPLICATION NUMBER: PCT/US93/09297
;  PRIOR FILING DATE: 1993-09-29
;  PRIOR APPLICATION NUMBER: 07/954,185
;  PRIOR FILING DATE: 1992-09-29
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;  PRIOR APPLICATION NUMBER: 10/515,546
;  PRIOR FILING DATE: 2004-11-23
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
;   LENGTH: 1316
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (102)...(863)
US-11-089-191-3

  Query Match             11.0%;  Score 65;  DB 15;  Length 1316;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 812

Qy        544 ATTCG 548
              |||||
Db        813 ATTCG 817


RESULT 100
US-09-924-703-5
; Sequence 5, Application US/09924703
; Patent No. US20020137898A1
; GENERAL INFORMATION:
;  APPLICANT: TRINCHIERI, GIORGIO
;  APPLICANT:  PERUSSIA, BICE
;  APPLICANT:  CLARK, STEVEN C.
;  APPLICANT:  WONG, GORDON G.
;  APPLICANT:  HEWICK, RODNEY
;  APPLICANT:  KOBAYASHI, MICHIKO
;  TITLE OF INVENTION: ANTIBODIES TO NATURAL KILLER STIMULATORY FACTOR
;  FILE REFERENCE: 01142.0142.0100
;  CURRENT APPLICATION NUMBER: US/09/924,703
;  CURRENT FILING DATE:  2001-08-09
;  PRIOR APPLICATION NUMBER: 09/325,958
;  PRIOR FILING DATE: 1999-06-04
;  PRIOR APPLICATION NUMBER: 08/858,000
;  PRIOR FILING DATE: 1997-05-16
;  PRIOR APPLICATION NUMBER: 08/403,013
;  PRIOR FILING DATE: 1995-03-13
;  PRIOR APPLICATION NUMBER: 07/584,941
;  PRIOR FILING DATE: 1990-09-18
;  PRIOR APPLICATION NUMBER: 07/307,817
;  PRIOR FILING DATE: 1989-02-07
;  PRIOR APPLICATION NUMBER: 07/269,945
;  PRIOR FILING DATE: 1988-11-10
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 1395
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
;   OTHER INFORMATION: sequence of the 30 kD subunit of NKSF
;   NAME/KEY: CDS
;   LOCATION: (114)..(872)
US-09-924-703-5

  Query Match             11.0%;  Score 65;  DB 3;  Length 1395;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 543
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Db        765 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 824

Qy        544 ATTCG 548
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Db        825 ATTCG 829


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OM nucleic - nucleic search, using sw model

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8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	18	3.0	22	7	US-11-266-409-9	Sequence 9, Appli
	2	18	3.0	2324	7	US-11-293-697-1624	Sequence 1624, Ap
c	3	17	2.9	918	7	US-11-217-529-1610	Sequence 1610, Ap
c	4	17	2.9	2024	7	US-11-293-697-1253	Sequence 1253, Ap
c	5	17	2.9	5298	7	US-11-217-529-1583	Sequence 1583, Ap
	6	16	2.7	360	6	US-10-488-619-237	Sequence 237, App
	7	16	2.7	861	7	US-11-217-529-585	Sequence 585, App
	8	16	2.7	1159	6	US-10-953-349-19286	Sequence 19286, A
	9	16	2.7	1186	6	US-10-953-349-20117	Sequence 20117, A
c	10	16	2.7	1203	6	US-10-953-349-36627	Sequence 36627, A
c	11	16	2.7	1437	7	US-11-183-218-9	Sequence 9, Appli
	12	16	2.7	1536	6	US-10-471-571A-2411	Sequence 2411, Ap
	13	16	2.7	1575	6	US-10-953-349-16963	Sequence 16963, A
	14	16	2.7	1676	6	US-10-953-349-34653	Sequence 34653, A
	15	16	2.7	1859	7	US-11-293-697-326	Sequence 326, App
c	16	16	2.7	1944	7	US-11-217-529-78920	Sequence 78920, A
c	17	16	2.7	2243	6	US-10-511-937-2883	Sequence 2883, Ap
c	18	16	2.7	2836	7	US-11-293-697-520	Sequence 520, App
	19	16	2.7	4293	7	US-11-217-529-76344	Sequence 76344, A
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	21	16	2.7	6383	6	US-10-511-937-2838	Sequence 2838, Ap
	22	16	2.7	138941	6	US-10-489-730-10	GENERAL INFORMATI
c	23	16	2.7	138941	6	US-10-489-730-10	GENERAL INFORMATI
c	24	15	2.5	25	7	US-11-217-529-105697	Sequence 105697,
	25	15	2.5	25	7	US-11-217-529-155757	Sequence 155757,
c	26	15	2.5	25	7	US-11-217-529-191540	Sequence 191540,
c	27	15	2.5	25	7	US-11-217-529-191845	Sequence 191845,
c	28	15	2.5	400	6	US-10-488-619-2364	Sequence 2364, Ap
	29	15	2.5	418	6	US-10-488-619-857	Sequence 857, App
	30	15	2.5	425	6	US-10-473-173-354	Sequence 354, App
	31	15	2.5	425	6	US-10-488-619-858	Sequence 858, App
	32	15	2.5	429	7	US-11-217-529-190905	Sequence 190905,
	33	15	2.5	438	6	US-10-488-619-2365	Sequence 2365, Ap
	34	15	2.5	441	6	US-10-488-619-1356	Sequence 1356, Ap
	35	15	2.5	459	7	US-11-217-529-166946	Sequence 166946,
	36	15	2.5	462	7	US-11-217-529-190985	Sequence 190985,
	37	15	2.5	507	7	US-11-217-529-81573	Sequence 81573, A
	38	15	2.5	510	7	US-11-217-529-79785	Sequence 79785, A
	39	15	2.5	576	7	US-11-217-529-81860	Sequence 81860, A
c	40	15	2.5	608	6	US-10-953-349-39845	Sequence 39845, A
c	41	15	2.5	612	7	US-11-217-529-77395	Sequence 77395, A
c	42	15	2.5	624	6	US-10-488-619-2292	Sequence 2292, Ap
	43	15	2.5	630	6	US-10-953-349-12334	Sequence 12334, A
	44	15	2.5	630	6	US-10-953-349-25972	Sequence 25972, A
c	45	15	2.5	768	7	US-11-217-529-190869	Sequence 190869,
	46	15	2.5	778	6	US-10-953-349-355	Sequence 355, App
c	47	15	2.5	782	6	US-10-488-619-1355	Sequence 1355, Ap
	48	15	2.5	814	6	US-10-953-349-33201	Sequence 33201, A
c	49	15	2.5	830	6	US-10-953-349-39705	Sequence 39705, A
c	50	15	2.5	906	7	US-11-217-529-5224	Sequence 5224, Ap
	51	15	2.5	906	7	US-11-217-529-174189	Sequence 174189,
	52	15	2.5	1046	6	US-10-953-349-39221	Sequence 39221, A
c	53	15	2.5	1124	6	US-10-953-349-17993	Sequence 17993, A
	54	15	2.5	1151	6	US-10-953-349-32852	Sequence 32852, A
c	55	15	2.5	1156	6	US-10-953-349-31118	Sequence 31118, A
	56	15	2.5	1176	7	US-11-217-529-79991	Sequence 79991, A
	57	15	2.5	1190	6	US-10-953-349-26534	Sequence 26534, A
	58	15	2.5	1206	6	US-10-953-349-19889	Sequence 19889, A
	59	15	2.5	1269	7	US-11-217-529-79181	Sequence 79181, A
	60	15	2.5	1271	6	US-10-953-349-32614	Sequence 32614, A
	61	15	2.5	1302	6	US-10-953-349-9401	Sequence 9401, Ap
	62	15	2.5	1305	7	US-11-217-529-79465	Sequence 79465, A
c	63	15	2.5	1404	7	US-11-217-529-190840	Sequence 190840,
	64	15	2.5	1406	6	US-10-953-349-3438	Sequence 3438, Ap
	65	15	2.5	1451	6	US-10-953-349-31780	Sequence 31780, A
c	66	15	2.5	1493	6	US-10-953-349-20272	Sequence 20272, A
	67	15	2.5	1504	6	US-10-953-349-10170	Sequence 10170, A
	68	15	2.5	1511	6	US-10-953-349-34123	Sequence 34123, A
c	69	15	2.5	1551	7	US-11-217-529-1240	Sequence 1240, Ap
c	70	15	2.5	1578	6	US-10-953-349-33142	Sequence 33142, A
	71	15	2.5	1821	6	US-10-953-349-1943	Sequence 1943, Ap
	72	15	2.5	1869	6	US-10-953-349-12445	Sequence 12445, A
	73	15	2.5	1902	7	US-11-293-697-2269	Sequence 2269, Ap
c	74	15	2.5	2043	7	US-11-293-697-773	Sequence 773, App
c	75	15	2.5	2105	6	US-10-953-349-11750	Sequence 11750, A
	76	15	2.5	2151	7	US-11-293-697-153	Sequence 153, App
	77	15	2.5	2205	7	US-11-293-697-56	Sequence 56, Appl
	78	15	2.5	2241	7	US-11-217-529-2489	Sequence 2489, Ap
c	79	15	2.5	2400	7	US-11-217-529-80988	Sequence 80988, A
c	80	15	2.5	2537	7	US-11-293-697-2092	Sequence 2092, Ap
	81	15	2.5	2553	7	US-11-217-529-1141	Sequence 1141, Ap
c	82	15	2.5	2650	7	US-11-293-697-749	Sequence 749, App
c	83	15	2.5	3350	6	US-10-505-928-637	Sequence 637, App
c	84	15	2.5	3350	6	US-10-505-928-641	Sequence 641, App
	85	15	2.5	4533	7	US-11-217-529-1172	Sequence 1172, Ap
	86	15	2.5	5171	6	US-10-501-834-216	Sequence 216, App
	87	15	2.5	5703	7	US-11-217-529-191092	Sequence 191092,
c	88	15	2.5	5734	6	US-10-505-928-28	Sequence 28, Appl
	89	15	2.5	5747	6	US-10-199-229-1	Sequence 1, Appli
c	90	15	2.5	6826	6	US-10-505-928-330	Sequence 330, App
	91	15	2.5	128361	6	US-10-505-928-151	Sequence 151, App
	92	15	2.5	261789	7	US-11-260-842-1	Sequence 1, Appli
c	93	15	2.5	261789	7	US-11-260-842-1	Sequence 1, Appli
	94	14	2.4	25	7	US-11-217-529-26117	Sequence 26117, A
	95	14	2.4	25	7	US-11-217-529-40959	Sequence 40959, A
	96	14	2.4	25	7	US-11-217-529-124406	Sequence 124406,
c	97	14	2.4	25	7	US-11-217-529-136455	Sequence 136455,
c	98	14	2.4	25	7	US-11-217-529-148494	Sequence 148494,

c 99	14	2.4	50	6	US-10-511-937-3058	Sequence 3058, Ap
c 100	14	2.4	258	6	US-10-471-571A-1747	Sequence 1747, Ap
c 101	14	2.4	312	7	US-11-217-529-5872	Sequence 5872, Ap
c 102	14	2.4	330	7	US-11-217-529-76063	Sequence 76063, A
103	14	2.4	345	7	US-11-217-529-166727	Sequence 166727,
104	14	2.4	360	6	US-10-471-571A-127	Sequence 127, App
105	14	2.4	381	7	US-11-217-529-166773	Sequence 166773,
c 106	14	2.4	410	6	US-10-473-173-293	Sequence 293, App
107	14	2.4	426	6	US-10-488-619-2658	Sequence 2658, Ap
108	14	2.4	449	6	US-10-473-173-445	Sequence 445, App
109	14	2.4	453	7	US-11-217-529-82632	Sequence 82632, A
110	14	2.4	455	7	US-11-024-545-26	Sequence 26, Appl
111	14	2.4	455	7	US-11-190-750-19	Sequence 19, Appl
112	14	2.4	467	6	US-10-488-619-943	Sequence 943, App
c 113	14	2.4	470	6	US-10-473-173-454	Sequence 454, App
114	14	2.4	510	7	US-11-217-529-3168	Sequence 3168, Ap
115	14	2.4	541	6	US-10-488-619-949	Sequence 949, App
116	14	2.4	552	7	US-11-301-554-137	Sequence 137, App
117	14	2.4	555	7	US-11-217-529-76962	Sequence 76962, A
c 118	14	2.4	569	6	US-10-488-619-2455	Sequence 2455, Ap
119	14	2.4	578	6	US-10-488-619-1525	Sequence 1525, Ap
c 120	14	2.4	581	6	US-10-488-619-1940	Sequence 1940, Ap
121	14	2.4	586	6	US-10-488-619-1222	Sequence 1222, Ap
c 122	14	2.4	605	6	US-10-488-619-1416	Sequence 1416, Ap
123	14	2.4	606	6	US-10-488-619-2488	Sequence 2488, Ap
c 124	14	2.4	614	7	US-11-301-554-1307	Sequence 1307, Ap
c 125	14	2.4	615	7	US-11-217-529-81209	Sequence 81209, A
c 126	14	2.4	627	6	US-10-471-571A-3259	Sequence 3259, Ap
127	14	2.4	637	6	US-10-953-349-15754	Sequence 15754, A
c 128	14	2.4	649	6	US-10-953-349-16024	Sequence 16024, A
129	14	2.4	654	7	US-11-024-545-19	Sequence 19, Appl
130	14	2.4	654	7	US-11-190-750-11	Sequence 11, Appl
131	14	2.4	667	6	US-10-953-349-26444	Sequence 26444, A
132	14	2.4	674	7	US-11-024-545-31	Sequence 31, Appl
133	14	2.4	674	7	US-11-190-750-24	Sequence 24, Appl
c 134	14	2.4	683	6	US-10-505-928-808	Sequence 808, App
135	14	2.4	714	7	US-11-217-529-173285	Sequence 173285,
c 136	14	2.4	717	6	US-10-471-571A-1489	Sequence 1489, Ap
137	14	2.4	747	6	US-10-953-349-30349	Sequence 30349, A
c 138	14	2.4	756	6	US-10-488-619-2529	Sequence 2529, Ap
c 139	14	2.4	756	7	US-11-217-529-173433	Sequence 173433,
140	14	2.4	759	7	US-11-217-529-5972	Sequence 5972, Ap
c 141	14	2.4	768	6	US-10-471-571A-1189	Sequence 1189, Ap
c 142	14	2.4	788	6	US-10-953-349-25425	Sequence 25425, A
143	14	2.4	795	7	US-11-217-529-190902	Sequence 190902,
144	14	2.4	802	6	US-10-953-349-16472	Sequence 16472, A
145	14	2.4	810	6	US-10-488-619-2332	Sequence 2332, Ap
146	14	2.4	810	6	US-10-953-349-9058	Sequence 9058, Ap
147	14	2.4	818	6	US-10-488-619-2757	Sequence 2757, Ap
c 148	14	2.4	831	7	US-11-217-529-80137	Sequence 80137, A
c 149	14	2.4	847	6	US-10-953-349-6957	Sequence 6957, Ap
150	14	2.4	856	6	US-10-953-349-25491	Sequence 25491, A
c 151	14	2.4	879	7	US-11-217-529-76034	Sequence 76034, A
c 152	14	2.4	884	6	US-10-953-349-297	Sequence 297, App
153	14	2.4	909	6	US-10-953-349-26362	Sequence 26362, A
c 154	14	2.4	925	6	US-10-953-349-28311	Sequence 28311, A
c 155	14	2.4	932	6	US-10-953-349-22368	Sequence 22368, A
c 156	14	2.4	933	6	US-10-471-571A-5273	Sequence 5273, Ap
157	14	2.4	935	6	US-10-953-349-35334	Sequence 35334, A
c 158	14	2.4	948	7	US-11-217-529-2070	Sequence 2070, Ap
c 159	14	2.4	956	6	US-10-953-349-3171	Sequence 3171, Ap
160	14	2.4	995	6	US-10-953-349-16178	Sequence 16178, A
161	14	2.4	996	7	US-11-024-545-1	Sequence 1, Appli
162	14	2.4	996	7	US-11-190-750-29	Sequence 29, Appl
163	14	2.4	996	7	US-11-264-784-95	Sequence 95, Appl
164	14	2.4	996	7	US-11-264-737-136	Sequence 136, App
165	14	2.4	996	7	US-11-265-761-108	Sequence 108, App
c 166	14	2.4	1000	6	US-10-953-349-22396	Sequence 22396, A
167	14	2.4	1010	6	US-10-953-349-18832	Sequence 18832, A
c 168	14	2.4	1011	7	US-11-217-529-4300	Sequence 4300, Ap
c 169	14	2.4	1014	7	US-11-321-475-1	Sequence 1, Appli
c 170	14	2.4	1017	7	US-11-217-529-1998	Sequence 1998, Ap
171	14	2.4	1021	6	US-10-953-349-36776	Sequence 36776, A
c 172	14	2.4	1023	6	US-10-471-571A-255	Sequence 255, App
173	14	2.4	1032	7	US-11-217-529-4293	Sequence 4293, Ap
c 174	14	2.4	1040	6	US-10-953-349-7739	Sequence 7739, Ap
175	14	2.4	1044	6	US-10-953-349-14244	Sequence 14244, A
c 176	14	2.4	1083	6	US-10-471-571A-1795	Sequence 1795, Ap
177	14	2.4	1087	6	US-10-953-349-14786	Sequence 14786, A
178	14	2.4	1095	6	US-10-196-749-231	Sequence 231, App
179	14	2.4	1097	6	US-10-953-349-101	Sequence 101, App
c 180	14	2.4	1106	6	US-10-953-349-1012	Sequence 1012, Ap
181	14	2.4	1125	7	US-11-217-529-76126	Sequence 76126, A
182	14	2.4	1125	7	US-11-217-529-81925	Sequence 81925, A
c 183	14	2.4	1133	6	US-10-953-349-7324	Sequence 7324, Ap
c 184	14	2.4	1160	6	US-10-953-349-14240	Sequence 14240, A
c 185	14	2.4	1174	6	US-10-953-349-7440	Sequence 7440, Ap
186	14	2.4	1176	7	US-11-121-154-118	Sequence 118, App
c 187	14	2.4	1177	6	US-10-196-749-381	Sequence 381, App
c 188	14	2.4	1177	7	US-11-101-316-129	Sequence 129, App
c 189	14	2.4	1178	6	US-10-953-349-17819	Sequence 17819, A
190	14	2.4	1185	7	US-11-217-529-5626	Sequence 5626, Ap
c 191	14	2.4	1197	7	US-11-122-986-301	Sequence 301, App
c 192	14	2.4	1197	7	US-11-122-986-303	Sequence 303, App
193	14	2.4	1212	6	US-10-953-349-20909	Sequence 20909, A
194	14	2.4	1227	6	US-10-713-648A-43	Sequence 43, Appl
c 195	14	2.4	1227	6	US-10-471-571A-391	Sequence 391, App
c 196	14	2.4	1253	6	US-10-953-349-1509	Sequence 1509, Ap
197	14	2.4	1266	7	US-11-217-529-4799	Sequence 4799, Ap
198	14	2.4	1272	7	US-11-217-529-1909	Sequence 1909, Ap
c 199	14	2.4	1274	6	US-10-953-349-28054	Sequence 28054, A
200	14	2.4	1284	7	US-11-217-529-5325	Sequence 5325, Ap

ALIGNMENTS

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RESULT 1
US-11-266-409-9
; Sequence 9, Application US/11266409
; Publication No. US20060093578A1
; GENERAL INFORMATION:
;  APPLICANT: SUZUMURA, AKIO
;  TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATING MULTIPLE SCLEROSIS
;  FILE REFERENCE: 279847US40
;  CURRENT APPLICATION NUMBER: US/11/266,409
;  CURRENT FILING DATE:  2005-11-04
;  PRIOR APPLICATION NUMBER: US 60/624,851
;  PRIOR FILING DATE: 2004-11-04
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA
US-11-266-409-9

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Qy        322 GACTTGAAGATGTACCAG 339
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Db          1 GACTTGAAGATGTACCAG 18


RESULT 2
US-11-293-697-1624
; Sequence 1624, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
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;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1624
;   LENGTH: 2324
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1624

  Query Match             3.0%;  Score 18;  DB 7;  Length 2324;
  Best Local Similarity   100.0%;  Pred. No. 2.1;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        259 AGTTGCCTGGCCTCCAGA 276
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Db        170 AGTTGCCTGGCCTCCAGA 187


RESULT 3
US-11-217-529-1610/c
; Sequence 1610, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1610
;   LENGTH: 918
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-1610

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Qy        144 TCATGAAGATATCACAA 160
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Db        223 TCATGAAGATATCACAA 207


RESULT 4
US-11-293-697-1253/c
; Sequence 1253, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1253
;   LENGTH: 2024
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1253

  Query Match             2.9%;  Score 17;  DB 7;  Length 2024;
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Qy        440 CCCTGAATGTCAACAGT 456
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Db        191 CCCTGAATGTCAACAGT 175


RESULT 5
US-11-217-529-1583/c
; Sequence 1583, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1583
;   LENGTH: 5298
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-1583

  Query Match             2.9%;  Score 17;  DB 7;  Length 5298;
  Best Local Similarity   100.0%;  Pred. No. 7.5;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        526 CTTCTTCATGCTTTCAG 542
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Db       1938 CTTCTTCATGCTTTCAG 1922


RESULT 6
US-10-488-619-237
; Sequence 237, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations W
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 237
;   LENGTH: 360
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(444)
;   OTHER INFORMATION: N IS G, C, A OR T
US-10-488-619-237

  Query Match             2.7%;  Score 16;  DB 6;  Length 360;
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Qy        133 GAAGAGATTGATCATG 148
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RESULT 7
US-11-217-529-585
; Sequence 585, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 585
;   LENGTH: 861
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-585

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Qy        321 GGACTTGAAGATGTAC 336
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Db        370 GGACTTGAAGATGTAC 385


RESULT 8
US-10-953-349-19286
; Sequence 19286, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19286
;   LENGTH: 1159
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-19286

  Query Match             2.7%;  Score 16;  DB 6;  Length 1159;
  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        321 GGACTTGAAGATGTAC 336
              ||||||||||||||||
Db        561 GGACTTGAAGATGTAC 576


RESULT 9
US-10-953-349-20117
; Sequence 20117, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20117
;   LENGTH: 1186
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-20117

  Query Match             2.7%;  Score 16;  DB 6;  Length 1186;
  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 CCCACACCCACACCAA 25
              ||||||||||||||||
Db        155 CCCACACCCACACCAA 170


RESULT 10
US-10-953-349-36627/c
; Sequence 36627, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36627
;   LENGTH: 1203
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-36627

  Query Match             2.7%;  Score 16;  DB 6;  Length 1203;
  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        522 CATACTTCTTCATGCT 537
              ||||||||||||||||
Db        531 CATACTTCTTCATGCT 516


RESULT 11
US-11-183-218-9/c
; Sequence 9, Application US/11183218
; Publication No. US20060088906A1
; GENERAL INFORMATION:
;  APPLICANT: Neose Technologies, Inc.
;  APPLICANT:  DeFrees, Shawn
;  APPLICANT:  Zopf, David
;  APPLICANT:  Bayer, Robert
;  APPLICANT:  Hakes, David
;  APPLICANT:  Chen, Xi
;  APPLICANT:  Bowe, Caryne
;  TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND
;  TITLE OF INVENTION: GLYCOCONJUGATION OF ERYTHROPOIETIN
;  FILE REFERENCE: 040853-01-5083-US02
;  CURRENT APPLICATION NUMBER: US/11/183,218
;  CURRENT FILING DATE:  2005-07-15
;  PRIOR APPLICATION NUMBER: US 10/410,945
;  PRIOR FILING DATE: 2003-04-09
;  PRIOR APPLICATION NUMBER: PCT/US02/32263
;  PRIOR FILING DATE: 2002-10-09
;  PRIOR APPLICATION NUMBER: US 60/407,527
;  PRIOR FILING DATE: 2002-08-28
;  PRIOR APPLICATION NUMBER: US 60/404,249
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;  PRIOR FILING DATE: 2002-08-16
;  PRIOR APPLICATION NUMBER: US 60/396,594
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: US 60/391,777
;  PRIOR FILING DATE: 2002-06-25
;  PRIOR APPLICATION NUMBER: US 60/387,292
;  PRIOR FILING DATE: 2002-06-07
;  PRIOR APPLICATION NUMBER: US 60/344,692
;  PRIOR FILING DATE: 2001-11-19
;  PRIOR APPLICATION NUMBER: US 60/334,301
;  PRIOR FILING DATE: 2001-11-28
;  PRIOR APPLICATION NUMBER: US 60/334,233
;  PRIOR FILING DATE: 2001-11-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
;   LENGTH: 1437
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-183-218-9

  Query Match             2.7%;  Score 16;  DB 7;  Length 1437;
  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        377 ATCCTAAAAGGCAGAT 392
              ||||||||||||||||
Db         64 ATCCTAAAAGGCAGAT 49


RESULT 12
US-10-471-571A-2411
; Sequence 2411, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 2411
;   LENGTH: 1536
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-2411

  Query Match             2.7%;  Score 16;  DB 6;  Length 1536;
  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        500 ATAAAACTAAAATCAA 515
              ||||||||||||||||
Db        983 ATAAAACTAAAATCAA 998


RESULT 13
US-10-953-349-16963
; Sequence 16963, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16963
;   LENGTH: 1575
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-16963

  Query Match             2.7%;  Score 16;  DB 6;  Length 1575;
  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        344 AGTTCAAGGCCATGAA 359
              ||||||||||||||||
Db        613 AGTTCAAGGCCATGAA 628


RESULT 14
US-10-953-349-34653
; Sequence 34653, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34653
;   LENGTH: 1676
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-34653

  Query Match             2.7%;  Score 16;  DB 6;  Length 1676;
  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        144 TCATGAAGATATCACA 159
              ||||||||||||||||
Db       1426 TCATGAAGATATCACA 1441


RESULT 15
US-11-293-697-326
; Sequence 326, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 326
;   LENGTH: 1859
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-326

  Query Match             2.7%;  Score 16;  DB 7;  Length 1859;
  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        334 TACCAGGTGGAGTTCA 349
              ||||||||||||||||
Db        386 TACCAGGTGGAGTTCA 401


RESULT 16
```

US-11-217-529-78920/c
; Sequence 78920, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78920
; LENGTH: 1944
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78920

Query Match 2.7%; Score 16; DB 7; Length 1944;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 71 GAGCCATCAGCAACAC 86
||||||||||||||||
Db 1790 GAGCCATCAGCAACAC 1775

RESULT 17
US-10-511-937-2883/c
; Sequence 2883, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2883
; LENGTH: 2243
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (39)..(39)
; OTHER INFORMATION: n is a, c, g, t or u
US-10-511-937-2883

Query Match 2.7%; Score 16; DB 6; Length 2243;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 208 ATGAATGAGAGTTGCC 223
||||||||||||||||
Db 560 ATGAATGAGAGTTGCC 545

RESULT 18
US-11-293-697-520/c
; Sequence 520, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 520
; LENGTH: 2836
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-520

Query Match 2.7%; Score 16; DB 7; Length 2836;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 387 GCAGATCTTTCTGGAT 402
||||||||||||||||
Db 2681 GCAGATCTTTCTGGAT 2666

RESULT 19
US-11-217-529-76344
; Sequence 76344, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76344
; LENGTH: 4293
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76344

Query Match 2.7%; Score 16; DB 7; Length 4293;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 420 TATTGATGAGCTGTTA 435
||||||||||||||||
Db 1146 TATTGATGAGCTGTTA 1161

RESULT 20
US-11-248-986-13/c
; Sequence 13, Application US/11248986
; Publication No. US20060112448A1
; GENERAL INFORMATION:

```
;  APPLICANT: OSBOURN, ANNE E.
;  APPLICANT:  QI, XIAOQUAN
;  TITLE OF INVENTION: ENZYMES INVOLVED IN TRITERPENE SYNTHESIS
;  FILE REFERENCE: BB1550 US NA
;  CURRENT APPLICATION NUMBER: US/11/248,986
;  CURRENT FILING DATE:  2005-10-12
;  PRIOR APPLICATION NUMBER: 60/619,203
;  PRIOR FILING DATE: 2004-10-15
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
;   LENGTH: 5992
;   TYPE: DNA
;   ORGANISM: Avena strigosa
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(5992)
;   OTHER INFORMATION: Genomic sequence for AsCYP51H
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(5992)
;   OTHER INFORMATION: Genomic sequence for AsCYP51H10
US-11-248-986-13

  Query Match             2.7%;  Score 16;  DB 7;  Length 5992;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         502 AAAACTAAAATCAAGC 517
               ||||||||||||||||
Db        2978 AAAACTAAAATCAAGC 2963


RESULT 21
US-10-511-937-2838
; Sequence 2838, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
;  APPLICANT: EXPRESSION DIAGNOSTICS, INC.
;  APPLICANT:  Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  APPLICANT:  Prentice, James
;  APPLICANT:  Morris, MacDonald
;  APPLICANT:  Rosenberg, Steven
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
;  TITLE OF INVENTION:  AND MONITORING TRANSPLANT REJECTION
;  FILE REFERENCE: 506612000104
;  CURRENT APPLICATION NUMBER: US/10/511,937
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: PCT/US2003/012946
;  PRIOR FILING DATE: 2003-04-24
;  PRIOR APPLICATION NUMBER: US 10/131,831
;  PRIOR FILING DATE: 2002-04-24
;  PRIOR APPLICATION NUMBER: US 10/325,899
;  PRIOR FILING DATE: 2002-12-20
;  NUMBER OF SEQ ID NOS: 3117
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2838
;   LENGTH: 6383
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-511-937-2838

  Query Match             2.7%;  Score 16;  DB 6;  Length 6383;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         274 AGAAAGACCTCTTTTA 289
               ||||||||||||||||
Db         438 AGAAAGACCTCTTTTA 453


RESULT 22
US-10-489-730-10
; GENERAL INFORMATION:
;  APPLICANT: Melino, Gennaro
;  APPLICANT:  Hayes, Ian
;  APPLICANT:  de Laurenzi, Vincenzo
;  APPLICANT:  Barcaroli, Daniela
;  APPLICANT:  Candi, Eleonora
;  APPLICANT:  Bernassola, Francesca
;  APPLICANT:  Tobler, Andreas
;  APPLICANT:  Novak, Urban
;  TITLE OF INVENTION: Human Delta-N p73 Molecules and Uses Thereof
;  FILE REFERENCE: 19319.002
;  CURRENT APPLICATION NUMBER: US/10/489,730
;  CURRENT FILING DATE:  2004-03-16
;  PRIOR APPLICATION NUMBER: PCT/GB02/04238
;  PRIOR FILING DATE: 2002-09-17
;  PRIOR APPLICATION NUMBER: US 60/322,436
;  PRIOR FILING DATE: 2001-09-17
;  NUMBER OF SEQ ID NOS: 39
;   OTHER INFORMATION: reverse complement of exons 14 through 1 as reported in GenBank Ac
US-10-489-730-10

  Query Match             2.7%;  Score 16;  DB 6;  Length 138941;
  Best Local Similarity   100.0%;  Pred. No. 29;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          90 TCAGAAGGCCAGACAA 105
               ||||||||||||||||
Db       28208 TCAGAAGGCCAGACAA 28223


RESULT 23
US-10-489-730-10/c
; GENERAL INFORMATION:
;  APPLICANT: Melino, Gennaro
;  APPLICANT:  Hayes, Ian
;  APPLICANT:  de Laurenzi, Vincenzo
;  APPLICANT:  Barcaroli, Daniela
;  APPLICANT:  Candi, Eleonora
;  APPLICANT:  Bernassola, Francesca
;  APPLICANT:  Tobler, Andreas
;  APPLICANT:  Novak, Urban
;  TITLE OF INVENTION: Human Delta-N p73 Molecules and Uses Thereof
;  FILE REFERENCE: 19319.002
;  CURRENT APPLICATION NUMBER: US/10/489,730
;  CURRENT FILING DATE:  2004-03-16
;  PRIOR APPLICATION NUMBER: PCT/GB02/04238
;  PRIOR FILING DATE: 2002-09-17
;  PRIOR APPLICATION NUMBER: US 60/322,436
;  PRIOR FILING DATE: 2001-09-17
;  NUMBER OF SEQ ID NOS: 39
;   OTHER INFORMATION: reverse complement of exons 14 through 1 as reported in GenBank Ac
US-10-489-730-10

  Query Match             2.7%;  Score 16;  DB 6;  Length 138941;
  Best Local Similarity   100.0%;  Pred. No. 29;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         495 TTTTTATAAAACTAAA 510
               ||||||||||||||||
Db       33604 TTTTTATAAAACTAAA 33589


RESULT 24
US-11-217-529-105697/c
; Sequence 105697, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
```

; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 105697
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-105697

Query Match 2.5%; Score 15; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 339 GGTGGAGTTCAAGGC 353
||||||||||||||
Db 17 GGTGGAGTTCAAGGC 3

RESULT 25
US-11-217-529-155757
; Sequence 155757, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 155757
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-155757

Query Match 2.5%; Score 15; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 518 TCTGCATACTTCTTC 532
|||||||||||||||
Db 5 TCTGCATACTTCTTC 19

RESULT 26
US-11-217-529-191540/c
; Sequence 191540, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 191540
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-191540

Query Match 2.5%; Score 15; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 147 TGAAGATATCACAAA 161
|||||||||||||||
Db 19 TGAAGATATCACAAA 5

RESULT 27
US-11-217-529-191845/c
; Sequence 191845, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 191845
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-191845

Query Match 2.5%; Score 15; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 235 GAGATCTCTCTGATA 249
|||||||||||||||
Db 17 GAGATCTCTCTGATA 3

RESULT 28
US-10-488-619-2364/c
; Sequence 2364, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations W
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2364
; LENGTH: 400
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2364

```
  Query Match             2.5%;  Score 15;  DB 6;  Length 400;
  Best Local Similarity   100.0%;  Pred. No. 82;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        444 GAATGTCAACAGTGT 458
              |||||||||||||||
Db        285 GAATGTCAACAGTGT 271


RESULT 29
US-10-488-619-857
; Sequence 857, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 857
;   LENGTH: 418
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(418)
;   OTHER INFORMATION: n is g, c, a or t
US-10-488-619-857

  Query Match             2.5%;  Score 15;  DB 6;  Length 418;
  Best Local Similarity   100.0%;  Pred. No. 82;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        207 CATGAATGAGAGTTG 221
              |||||||||||||||
Db         24 CATGAATGAGAGTTG 38


RESULT 30
US-10-473-173-354
; Sequence 354, Application US/10473173
; Publication No. US20060088823A1
; GENERAL INFORMATION:
;  APPLICANT: VAN ANDEL INSTITUTE
;  TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell
;  TITLE OF INVENTION:  Carcinoma: Prognosis and Drug Target Identification
;  FILE REFERENCE: 38345-170094
;  CURRENT APPLICATION NUMBER: US/10/473,173
;  CURRENT FILING DATE:  2003-09-29
;  PRIOR APPLICATION NUMBER: US 60/279,411
;  PRIOR FILING DATE: 2001-03-29
;  NUMBER OF SEQ ID NOS: 498
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 354
;   LENGTH: 425
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: n can be a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (23)..(24)
;   OTHER INFORMATION: n can be a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (425)..(425)
;   OTHER INFORMATION: n can be a, c, g or t
US-10-473-173-354

  Query Match             2.5%;  Score 15;  DB 6;  Length 425;
  Best Local Similarity   100.0%;  Pred. No. 83;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        207 CATGAATGAGAGTTG 221
              |||||||||||||||
Db         26 CATGAATGAGAGTTG 40


RESULT 31
US-10-488-619-858
; Sequence 858, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations W
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 858
;   LENGTH: 425
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(425)
;   OTHER INFORMATION: n is g, a, c or t
US-10-488-619-858

  Query Match             2.5%;  Score 15;  DB 6;  Length 425;
  Best Local Similarity   100.0%;  Pred. No. 83;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        207 CATGAATGAGAGTTG 221
              |||||||||||||||
Db         26 CATGAATGAGAGTTG 40


RESULT 32
US-11-217-529-190905
; Sequence 190905, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 190905
;   LENGTH: 429
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-190905

  Query Match             2.5%;  Score 15;  DB 7;  Length 429;
  Best Local Similarity   100.0%;  Pred. No. 83;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 CCCACACCCACACCA 24
```

```
                ||||||||||||||||
Db        112 CCCACACCCACACCA 126


RESULT 33
US-10-488-619-2365
; Sequence 2365, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2365
;   LENGTH: 438
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(438)
;   OTHER INFORMATION: n is g, c, a or t
US-10-488-619-2365

  Query Match             2.5%;  Score 15;  DB 6;  Length 438;
  Best Local Similarity   100.0%;  Pred. No. 83;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        444 GAATGTCAACAGTGT 458
                ||||||||||||||||
Db        105 GAATGTCAACAGTGT 119


RESULT 34
US-10-488-619-1356
; Sequence 1356, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1356
;   LENGTH: 441
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-488-619-1356

  Query Match             2.5%;  Score 15;  DB 6;  Length 441;
  Best Local Similarity   100.0%;  Pred. No. 83;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        158 CAAAAGATAAAACCA 172
                ||||||||||||||||
Db        121 CAAAAGATAAAACCA 135


RESULT 35
US-11-217-529-166946
; Sequence 166946, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 166946
;   LENGTH: 459
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-166946

  Query Match             2.5%;  Score 15;  DB 7;  Length 459;
  Best Local Similarity   100.0%;  Pred. No. 83;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 CCCACACCCACACCA 24
                ||||||||||||||||
Db         56 CCCACACCCACACCA 70


RESULT 36
US-11-217-529-190985
; Sequence 190985, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 190985
;   LENGTH: 462
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-190985

  Query Match             2.5%;  Score 15;  DB 7;  Length 462;
  Best Local Similarity   100.0%;  Pred. No. 83;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 CCCACACCCACACCA 24
                ||||||||||||||||
Db        121 CCCACACCCACACCA 135


RESULT 37
US-11-217-529-81573
; Sequence 81573, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
```

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;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81573
;   LENGTH: 507
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-81573

  Query Match             2.5%;  Score 15;  DB 7;  Length 507;
  Best Local Similarity   100.0%;  Pred. No. 83;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        560 TCAATAGAATGATGA 574
              |||||||||||||||
Db         23 TCAATAGAATGATGA 37


RESULT 38
US-11-217-529-79785
; Sequence 79785, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79785
;   LENGTH: 510
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-79785

  Query Match             2.5%;  Score 15;  DB 7;  Length 510;
  Best Local Similarity   100.0%;  Pred. No. 83;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        131 CCGAAGAGATTGATC 145
              |||||||||||||||
Db         80 CCGAAGAGATTGATC 94


RESULT 39
US-11-217-529-81860
; Sequence 81860, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81860
;   LENGTH: 576
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-81860

  Query Match             2.5%;  Score 15;  DB 7;  Length 576;
  Best Local Similarity   100.0%;  Pred. No. 84;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        518 TCTGCATACTTCTTC 532
              |||||||||||||||
Db        328 TCTGCATACTTCTTC 342


RESULT 40
US-10-953-349-39845/c
; Sequence 39845, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39845
;   LENGTH: 608
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-39845

  Query Match             2.5%;  Score 15;  DB 6;  Length 608;
  Best Local Similarity   100.0%;  Pred. No. 84;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        237 GATCTCTCTGATAAC 251
              |||||||||||||||
Db         67 GATCTCTCTGATAAC 53


RESULT 41
US-11-217-529-77395/c
; Sequence 77395, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77395
;   LENGTH: 612
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-77395

  Query Match             2.5%;  Score 15;  DB 7;  Length 612;
  Best Local Similarity   100.0%;  Pred. No. 84;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        339 GGTGGAGTTCAAGGC 353
```

```
              ||||||||||||||||
Db         24 GGTGGAGTTCAAGGC 10


RESULT 42
US-10-488-619-2292/c
; Sequence 2292, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2292
;   LENGTH: 624
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-488-619-2292

  Query Match             2.5%;  Score 15;  DB 6;  Length 624;
  Best Local Similarity   100.0%;  Pred. No. 84;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        477 CTCCTTGGAAGAACC 491
              ||||||||||||||||
Db         51 CTCCTTGGAAGAACC 37


RESULT 43
US-10-953-349-12334
; Sequence 12334, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12334
;   LENGTH: 630
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (591)..(591)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-12334

  Query Match             2.5%;  Score 15;  DB 6;  Length 630;
  Best Local Similarity   100.0%;  Pred. No. 84;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         51 CCACTCCCAAACCCT 65
              ||||||||||||||||
Db         14 CCACTCCCAAACCCT 28


RESULT 44
US-10-953-349-25972
; Sequence 25972, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25972
;   LENGTH: 630
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-10-953-349-25972

  Query Match             2.5%;  Score 15;  DB 6;  Length 630;
  Best Local Similarity   100.0%;  Pred. No. 84;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         51 CCACTCCCAAACCCT 65
              ||||||||||||||||
Db         14 CCACTCCCAAACCCT 28


RESULT 45
US-11-217-529-190869/c
; Sequence 190869, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 190869
;   LENGTH: 768
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-190869

  Query Match             2.5%;  Score 15;  DB 7;  Length 768;
  Best Local Similarity   100.0%;  Pred. No. 85;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        235 GAGATCTCTCTGATA 249
              ||||||||||||||||
Db        163 GAGATCTCTCTGATA 149


RESULT 46
US-10-953-349-355
; Sequence 355, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 355
;   LENGTH: 778
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-355

  Query Match             2.5%;  Score 15;  DB 6;  Length 778;
```

```
  Best Local Similarity   100.0%;  Pred. No. 85;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        128 CTTCCGAAGAGATTG 142
              |||||||||||||||
Db         41 CTTCCGAAGAGATTG 55


RESULT 47
US-10-488-619-1355/c
; Sequence 1355, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1355
;   LENGTH: 782
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(782)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-488-619-1355

  Query Match             2.5%;  Score 15;  DB 6;  Length 782;
  Best Local Similarity   100.0%;  Pred. No. 85;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        158 CAAAAGATAAAACCA 172
              |||||||||||||||
Db        663 CAAAAGATAAAACCA 649


RESULT 48
US-10-953-349-33201
; Sequence 33201, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33201
;   LENGTH: 814
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-33201

  Query Match             2.5%;  Score 15;  DB 6;  Length 814;
  Best Local Similarity   100.0%;  Pred. No. 85;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 CCCACACCCACACCA 24
              |||||||||||||||
Db         39 CCCACACCCACACCA 53


RESULT 49
US-10-953-349-39705/c
; Sequence 39705, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39705
;   LENGTH: 830
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-39705

  Query Match             2.5%;  Score 15;  DB 6;  Length 830;
  Best Local Similarity   100.0%;  Pred. No. 85;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GAACCTCCCCACACC 17
              |||||||||||||||
Db        472 GAACCTCCCCACACC 458


RESULT 50
US-11-217-529-5224/c
; Sequence 5224, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5224
;   LENGTH: 906
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-5224

  Query Match             2.5%;  Score 15;  DB 7;  Length 906;
  Best Local Similarity   100.0%;  Pred. No. 85;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        301 TGCCTTAGCAGTATC 315
              |||||||||||||||
Db        852 TGCCTTAGCAGTATC 838


RESULT 51
US-11-217-529-174189
; Sequence 174189, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
```

; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174189
; LENGTH: 906
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-174189

Query Match 2.5%; Score 15; DB 7; Length 906;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 364 AAGCTGTTAATGGAT 378
||||||||||||||||
Db 614 AAGCTGTTAATGGAT 628

RESULT 52
US-10-953-349-39221
; Sequence 39221, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39221
; LENGTH: 1046
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
US-10-953-349-39221

Query Match 2.5%; Score 15; DB 6; Length 1046;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 406 AACATGCTGACAGCT 420
||||||||||||||||
Db 383 AACATGCTGACAGCT 397

RESULT 53
US-10-953-349-17993/c
; Sequence 17993, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17993
; LENGTH: 1124
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-17993

Query Match 2.5%; Score 15; DB 6; Length 1124;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 146 ATGAAGATATCACAA 160
||||||||||||||||
Db 883 ATGAAGATATCACAA 869

RESULT 54
US-10-953-349-32852
; Sequence 32852, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32852
; LENGTH: 1151
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
US-10-953-349-32852

Query Match 2.5%; Score 15; DB 6; Length 1151;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 CCACACCCACACCAA 25
||||||||||||||||
Db 517 CCACACCCACACCAA 531

RESULT 55
US-10-953-349-31118/c
; Sequence 31118, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31118
; LENGTH: 1156
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-953-349-31118

Query Match 2.5%; Score 15; DB 6; Length 1156;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 246 GATAACTAATGGGAG 260
||||||||||||||||
Db 1030 GATAACTAATGGGAG 1016

RESULT 56
US-11-217-529-79991
; Sequence 79991, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182

; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79991
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79991

Query Match 2.5%; Score 15; DB 7; Length 1176;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 206 CCATGAATGAGAGTT 220
||||||||||||||||
Db 842 CCATGAATGAGAGTT 856

RESULT 57
US-10-953-349-26534
; Sequence 26534, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26534
; LENGTH: 1190
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-953-349-26534

Query Match 2.5%; Score 15; DB 6; Length 1190;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 414 GACAGCTATTGATGA 428
||||||||||||||||
Db 884 GACAGCTATTGATGA 898

RESULT 58
US-10-953-349-19889
; Sequence 19889, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19889
; LENGTH: 1206
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-19889

Query Match 2.5%; Score 15; DB 6; Length 1206;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 509 AAATCAAGCTCTGCA 523
||||||||||||||||
Db 1008 AAATCAAGCTCTGCA 1022

RESULT 59
US-11-217-529-79181
; Sequence 79181, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79181
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79181

Query Match 2.5%; Score 15; DB 7; Length 1269;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 132 CGAAGAGATTGATCA 146
||||||||||||||||
Db 348 CGAAGAGATTGATCA 362

RESULT 60
US-10-953-349-32614
; Sequence 32614, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32614
; LENGTH: 1271
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-953-349-32614

Query Match 2.5%; Score 15; DB 6; Length 1271;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 345 GTTCAAGGCCATGAA 359
||||||||||||||||
Db 1052 GTTCAAGGCCATGAA 1066

RESULT 61
US-10-953-349-9401
; Sequence 9401, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349

```
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9401
;   LENGTH: 1302
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-9401

  Query Match             2.5%;  Score 15;  DB 6;  Length 1302;
  Best Local Similarity   100.0%;  Pred. No. 86;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        395 TTCTGGATCAAAACA 409
              |||||||||||||||
Db        546 TTCTGGATCAAAACA 560


RESULT 62
US-11-217-529-79465
; Sequence 79465, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79465
;   LENGTH: 1305
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-79465

  Query Match             2.5%;  Score 15;  DB 7;  Length 1305;
  Best Local Similarity   100.0%;  Pred. No. 86;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TATCACAAAAGATAA 167
              |||||||||||||||
Db       1291 TATCACAAAAGATAA 1305


RESULT 63
US-11-217-529-190840/c
; Sequence 190840, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 190840
;   LENGTH: 1404
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-190840

  Query Match             2.5%;  Score 15;  DB 7;  Length 1404;
  Best Local Similarity   100.0%;  Pred. No. 87;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        147 TGAAGATATCACAAA 161
              |||||||||||||||
Db        838 TGAAGATATCACAAA 824


RESULT 64
US-10-953-349-3438
; Sequence 3438, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3438
;   LENGTH: 1406
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-3438

  Query Match             2.5%;  Score 15;  DB 6;  Length 1406;
  Best Local Similarity   100.0%;  Pred. No. 87;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        366 GCTGTTAATGGATCC 380
              |||||||||||||||
Db        976 GCTGTTAATGGATCC 990


RESULT 65
US-10-953-349-31780
; Sequence 31780, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31780
;   LENGTH: 1451
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-10-953-349-31780

  Query Match             2.5%;  Score 15;  DB 6;  Length 1451;
  Best Local Similarity   100.0%;  Pred. No. 87;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 CCACACCAAGCCCAG 31
              |||||||||||||||
Db        480 CCACACCAAGCCCAG 494


RESULT 66
US-10-953-349-20272/c
; Sequence 20272, Application US/10953349
; Publication No. US20060107345A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20272
;   LENGTH: 1493
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-20272

  Query Match             2.5%;  Score 15;  DB 6;  Length 1493;
  Best Local Similarity   100.0%;  Pred. No. 87;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        166 AAAACCAGCACAGTG 180
              |||||||||||||||
Db        184 AAAACCAGCACAGTG 170


RESULT 67
US-10-953-349-10170
; Sequence 10170, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10170
;   LENGTH: 1504
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-10170

  Query Match             2.5%;  Score 15;  DB 6;  Length 1504;
  Best Local Similarity   100.0%;  Pred. No. 87;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        395 TTCTGGATCAAAACA 409
              |||||||||||||||
Db        583 TTCTGGATCAAAACA 597


RESULT 68
US-10-953-349-34123
; Sequence 34123, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34123
;   LENGTH: 1511
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-34123

  Query Match             2.5%;  Score 15;  DB 6;  Length 1511;
  Best Local Similarity   100.0%;  Pred. No. 87;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 CCCCACACCCACACC 23
              |||||||||||||||
Db       1045 CCCCACACCCACACC 1059


RESULT 69
US-11-217-529-1240/c
; Sequence 1240, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1240
;   LENGTH: 1551
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-1240

  Query Match             2.5%;  Score 15;  DB 7;  Length 1551;
  Best Local Similarity   100.0%;  Pred. No. 87;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        150 AGATATCACAAAAGA 164
              |||||||||||||||
Db        673 AGATATCACAAAAGA 659


RESULT 70
US-10-953-349-33142/c
; Sequence 33142, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33142
;   LENGTH: 1578
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-33142

  Query Match             2.5%;  Score 15;  DB 6;  Length 1578;
  Best Local Similarity   100.0%;  Pred. No. 87;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        481 TTGGAAGAACCGGAT 495
              |||||||||||||||
Db         90 TTGGAAGAACCGGAT 76


RESULT 71
US-10-953-349-1943
; Sequence 1943, Application US/10953349
; Publication No. US20060107345A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1943
;   LENGTH: 1821
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-1943

  Query Match             2.5%;  Score 15;  DB 6;  Length 1821;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        417 AGCTATTGATGAGCT 431
              |||||||||||||||
Db        600 AGCTATTGATGAGCT 614


RESULT 72
US-10-953-349-12445
; Sequence 12445, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12445
;   LENGTH: 1869
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (532)..(532)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-12445

  Query Match             2.5%;  Score 15;  DB 6;  Length 1869;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        222 CCTGGCTTCCAGAGA 236
              |||||||||||||||
Db        144 CCTGGCTTCCAGAGA 158


RESULT 73
US-11-293-697-2269
; Sequence 2269, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2269
;   LENGTH: 1902
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-2269

  Query Match             2.5%;  Score 15;  DB 7;  Length 1902;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        451 AACAGTGTGACTGTG 465
              |||||||||||||||
Db        235 AACAGTGTGACTGTG 249


RESULT 74
US-11-293-697-773/c
; Sequence 773, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 773
;   LENGTH: 2043
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-773

  Query Match             2.5%;  Score 15;  DB 7;  Length 2043;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        245 TGATAACTAATGGGA 259
              |||||||||||||||
Db        802 TGATAACTAATGGGA 788


RESULT 75
US-10-953-349-11750/c
; Sequence 11750, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11750
;   LENGTH: 2105
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-11750

  Query Match             2.5%;  Score 15;  DB 6;  Length 2105;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         19 ACACCAAGCCCAGGA 33
              |||||||||||||||
Db       2085 ACACCAAGCCCAGGA 2071


RESULT 76
US-11-293-697-153
; Sequence 153, Application US/11293697
; Publication No. US20060105376A1
```

; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 153
; LENGTH: 2151
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-153

Query Match 2.5%; Score 15; DB 7; Length 2151;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 ACCCTGCTGCGAGCC 75
||||||||||||||||
Db 1116 ACCCTGCTGCGAGCC 1130

RESULT 77
US-11-293-697-56
; Sequence 56, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 2205
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-56

Query Match 2.5%; Score 15; DB 7; Length 2205;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 566 GAATGATGAGCTATC 580
||||||||||||||||
Db 1538 GAATGATGAGCTATC 1552

RESULT 78
US-11-217-529-2489
; Sequence 2489, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2489
; LENGTH: 2241
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-2489

Query Match 2.5%; Score 15; DB 7; Length 2241;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 322 GACTTGAAGATGTAC 336
||||||||||||||||
Db 1711 GACTTGAAGATGTAC 1725

RESULT 79
US-11-217-529-80988/c
; Sequence 80988, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80988
; LENGTH: 2400
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-80988

Query Match 2.5%; Score 15; DB 7; Length 2400;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 394 TTTCTGGATCAAAAC 408
||||||||||||||||
Db 472 TTTCTGGATCAAAAC 458

RESULT 80
US-11-293-697-2092/c
; Sequence 2092, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2092
; LENGTH: 2537
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-2092

Query Match 2.5%; Score 15; DB 7; Length 2537;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          44 GCCTCAACCACTCCC 58
               ||||||||||||||
Db        1344 GCCTCAACCACTCCC 1330


RESULT 81
US-11-217-529-1141
; Sequence 1141, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1141
;   LENGTH: 2553
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-1141

  Query Match             2.5%;  Score 15;  DB 7;  Length 2553;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         474 CTCCTCCTTGGAAGA 488
               |||||||||||||||
Db         402 CTCCTCCTTGGAAGA 416


RESULT 82
US-11-293-697-749/c
; Sequence 749, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 749
;   LENGTH: 2650
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-749

  Query Match             2.5%;  Score 15;  DB 7;  Length 2650;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         392 TCTTTCTGGATCAAA 406
               |||||||||||||||
Db        1786 TCTTTCTGGATCAAA 1772


RESULT 83
US-10-505-928-637/c
; Sequence 637, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
;  APPLICANT: Ludwig Institute for Cancer Research et al.
;  TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
;  FILE REFERENCE: 28967/39178
;  CURRENT APPLICATION NUMBER: US/10/505,928
;  CURRENT FILING DATE:  2004-08-27
;  PRIOR APPLICATION NUMBER: US 60/363,019
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: PatentIn 3.2
; SEQ ID NO 637
;   LENGTH: 3350
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-505-928-637

  Query Match             2.5%;  Score 15;  DB 6;  Length 3350;
  Best Local Similarity   100.0%;  Pred. No. 90;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           6 CCTCCCCACACCCAC 20
               |||||||||||||||
Db         973 CCTCCCCACACCCAC 959


RESULT 84
US-10-505-928-641/c
; Sequence 641, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
;  APPLICANT: Ludwig Institute for Cancer Research et al.
;  TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
;  FILE REFERENCE: 28967/39178
;  CURRENT APPLICATION NUMBER: US/10/505,928
;  CURRENT FILING DATE:  2004-08-27
;  PRIOR APPLICATION NUMBER: US 60/363,019
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: PatentIn 3.2
; SEQ ID NO 641
;   LENGTH: 3350
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-505-928-641

  Query Match             2.5%;  Score 15;  DB 6;  Length 3350;
  Best Local Similarity   100.0%;  Pred. No. 90;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           6 CCTCCCCACACCCAC 20
               |||||||||||||||
Db         973 CCTCCCCACACCCAC 959


RESULT 85
US-11-217-529-1172
; Sequence 1172, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1172
```

```
;   LENGTH: 4533
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-1172

  Query Match             2.5%;  Score 15;  DB 7;  Length 4533;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        138 GATTGATCATGAAGA 152
              ||||||||||||||||
Db       2550 GATTGATCATGAAGA 2564


RESULT 86
US-10-501-834-216
; Sequence 216, Application US/10501834
; Publication No. US20060088828A1
; GENERAL INFORMATION:
;  APPLICANT: Harris, Peter C., Ward, Christopher J., Rossetti, Sandro, and Torres,
;  APPLICANT:  Vicente E.
;  TITLE OF INVENTION: Polycystic Kidney Disease Nucleic Acids
;  TITLE OF INVENTION:  and Proteins
;  FILE REFERENCE: 07039/386US1
;  CURRENT APPLICATION NUMBER: US/10/501,834
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: PCT/US03/02038
;  PRIOR FILING DATE: 2003-01-23
;  PRIOR APPLICATION NUMBER: 60/351,110
;  PRIOR FILING DATE: 2002-01-23
;  NUMBER OF SEQ ID NOS: 221
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 216
;   LENGTH: 5171
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-501-834-216

  Query Match             2.5%;  Score 15;  DB 6;  Length 5171;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        461 CTGTGCCACAGAACT 475
              ||||||||||||||||
Db       2813 CTGTGCCACAGAACT 2827


RESULT 87
US-11-217-529-191092
; Sequence 191092, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 191092
;   LENGTH: 5703
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-191092

  Query Match             2.5%;  Score 15;  DB 7;  Length 5703;
  Best Local Similarity   100.0%;  Pred. No. 92;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        364 AAGCTGTTAATGGAT 378
              |||||||||||||||
Db       5123 AAGCTGTTAATGGAT 5137


RESULT 88
US-10-505-928-28/c
; Sequence 28, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
;  APPLICANT: Ludwig Institute for Cancer Research et al.
;  TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
;  FILE REFERENCE: 28967/39178
;  CURRENT APPLICATION NUMBER: US/10/505,928
;  CURRENT FILING DATE:  2004-08-27
;  PRIOR APPLICATION NUMBER: US 60/363,019
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: PatentIn 3.2
; SEQ ID NO 28
;   LENGTH: 5734
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-505-928-28

  Query Match             2.5%;  Score 15;  DB 6;  Length 5734;
  Best Local Similarity   100.0%;  Pred. No. 92;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        458 TGACTGTGCCACAGA 472
              |||||||||||||||
Db       5362 TGACTGTGCCACAGA 5348


RESULT 89
US-10-199-229-1
; Sequence 1, Application US/10199229
; Publication No. US20060099701A1
; GENERAL INFORMATION:
;  APPLICANT: She, Jin-Xiong
;  APPLICANT:  Kumar, Pradeep
;  APPLICANT:  Wang, Cong-Yi
;  TITLE OF INVENTION: ACTIVATORS OF CYCLIN-DEPENDENT KINASES
;  FILE REFERENCE: 5853-210
;  CURRENT APPLICATION NUMBER: US/10/199,229
;  CURRENT FILING DATE:  2002-07-19
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 5747
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-199-229-1

  Query Match             2.5%;  Score 15;  DB 6;  Length 5747;
  Best Local Similarity   100.0%;  Pred. No. 92;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 ACCTCCCCACACCCA 19
              |||||||||||||||
Db       4618 ACCTCCCCACACCCA 4632


RESULT 90
US-10-505-928-330/c
; Sequence 330, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
;  APPLICANT: Ludwig Institute for Cancer Research et al.
;  TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
```

```
;  FILE REFERENCE: 28967/39178
;  CURRENT APPLICATION NUMBER: US/10/505,928
;  CURRENT FILING DATE:  2004-08-27
;  PRIOR APPLICATION NUMBER: US 60/363,019
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: PatentIn 3.2
; SEQ ID NO 330
;   LENGTH: 6826
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-505-928-330

  Query Match             2.5%;  Score 15;  DB 6;  Length 6826;
  Best Local Similarity   100.0%;  Pred. No. 92;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         51 CCACTCCCAAACCCT 65
              |||||||||||||||
Db       5759 CCACTCCCAAACCCT 5745


RESULT 91
US-10-505-928-151
; Sequence 151, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
;  APPLICANT: Ludwig Institute for Cancer Research et al.
;  TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
;  FILE REFERENCE: 28967/39178
;  CURRENT APPLICATION NUMBER: US/10/505,928
;  CURRENT FILING DATE:  2004-08-27
;  PRIOR APPLICATION NUMBER: US 60/363,019
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: PatentIn 3.2
; SEQ ID NO 151
;   LENGTH: 128361
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-505-928-151

  Query Match             2.5%;  Score 15;  DB 6;  Length 128361;
  Best Local Similarity   100.0%;  Pred. No. 99;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        345 GTTCAAGGCCATGAA 359
              |||||||||||||||
Db     117581 GTTCAAGGCCATGAA 117595


RESULT 92
US-11-260-842-1
; Sequence 1, Application US/11260842
; Publication No. US20060115845A1
; GENERAL INFORMATION:
;  APPLICANT: Vance, Jeffrey M.
;  APPLICANT:  Kraus, William E.
;  APPLICANT:  Goldschmidt, Pascal J.
;  APPLICANT:  Gregory, Simon G.
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING GENETIC MARKERS WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISEASE
;  FILE REFERENCE: 5405-347
;  CURRENT APPLICATION NUMBER: US/11/260,842
;  CURRENT FILING DATE:  2005-10-27
;  PRIOR APPLICATION NUMBER: US 60/662,447
;  PRIOR FILING DATE: 2004-10-27
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
;   LENGTH: 261789
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-260-842-1

  Query Match             2.5%;  Score 15;  DB 7;  Length 261789;
  Best Local Similarity   100.0%;  Pred. No. 96;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         32 GAATGTTCCAGTGCC 46
              |||||||||||||||
Db       9649 GAATGTTCCAGTGCC 9663


RESULT 93
US-11-260-842-1/c
; Sequence 1, Application US/11260842
; Publication No. US20060115845A1
; GENERAL INFORMATION:
;  APPLICANT: Vance, Jeffrey M.
;  APPLICANT:  Kraus, William E.
;  APPLICANT:  Goldschmidt, Pascal J.
;  APPLICANT:  Gregory, Simon G.
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING GENETIC MARKERS WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISEASE
;  FILE REFERENCE: 5405-347
;  CURRENT APPLICATION NUMBER: US/11/260,842
;  CURRENT FILING DATE:  2005-10-27
;  PRIOR APPLICATION NUMBER: US 60/662,447
;  PRIOR FILING DATE: 2004-10-27
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
;   LENGTH: 261789
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-260-842-1

  Query Match             2.5%;  Score 15;  DB 7;  Length 261789;
  Best Local Similarity   100.0%;  Pred. No. 96;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        558 CATCAATAGAATGAT 572
              |||||||||||||||
Db      29696 CATCAATAGAATGAT 29682


RESULT 94
US-11-217-529-26117
; Sequence 26117, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26117
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-26117

  Query Match             2.4%;  Score 14;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy        444 GAATGTCAACAGTG 457
              ||||||||||||||
Db          1 GAATGTCAACAGTG 14


RESULT 95
US-11-217-529-40959
; Sequence 40959, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 40959
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-40959

  Query Match             2.4%;  Score 14;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         42 GTGCCTCAACCACT 55
              ||||||||||||||
Db         11 GTGCCTCAACCACT 24


RESULT 96
US-11-217-529-124406
; Sequence 124406, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 124406
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-124406

  Query Match             2.4%;  Score 14;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        189 CTTACCACTGGAAT 202
              ||||||||||||||
Db          2 CTTACCACTGGAAT 15


RESULT 97
US-11-217-529-136455/c
; Sequence 136455, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 136455
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-136455

  Query Match             2.4%;  Score 14;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        294 GACCCTGTGCCTTA 307
              ||||||||||||||
Db         23 GACCCTGTGCCTTA 10


RESULT 98
US-11-217-529-148494/c
; Sequence 148494, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 148494
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-148494

  Query Match             2.4%;  Score 14;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        326 TGAAGATGTACCAG 339
              ||||||||||||||
Db         16 TGAAGATGTACCAG 3


RESULT 99
US-10-511-937-3058/c
; Sequence 3058, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: EXPRESSION DIAGNOSTICS, INC.
;  APPLICANT:  Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  APPLICANT:  Prentice, James
;  APPLICANT:  Morris, MacDonald
;  APPLICANT:  Rosenberg, Steven
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
;  TITLE OF INVENTION:  AND MONITORING TRANSPLANT REJECTION
;  FILE REFERENCE: 506612000104
;  CURRENT APPLICATION NUMBER: US/10/511,937
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: PCT/US2003/012946
;  PRIOR FILING DATE: 2003-04-24
;  PRIOR APPLICATION NUMBER: US 10/131,831
;  PRIOR FILING DATE: 2002-04-24
;  PRIOR APPLICATION NUMBER: US 10/325,899
;  PRIOR FILING DATE: 2002-12-20
;  NUMBER OF SEQ ID NOS: 3117
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3058
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-511-937-3058

  Query Match             2.4%;  Score 14;  DB 6;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        162 AGATAAAACCAGCA 175
              ||||||||||||||
Db         41 AGATAAAACCAGCA 28


RESULT 100
US-10-471-571A-1747/c
; Sequence 1747, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 1747
;   LENGTH: 258
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-1747

  Query Match             2.4%;  Score 14;  DB 6;  Length 258;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        499 TATAAAACTAAAAT 512
              ||||||||||||||
Db         92 TATAAAACTAAAAT 79


Search completed: June  9, 2006, 23:43:21
Job time : 15.6742 secs
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 12, 2006, 15:14:42 ; Search time 2671.26 Seconds
(without alignments)
7073.997 Million cell updates/sec

Title: US-10-821-670A-36
Perfect score: 1001
Sequence: 1 RNLPTPTPSPGMFQCLNHSQ.....HAFRIRAVTINRMMSYLNAS 197

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/abss/ABSSWEB_spool/US10821670/runat_07062006_110102_26152/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss06h
-USER=US10821670_@CGN_1_1_5308_@runat_07062006_110102_26152 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1001	100.0	591	2	AR595954	AR595954 Sequence
c 2	1001	100.0	591	2	AR595955	AR595955 Sequence
3	1001	100.0	666	2	AR595952	AR595952 Sequence
c 4	1001	100.0	666	2	AR595953	AR595953 Sequence
5	1001	100.0	669	14	FCIL12P35	Y07761 Felis catus
6	1001	100.0	1533	2	AR595959	AR595959 Sequence
c 7	1001	100.0	1533	2	AR595960	AR595960 Sequence
8	1001	100.0	1599	2	AR595956	AR595956 Sequence
c 9	1001	100.0	1599	2	AR595957	AR595957 Sequence
10	998	99.7	591	2	AR242439	AR242439 Sequence
11	998	99.7	591	2	AR280207	AR280207 Sequence
12	998	99.7	591	2	AR322422	AR322422 Sequence
13	998	99.7	689	2	AR242451	AR242451 Sequence
14	998	99.7	689	2	AR280219	AR280219 Sequence
15	998	99.7	689	2	AR322434	AR322434 Sequence
16	998	99.7	1441	2	AR242438	AR242438 Sequence
17	998	99.7	1441	2	AR280206	AR280206 Sequence
18	998	99.7	1441	2	AR322421	AR322421 Sequence
19	993	99.2	669	14	FCU83185	U83185 Felis catus
20	980	97.9	669	2	AX076201	AX076201 Sequence
21	980	97.9	669	2	AX076483	AX076483 Sequence
22	980	97.9	4201	2	AX076477	AX076477 Sequence
23	960	95.9	1533	2	AR595973	AR595973 Sequence
c 24	960	95.9	1533	2	AR595974	AR595974 Sequence
25	960	95.9	1599	2	AR595971	AR595971 Sequence
c 26	960	95.9	1599	2	AR595972	AR595972 Sequence
27	944	94.3	561	2	AR596007	AR596007 Sequence
c 28	944	94.3	561	2	AR596008	AR596008 Sequence
29	929	92.8	591	2	BD171284	BD171284 Novel can
30	929	92.8	591	2	AR595963	AR595963 Sequence
c 31	929	92.8	591	2	AR595964	AR595964 Sequence
32	929	92.8	666	2	AR595961	AR595961 Sequence
c 33	929	92.8	666	2	AR595962	AR595962 Sequence
34	929	92.8	669	2	AR151072	AR151072 Sequence
35	929	92.8	669	2	BD014664	BD014664 Process f
36	929	92.8	669	2	E15018	E15018 Canine mRNA
37	929	92.8	669	2	AR316471	AR316471 Sequence
38	929	92.8	1282	2	BD171283	BD171283 Novel can
39	929	92.8	1455	2	AR596009	AR596009 Sequence
c 40	929	92.8	1455	2	AR596010	AR596010 Sequence
41	924	92.3	669	2	AR151062	AR151062 Sequence
42	924	92.3	669	2	BD014654	BD014654 Process f
43	924	92.3	669	2	AR316461	AR316461 Sequence
44	916	91.5	669	14	CFU49085	U49085 Canis famil
45	910	90.9	657	8	AY191828	AY191828 Synthetic

ALIGNMENTS

RESULT 1
AR595954
LOCUS AR595954 591 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 35 from patent US 6818444.
ACCESSION AR595954
VERSION AR595954.1 GI:56646935
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 591)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 35 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .591
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.: 2.01e-104 Length: 591
Score: 1001.00 Matches: 197
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0

```
DB:                    2             Gaps:          0

US-10-821-670A-36 (1-197) x AR595954 (1-591)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591

RESULT 2
AR595955/c
LOCUS       AR595955                591 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 37 from patent US 6818444.
ACCESSION   AR595955
VERSION     AR595955.1  GI:56646936
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 37 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.01e-104       Length:         591
Score:                  1001.00         Matches:        197
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-36 (1-197) x AR595955 (1-591)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 3
AR595952
LOCUS       AR595952                666 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 32 from patent US 6818444.
ACCESSION   AR595952
VERSION     AR595952.1  GI:56646933
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 32 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.31e-104       Length:         666
Score:                  1001.00         Matches:        197
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-36 (1-197) x AR595952 (1-666)
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Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666
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RESULT 4
AR595953/c
LOCUS AR595953 666 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 34 from patent US 6818444.
ACCESSION AR595953
VERSION AR595953.1 GI:56646934
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 666)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 34 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .666
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Alignment Scores:

Pred. No.:	2.31e-104	Length:	666
Score:	1001.00	Matches:	197
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-36 (1-197) x AR595953 (1-666)

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Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
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RESULT 5
FCIL12P35
LOCUS FCIL12P35 669 bp mRNA linear MAM 18-APR-2005
DEFINITION Felis catus mRNA for interleukin-12 p35 chain.
ACCESSION Y07761
VERSION Y07761.1 GI:2102662
KEYWORDS interleukin-12 subunit p35.
SOURCE Felis catus (cat)
ORGANISM Felis catus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
Felinae; Felis.
REFERENCE 1
AUTHORS Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
TITLE Molecular cloning of cat interleukin-12
JOURNAL Immunogenetics 45 (6), 462-463 (1997)
PUBMED 9089110
REFERENCE 2 (bases 1 to 669)
AUTHORS Schijns,V.E.C.J.
TITLE Direct Submission
JOURNAL Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
Utrecht, NETHERLANDS
FEATURES Location/Qualifiers
source 1. .669
/organism="Felis catus"
/mol_type="mRNA"
/db_xref="taxon:9685"
/cell_type="lymphocyte"
/tissue_type="peripheral blood"
gene 1. .669
/gene="IL-12.p35"
CDS 1. .669
/gene="IL-12.p35"
/function="heterodimer with IL-12 p40 chain"

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                     /codon_start=1
                     /product="interleukin-12 p35 chain"
                     /protein_id="CAA69067.1"
                     /db_xref="GI:2102663"
                     /db_xref="GOA:O02743"
                     /db_xref="InterPro:IPR004281"
                     /db_xref="InterPro:IPR009079"
                     /db_xref="UniProtKB/Swiss-Prot:O02743"
                     /translation="MCPPRGLLLVTILVLLNHLDHLSLARNLPTPTPSPGMFQCLNHS
                     QTLLRAISNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
                     REISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAMNAKLLMDPKRQIFLDQ
                     NMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSY
                     LNAS"
ORIGIN

Alignment Scores:
Pred. No.:              2.32e-104       Length:         669
Score:                  1001.00         Matches:        197
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-36 (1-197) x FCIL12P35 (1-669)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666

RESULT 6
AR595959
LOCUS       AR595959               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 43 from patent US 6818444.
ACCESSION   AR595959
VERSION     AR595959.1  GI:56646940
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 43 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              6.07e-104       Length:         1533
Score:                  1001.00         Matches:        197
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-36 (1-197) x AR595959 (1-1533)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        943 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1002

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1003 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1062

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1122

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1123 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1182

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1183 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1242

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1243 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1302

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1303 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1362

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1363 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1422

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1423 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1482

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1483 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533

RESULT 7
AR595960/c
LOCUS       AR595960               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 45 from patent US 6818444.
ACCESSION   AR595960
VERSION     AR595960.1  GI:56646941
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
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REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 45 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                6.07e-104      Length:          1533
Score:                    1001.00        Matches:         197
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-36 (1-197) x AR595960 (1-1533)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
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Db        591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
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Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
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Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
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Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
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Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
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Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
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Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
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Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 8
AR595956
LOCUS       AR595956               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 38 from patent US 6818444.
ACCESSION   AR595956
VERSION     AR595956.1  GI:56646937
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 38 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                6.38e-104      Length:          1599
Score:                    1001.00        Matches:         197
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-36 (1-197) x AR595956 (1-1599)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
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Db       1009 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1068

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
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Db       1069 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1128

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
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Db       1129 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1188

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
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Db       1189 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1248

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
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Db       1249 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1308

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1309 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1368

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
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Db       1369 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1428

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
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Db       1429 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1488

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
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Db       1489 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1548

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
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Db       1549 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599

RESULT 9
AR595957/c
LOCUS       AR595957               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 40 from patent US 6818444.
ACCESSION   AR595957
VERSION     AR595957.1  GI:56646938
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 40 16-NOV-2004;
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          Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
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ORIGIN

Alignment Scores:
Pred. No.:                6.38e-104      Length:          1599
Score:                    1001.00        Matches:         197
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-36 (1-197) x AR595957 (1-1599)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
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Db        591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
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Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
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Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
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Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
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Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
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Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
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Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
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Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 10
AR242439
LOCUS       AR242439                 591 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 9 from patent US 6472509.
ACCESSION   AR242439
VERSION     AR242439.1  GI:27288856
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 9 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
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          EPX;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:                4.42e-104      Length:          591
Score:                    998.00         Matches:         196
Percent Similarity:       100.0%         Conservative:    1
Best Local Similarity:    99.5%          Mismatches:      0
Query Match:              99.7%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-36 (1-197) x AR242439 (1-591)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
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Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
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Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
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Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
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Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
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Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
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Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
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Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
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Db        481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
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Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 591

RESULT 11
AR280207
LOCUS       AR280207                 591 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 9 from patent US 6518045.
ACCESSION   AR280207
VERSION     AR280207.1  GI:29715597
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 9 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
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          EPX;
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              4.42e-104      Length:         591
Score:                  998.00         Matches:        196
Percent Similarity:     100.0%         Conservative:   1
Best Local Similarity:  99.5%          Mismatches:     0
Query Match:            99.7%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-36 (1-197) x AR280207 (1-591)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
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Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
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Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
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Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
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Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
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Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
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Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
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Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
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Db        481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||:::|||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 591

RESULT 12
AR322422
LOCUS       AR322422                 591 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 9 from patent US 6566097.
ACCESSION   AR322422
VERSION     AR322422.1  GI:33708175
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 9 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
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          EPX;
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              4.42e-104      Length:         591
Score:                  998.00         Matches:        196
Percent Similarity:     100.0%         Conservative:   1
Best Local Similarity:  99.5%          Mismatches:     0
Query Match:            99.7%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-36 (1-197) x AR322422 (1-591)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
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Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
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Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
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Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
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Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
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Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
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Db        481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
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Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 591

RESULT 13
AR242451
LOCUS       AR242451                 689 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 26 from patent US 6472509.
ACCESSION   AR242451
VERSION     AR242451.1  GI:27288868
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 26 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
```

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          EPX;
FEATURES             Location/Qualifiers
     source          1. .689
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              5.28e-104      Length:         689
Score:                  998.00         Matches:        196
Percent Similarity:     100.0%         Conservative:   1
Best Local Similarity:  99.5%          Mismatches:     0
Query Match:            99.7%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-36 (1-197) x AR242451 (1-689)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
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Db         82 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 141

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
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Db        142 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 201

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
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Db        202 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 261

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
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Db        262 GAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 321

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
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Db        322 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 381

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
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Db        382 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 441

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
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Db        442 GCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 501

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
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Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
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Db        562 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 621

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
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Db        622 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 672

RESULT 14
AR280219
LOCUS       AR280219                689 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 26 from patent US 6518045.
ACCESSION   AR280219
VERSION     AR280219.1  GI:29715609
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 26 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
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          EPX;
FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:              5.28e-104      Length:         689
Score:                  998.00         Matches:        196
Percent Similarity:     100.0%         Conservative:   1
Best Local Similarity:  99.5%          Mismatches:     0
Query Match:            99.7%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-36 (1-197) x AR280219 (1-689)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
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Db         82 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 141

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
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Db        142 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 201

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 261

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
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Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
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Db        322 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 381

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
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Db        382 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 441

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
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Db        442 GCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 501

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        502 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 561

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
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Db        562 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 621

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              ||||||||||||||||||||||||||||||||||||||||||:::|||
Db        622 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 672

RESULT 15
AR322434
LOCUS       AR322434                689 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 26 from patent US 6566097.
ACCESSION   AR322434
VERSION     AR322434.1  GI:33708187
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 26 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
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           EPX;
FEATURES             Location/Qualifiers
     source          1. .689
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              5.28e-104      Length:         689
Score:                  998.00         Matches:        196
Percent Similarity:     100.0%         Conservative:   1
Best Local Similarity:  99.5%          Mismatches:     0
Query Match:            99.7%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-36 (1-197) x AR322434 (1-689)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
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Db         82 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 141

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 201

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
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Db        202 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 261

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
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Db        262 GAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 321

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
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Db        322 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 381

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 441

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
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Db        442 GCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 501

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        502 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 561

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
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Db        562 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 621

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||:::|||
Db        622 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 672


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Job time : 2674.26 secs
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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 9, 2006, 23:43:41 ; Search time 420.528 Seconds
(without alignments)
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Title: US-10-821-670A-36
Perfect score: 1001
Sequence: 1 RNLPTPTPSPGMFQCLNHSQ.....HAFRIRAVTINRMMSYLNAS 197

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Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	2	1001	100.0	591	6	ABK98949	Abk98949 Feline in
	3	1001	100.0	591	14	ADV34688	Adv34688 Feline si
c	4	1001	100.0	591	14	ADV34690	Adv34690 Feline si
c	5	1001	100.0	666	6	ABK98947	Abk98947 Feline in
	6	1001	100.0	666	6	ABK98946	Abk98946 Feline in
	7	1001	100.0	666	14	ADV34685	Adv34685 Feline si
c	8	1001	100.0	666	14	ADV34687	Adv34687 Feline si
c	9	1001	100.0	1533	6	ABK98954	Abk98954 Feline in
	10	1001	100.0	1533	6	ABK98953	Abk98953 Feline in
c	11	1001	100.0	1533	14	ADV34697	Adv34697 Feline si
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c	16	1001	100.0	1599	14	ADV34693	Adv34693 Feline si
	17	998	99.7	591	2	AAV56629	Aav56629 Feline FL
	18	998	99.7	689	2	AAV56641	Aav56641 Feline FL
	19	998	99.7	1441	2	AAV56628	Aav56628 Feline FL
	20	980	97.9	669	4	AAF26083	Aaf26083 Feline IL
	21	980	97.9	669	4	AAF26086	Aaf26086 Feline IL
	22	980	97.9	4201	4	AAF26077	Aaf26077 Feline IL
	23	969	96.8	639	4	AAF26098	Aaf26098 Plasmid p
	24	964	96.3	679	4	AAF26097	Aaf26097 Feline fi
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	40	929	92.8	591	14	ADV34701	Adv34701 Canine si
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ALIGNMENTS

RESULT 1
ABK98948
ID ABK98948 standard; cDNA; 591 BP.
XX
AC ABK98948;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p35-591 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX

PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69305.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 1; Page 56-57; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 591 BP; 178 A; 149 C; 122 G; 142 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.66e-102	Length:	591
Score:	1001.00	Matches:	197
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-36 (1-197) x ABK98948 (1-591)

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Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
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Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
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Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
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Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
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Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591
```

RESULT 2
ABK98949/c
ID ABK98949 standard; cDNA; 591 BP.
XX
AC ABK98949;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p35-591 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Disclosure; Page 58; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 591 BP; 142 A; 122 C; 149 G; 178 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.66e-102	Length:	591
Score:	1001.00	Matches:	197
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-36 (1-197) x ABK98949 (1-591)

```
Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 3
ADV34688
ID   ADV34688 standard; cDNA; 591 BP.
XX
AC   ADV34688;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain mature IL-12p35 protein cDNA, nFeIL-12p35 591.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .591
FT                   /*tag=  a
FT                   /product= "PFeIL-12p35 197 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34689.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 23; SEQ ID NO 35; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain mature IL-12p35 subunit
CC   protein encoding cDNA.
XX
SQ   Sequence 591 BP; 178 A; 149 C; 122 G; 142 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              4.66e-102       Length:         591
Score:                  1001.00         Matches:        197
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-36 (1-197) x ADV34688 (1-591)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591

RESULT 4
ADV34690/c
ID   ADV34690 standard; DNA; 591 BP.
XX
AC   ADV34690;
XX
```

DT 24-FEB-2005 (first entry)
XX
DE Feline single chain mature IL-12p35 complementary DNA, nFeIL-12p35 591.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Felis catus.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 3; SEQ ID NO 37; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain mature IL-12p35 subunit
CC complementary DNA.
XX
SQ Sequence 591 BP; 142 A; 122 C; 149 G; 178 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.66e-102	Length:	591
Score:	1001.00	Matches:	197
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-36 (1-197) x ADV34690 (1-591)

```
Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
```

RESULT 5
ABK98947/c
ID ABK98947 standard; cDNA; 666 BP.
XX
AC ABK98947;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p35-666 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Example 3; Page 56; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 666 BP; 160 A; 138 C; 179 G; 189 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	5.49e-102	Length:	666
Score:	1001.00	Matches:	197
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-36 (1-197) x ABK98947 (1-666)

```
Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
```

RESULT 6
ABK98946
ID ABK98946 standard; cDNA; 666 BP.
XX
AC ABK98946;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p35-666 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69304.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 1; Page 54-55; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 666 BP; 189 A; 179 C; 138 G; 160 T; 0 U; 0 Other;

Pred. No.:	5.49e-102	Length:	666
Score:	1001.00	Matches:	197
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-36 (1-197) x ABK98946 (1-666)

```
Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
```

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666

RESULT 7
ADV34685
ID   ADV34685 standard; cDNA; 666 BP.
XX
AC   ADV34685;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12p35 full-length cDNA, nFeIL-12p35 666.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .666
FT                   /*tag= a
FT                   /product= "PFeIL-12p35 222 protein "
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34686.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 23; SEQ ID NO 32; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12p35 subunit protein
CC   encoding full-length cDNA.
XX
SQ   Sequence 666 BP; 189 A; 179 C; 138 G; 160 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              5.49e-102       Length:         666
Score:                  1001.00         Matches:        197
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-36 (1-197) x ADV34685 (1-666)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666

RESULT 8
ADV34687/c
ID   ADV34687 standard; DNA; 666 BP.
XX
AC   ADV34687;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12p35 complementary DNA, nFeIL-12p35 666.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
```

```
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 34; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12p35 subunit full-length
CC   complementary DNA.
XX
SQ   Sequence 666 BP; 160 A; 138 C; 179 G; 189 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              5.49e-102       Length:         666
Score:                  1001.00         Matches:        197
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-36 (1-197) x ADV34687 (1-666)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 9
ABK98954/c
ID   ABK98954 standard; cDNA; 1533 BP.
XX
AC   ABK98954;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1533 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 66-67; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.74e-101       Length:         1533
Score:                  1001.00         Matches:        197
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-36 (1-197) x ABK98954 (1-1533)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
```

RESULT 10
ABK98953
ID ABK98953 standard; cDNA; 1533 BP.
XX
AC ABK98953;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12-1533 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69307.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 63-64; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention

XX
SQ Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.74e-101	Length:	1533
Score:	1001.00	Matches:	197
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-36 (1-197) x ABK98953 (1-1533)

```
Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        943 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1002

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1003 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1062

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1122

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1123 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1182

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1183 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1242

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1243 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1302

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1303 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1362

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1363 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1422

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1423 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1482

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1483 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
```

RESULT 11
ADV34697/c
ID ADV34697 standard; DNA; 1533 BP.
XX
AC ADV34697;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain IL-12 complementary DNA, nFeIL-12 1533.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Felis catus.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.

```
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 45; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 complementary DNA.
XX
SQ   Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.74e-101      Length:         1533
Score:                  1001.00        Matches:        197
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     14             Gaps:           0

US-10-821-670A-36 (1-197) x ADV34697 (1-1533)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 12
ADV34695
ID   ADV34695 standard; cDNA; 1533 BP.
XX
AC   ADV34695;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1533
FT                   /*tag=  a
FT                   /product= "PFeIL-12 511 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34696.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 43; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.74e-101      Length:         1533
Score:                  1001.00        Matches:        197
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     14             Gaps:           0

US-10-821-670A-36 (1-197) x ADV34695 (1-1533)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        943 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1002
```

```
Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1003 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1062

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1122

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1123 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1182

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1183 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1242

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1243 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1302

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1303 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1362

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1363 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1422

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1423 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1482

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1483 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
```

RESULT 13
ABK98950
ID ABK98950 standard; cDNA; 1599 BP.
XX
AC ABK98950;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12-1599 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69306.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 58-60; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.84e-101	Length:	1599
Score:	1001.00	Matches:	197
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-36 (1-197) x ABK98950 (1-1599)

```
Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1009 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1068

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1069 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1128

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1129 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1188

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1189 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1248

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1249 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1308

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1309 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1368

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1369 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1428

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1429 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1488

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1489 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1548

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1549 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
```

RESULT 14
ABK98951/c
ID ABK98951 standard; cDNA; 1599 BP.
XX
AC ABK98951;
XX

```
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1599 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 61-62; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.84e-101      Length:         1599
Score:                  1001.00        Matches:        197
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     6              Gaps:           0

US-10-821-670A-36 (1-197) x ABK98951 (1-1599)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 15
ADV34691
ID   ADV34691 standard; cDNA; 1599 BP.
XX
AC   ADV34691;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1599
FT                   /*tag=  a
FT                   /product= "PFeIL-12p533 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34692.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 38; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
```

CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.84e-101	Length:	1599
Score:	1001.00	Matches:	197
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	14	Gaps:	0

US-10-821-670A-36 (1-197) x ADV34691 (1-1599)

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Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1009 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1068

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1069 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1128

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1129 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1188

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1189 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1248

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1249 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1308

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1309 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1368

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1369 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1428

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1429 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1488

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1489 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1548

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
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Db       1549 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599
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Search completed: June 10, 2006, 01:16:58
Job time : 424.528 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 10, 2006, 00:20:47 ; Search time 2414.57 Seconds
(without alignments)
6843.525 Million cell updates/sec

Title: US-10-821-670A-36
Perfect score: 1001
Sequence: 1 RNLPTPTPSPGMFQCLNHSQ.....HAFRIRAVTINRMMSYLNAS 197

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/abss/ABSSWEB_spool/US10821670/runat_07062006_110104_26172/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
-USER=US10821670_@CGN_1_1_27300_@runat_07062006_110104_26172 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
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3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	2	873	87.2	762	14	DQ033873	DQ033873 Pan trogl
	3	855.5	85.5	1136	4	CD013915	CD013915 90138132
	4	809	80.8	935	4	CD013914	CD013914 90138124
	5	748.5	74.8	1938	6	BC035571	BC035571 Homo sapi
	6	663	66.2	863	4	CD013916	CD013916 90138296
	7	460	46.0	1299	6	AK153729	AK153729 Mus muscu
	8	418.5	41.8	563	3	BU698113	BU698113 LL2in1206
	9	412.5	41.2	812	2	BG702253	BG702253 602683459
	10	404	40.4	589	1	AI050362	AI050362 ub30a07.r
c	11	374.5	37.4	1099	2	BI523344	BI523344 603175938
c	12	355	35.5	778	1	AJ820622	AJ820622 AJ820622
	13	349.5	34.9	561	3	BU699383	BU699383 LL2in1157
	14	345	34.5	373	7	BF552757	BF552757 UI-R-C0-i
	15	344	34.4	692	5	CJ137697	CJ137697 CJ137697
	16	321	32.1	456	10	DT913216	DT913216 S13.1426
	17	320	32.0	427	10	DT930939	DT930939 S13.1784
	18	312	31.2	832	2	BI523569	BI523569 603175938
	19	300	30.0	371	3	BU699957	BU699957 B4-79 Hem
	20	299	29.9	581	3	BP260963	BP260963 BP260963
	21	295	29.5	412	4	CB801533	CB801533 AMGNNUC:S
c	22	295	29.5	777	4	CB168830	CB168830 CWI602769
	23	287	28.7	354	4	BY230958	BY230958 BY230958
	24	265	26.5	777	14	CT080894	CT080894 Sus scrof
	25	231	23.1	571	3	BP261459	BP261459 BP261459
	26	221	22.1	551	10	DT919655	DT919655 PCRS30821
	27	215.5	21.5	373	3	BU695376	BU695376 B1-30 Hem
	28	203.5	20.3	571	9	DN829917	DN829917 pat.pk005
	29	177.5	17.7	342	2	BM257856	BM257856 521721 MA
c	30	156.5	15.6	940	14	BX963061	BX963061 Forward s
	31	150	15.0	840	11	BZ261813	BZ261813 CH230-420
	32	137	13.7	592	12	CE159257	CE159257 tigr-gss-
	33	136.5	13.6	817	3	BU474924	BU474924 603761859
	34	130	13.0	508	9	DA505380	DA505380 DA505380
	35	129	12.9	447	2	BI824638	BI824638 603033580
	36	126	12.6	382	4	CB809298	CB809298 AMGNNUC:T
	37	126	12.6	558	9	CX570753	CX570753 RVL1941 W
	38	125	12.5	463	9	DR007201	DR007201 TC124111
	39	115	11.5	451	4	BX258840	BX258840 BX258840
	40	114.5	11.4	361	3	BU694675	BU694675 B2-56 Hem
	41	114	11.4	344	14	BX537236	BX537236 INRA porc
c	42	102	10.2	528	1	AI332701	AI332701 qq19a07.x
	43	101	10.1	477	4	BX258839	BX258839 BX258839
	44	100	10.0	905	3	BU540821	BU540821 AGENCOURT
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ALIGNMENTS

RESULT 1
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LOCUS DQ033872 762 bp DNA linear GSS 02-JUN-2005
DEFINITION Homo sapiens IL12A gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION DQ033872
VERSION DQ033872.1 GI:66885081
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 762)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 762)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

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COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.  Translation starts at the beginning of
            alignment.
FEATURES             Location/Qualifiers
     source          1. .762
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
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                     /gene="IL12A"
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ORIGIN

Alignment Scores:
Pred. No.:              7.48e-93        Length:         762
Score:                  883.00          Matches:        173
Percent Similarity:     90.4%           Conservative:   5
Best Local Similarity:  87.8%           Mismatches:     19
Query Match:            88.2%           Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-36 (1-197) x DQ033872 (1-762)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||      ||||||   ||||||||||||   ||||||:::||||||||
Db        169 AGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 228

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
                ||||||||||||:::||||||   ||||||||||||||||||||||||||||||||
Db        229 AACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTTTAC 288

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 CCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 348

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||   ||||||||||||||   |||||||||
Db        349 GAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGAGAGACC 408

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              |||   ||||||||||||||||||||||||||||||||||||||||||||       |||
Db        409 TCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATGGCCCTG 468

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        469 TGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAAT 528

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        529 GCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCAGTT 588

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||:::||||||||||||   ||||||   ||||||||||||   ||||||
Db        589 ATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCC 648

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        649 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 708

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||:::|||:::||||||||||||||||||||
Db        709 AGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTCC 759

RESULT 2
DQ033873
LOCUS       DQ033873                762 bp    DNA     linear   GSS 02-JUN-2005
DEFINITION  Pan troglodytes IL12A gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   DQ033873
VERSION     DQ033873.1  GI:66885082
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     A Scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
  JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
   PUBMED   15869325
REFERENCE   2  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.  Translation starts at the beginning of
            alignment.
FEATURES             Location/Qualifiers
     source          1. .762
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     gene            <1. .>762
                     /gene="IL12A"
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Score:                  873.00          Matches:        172
Percent Similarity:     89.8%           Conservative:   5
Best Local Similarity:  87.3%           Mismatches:     20
Query Match:            87.2%           Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-36 (1-197) x DQ033873 (1-762)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
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Db        169 AGAAACCTCCCCGTGGCCACCCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 228

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
                ||||||||||||:::||||||   ||||||||||||||||||||||||||||||||
Db        229 AACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTTTAC 288

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 CCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 348

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||   ||||||||||||||   |||||||||
Db        349 GAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGAGAGACC 408

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              |||   ||||||||||||||||||||||||||||||||||||||||||||       |||
Db        409 TCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATGGCCCTG 468

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        469 TGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAAT 528

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        529 GCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCAGTT 588

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||:::||||||||||||   ||||||   ||||||||||||   ||||||
Db        589 ATTGACGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCC 648
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Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
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Db        649 CTTGAAGAACTGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 708

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              ||||||||||||||||||:::|||:::||||||||||||||||||||||
Db        709 AGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTCC 759

RESULT 3
CD013915
LOCUS       CD013915                1136 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION  90138132 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD013915
VERSION     CD013915.1  GI:37777445
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1136)
  AUTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
            Au-Young,J. and Stuve,L.L.
  TITLE     PCR isolation and cloning of novel splice variant mRNAs from known
            drug target genes
  JOURNAL   Genomics 83 (4), 566-571 (2004)
   PUBMED   15028279
COMMENT     Contact: Jin, P.
            Incyte Corporation
            3160 Porter Drive, Palo Alto, CA 94304, USA
            Tel: 650 621 8639
            Fax: 650 621 8965
            Email: pjin@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .1136
                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
                     /clone_lib="Single gene library"
                     /note="Vector: pDrive Cloning Vector; RT-PCR was performed
                     using gene-specific primers flanking the open-reading
                     frame. PCR products were subcloned into pDrive Cloning
                     Vector and sequenced completely using M13 forward and
                     reverse primers. Sequencing gaps were closed by
                     re-sequencig using primers flanking the gapped areas."
ORIGIN

Alignment Scores:
Pred. No.:              2.26e-89      Length:         1136
Score:                  855.50        Matches:        172
Percent Similarity:     80.2%         Conservative:   6
Best Local Similarity:  77.5%         Mismatches:     19
Query Match:            85.5%         Indels:         25
DB:                     4             Gaps:           1

US-10-821-670A-36 (1-197) x CD013915 (1-1136)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              |||:::||||||      ||||||   ||||||||||||   ||||||:::|||||||||
Db        356 AGAGACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 415

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||:::||||||   ||||||||||||||||||||||||||||||||||||
Db        416 AACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTTTAC 475

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
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Db        476 CCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 535

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              |||||||||||||||||||||||||   ||||||||||||||   |||||||||
Db        536 GAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGAGAGACC 595

Qy         81 SerLeuIleThr---------------------------------------------- 84
              |||   ||||||
Db        596 TCTTTCATAACTGTAAGTCAAAAAATGAAAAGTTTCAGCCTGTATGATGAATTCATATCA 655

Qy         85 --------------------------AsnGlySerCysLeuAlaSerArgLysThrSer 95
                                         ||||||||||||||||||||||||||||||
Db        656 CTGATGTCTGATTATTTTTTCCTCTAGAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 715

Qy         96 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 115
              ||||||      ||||||||||||||||||||||||||||||||||||||||||||||||
Db        716 TTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAG 775

Qy        116 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 135
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        776 TTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAA 835

Qy        136 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 155
              |||||||||      ||||||||||:::|||||||||||   ||||||   ||||||
Db        836 AACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTG 895

Qy        156 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 175
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        896 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 955

Qy        176 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 195
              ||||||||||||||||||||||||||||||||:::|||:::|||||||||||||||||
Db        956 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAAT 1015

Qy        196 AlaSer 197
              ||||||
Db       1016 GCTTCC 1021

RESULT 4
CD013914
LOCUS       CD013914                 935 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION  90138124 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD013914
VERSION     CD013914.1  GI:37777444
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 935)
  AUTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
            Au-Young,J. and Stuve,L.L.
  TITLE     PCR isolation and cloning of novel splice variant mRNAs from known
            drug target genes
  JOURNAL   Genomics 83 (4), 566-571 (2004)
   PUBMED   15028279
COMMENT     Contact: Jin, P.
            Incyte Corporation
            3160 Porter Drive, Palo Alto, CA 94304, USA
            Tel: 650 621 8639
            Fax: 650 621 8965
            Email: pjin@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .935
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Single gene library"
                     /note="Vector: pDrive Cloning Vector; RT-PCR was performed
                     using gene-specific primers flanking the open-reading
                     frame. PCR products were subcloned into pDrive Cloning
                     Vector and sequenced completely using M13 forward and
                     reverse primers. Sequencing gaps were closed by
                     re-sequencig using primers flanking the gapped areas."
ORIGIN

Alignment Scores:
```

```
Pred. No.:              5e-84          Length:         935
Score:                  809.00         Matches:        161
Percent Similarity:     84.8%          Conservative:   6
Best Local Similarity:  81.7%          Mismatches:     16
Query Match:            80.8%          Indels:         14
DB:                     4              Gaps:           1

US-10-821-670A-36 (1-197) x CD013914 (1-935)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              |||:::||||||      ||||||   ||||||||||||   ||||||:::|||||||||
Db        272 AGAGACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 331

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
                ||||||||||||:::||||||   ||||||||||||||||||||||||||||||||
Db        332 AACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTTTAC 391

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 CCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 451

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||
Db        452 GAGGCCTGTTTACCATTGGAATTAACC------------------------------ 478

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
                         ||||||||||||||||||||||||||||||||||||||||      |||
Db        479 ---------AAGAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATGGCCCTG 529

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        530 TGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAAT 589

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        590 GCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCAGTT 649

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||:::||||||||||||   ||||||   ||||||||||||   ||||||
Db        650 ATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCC 709

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        710 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 769

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              ||||||||||||||||||||:::|||:::||||||||||||||||||||
Db        770 AGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTCC 820

RESULT 5
BC035571
LOCUS       BC035571               1938 bp    mRNA    linear   HTC 04-MAR-2003
DEFINITION  Homo sapiens, clone IMAGE:5240216, mRNA.
ACCESSION   BC035571
VERSION     BC035571.1  GI:23958681
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1938)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 69 Row: b Column: 15
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 4504638
            This clone has the following problem: retained intron.
FEATURES             Location/Qualifiers
     source          1. .1938
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240216"
                     /tissue_type="Brain, fetal, whole pooled"
                     /clone_lib="NIH_MGC_121"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
ORIGIN

Alignment Scores:
Pred. No.:              1.83e-76       Length:         1938
Score:                  748.50         Matches:        173
Percent Similarity:     49.4%          Conservative:   6
Best Local Similarity:  47.8%          Mismatches:     18
Query Match:            74.8%          Indels:         165
DB:                     6              Gaps:           3

US-10-821-670A-36 (1-197) x BC035571 (1-1938)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||      ||||||   ||||||||||||   ||||||:::|||||||||
Db        361 AGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 420

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
                ||||||||||||:::||||||   ||||||||||||||||||||||||||||||||
Db        421 AACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTTTAC 480

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 540

Qy         61 GluAlaCysLeuProLeuGluLeuThr------------------------------ 69
              ||||||||||||||||||||||||||
Db        541 GAGGCCTGTTTACCATTGGAATTAACCAAGGTATAAAGGATTTTCCTCCCAGAGCATGCA 600

Qy         69 ------------------------------------------------------------ 69

Db        601 GTGTGGTTAAAAACTGTGCATCAAATCTCACCTGCTTCTAAAAATTCACGTTTCTGGTAT 660

Qy         69 ------------------------------------------------------------ 69

Db        661 CCATCATTATGGGATTTTAACTGGTCCTACTTCAGAAGTTAGATTTGGGAGAAAAATTAT 720

Qy         69 ------------------------------------------------------------ 69

Db        721 TTTTAAAAAATGGTTTTTTTTGCAACAATGTGAATACACTTAACACTTAAAAATAGTTCA 780

Qy         69 ------------------------------------------------------------ 69
```

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Db        781 GATGCTAAATATTATGATATGTGTTTTTACCATAATAAAAAAAATTTGAGACCTGAAGAG 840

Qy         70 ----------------------------------------------------Met-AsnGl  72
                                                                  ::: |||||
Db        841 TCAGAAAGATTTATACTAAGAATTAATACTTTGATATATGATTTTTTCCCTCTAGAATGA 900

Qy         72 uSerCysLeuAlaSerArgGluIleSerLeuIleThr---------------------- 84
               ||||||||||   |||||||||   |||   ||||||
Db        901 GAGTTGCCTAAATTCCAGAGAGACCTCTTTCATAACTGTAAGTCAAAAAATGAAAAGTTT 960

Qy         85 ----------------------------------------------------AsnGlySe  87
                                                                  ||||||||
Db        961 CAGCCTGTATGATGAATTCATATCACTGATGTCTGATTATTTTTTCCTCTAGAATGGGAG 1020

Qy         87 rCysLeuAlaSerArgLysThrSerPheMet---------------------------- 97
               ||||||||||||||||||||||||||||
Db       1021 TTGCCTGGCCTCCAGAAAGACCTCTTTTATGATGGTAAGACACACAGCTCTTTCCTCAAA 1080

Qy         97 ------------------------------------------------------------ 97

Db       1081 TGCAATGGGGGAAATGTTTTTAGCCCATCTCAATGGATACTTCCCCATCTTGTCATGTCA 1140

Qy         98 --ThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheL 117
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CCCAGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCA 1200

Qy        117 ysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnM 137
               ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACA 1260

Qy        137 etLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProG 157
               |||||      ||||||||||:::||||||||||   ||||||   ||||||||||
Db       1261 TGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCAC 1320

Qy        157 lnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuL 177
               ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTC 1380

Qy        177 euHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaS 197
               ||||||||||||||||||||||||||||:::|||:::||||||||||||||||||||||
Db       1381 TTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAATGCTT 1440

Qy        197 er 197
               ||
Db       1441 CC 1442
```

RESULT 6
CD013916

```
LOCUS       CD013916                863 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION  90138296 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD013916
VERSION     CD013916.1  GI:37777446
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 863)
  AUTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
            Au-Young,J. and Stuve,L.L.
  TITLE     PCR isolation and cloning of novel splice variant mRNAs from known
            drug target genes
  JOURNAL   Genomics 83 (4), 566-571 (2004)
   PUBMED   15028279
COMMENT     Contact: Jin, P.
            Incyte Corporation
            3160 Porter Drive, Palo Alto, CA 94304, USA
            Tel: 650 621 8639
            Fax: 650 621 8965
            Email: pjin@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .863
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Single gene library"
                     /note="Vector: pDrive Cloning Vector; RT-PCR was performed
                     using gene-specific primers flanking the open-reading
                     frame. PCR products were subcloned into pDrive Cloning
                     Vector and sequenced completely using M13 forward and
                     reverse primers. Sequencing gaps were closed by
                     re-sequencig using primers flanking the gapped areas."
ORIGIN
```

Alignment Scores:

Pred. No.:	6.49e-67	Length:	863
Score:	663.00	Matches:	136
Percent Similarity:	72.1%	Conservative:	6
Best Local Similarity:	69.0%	Mismatches:	17
Query Match:	66.2%	Indels:	38
DB:	4	Gaps:	1

US-10-821-670A-36 (1-197) x CD013916 (1-863)

```
Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              |||:::||||||      ||||||   ||||||||||||   ||||||:::|||||||||
Db        272 AGAGACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 331

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
                 ||||||||||||:::||||||   |||||||||
Db        332 AACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAG---------------------- 367

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60

Db        367 ------------------------------------------------------------ 367

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
                                                 ||||||||||||||   |||||||||
Db        368 ------------------------------AATGAGAGTTGCCTAAATTCCAGAGAGACC 397

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              |||   ||||||||||||||||||||||||||||||||||||||||||||      |||
Db        398 TCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATGGCCCTG 457

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        458 TGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAAT 517

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 GCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCAGTT 577

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||:::|||||||||||   ||||||   ||||||||||||   ||||||
Db        578 ATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCC 637

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        638 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 697

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              ||||||||||||||||||||:::|||:::||||||||||||||||||||
Db        698 AGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTCC 748
```

RESULT 7
AK153729

```
LOCUS       AK153729                1299 bp    mRNA    linear   HTC 21-SEP-2005
DEFINITION  Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
            library, clone:A630064E02 product:interleukin 12a, full insert
            sequence.
ACCESSION   AK153729
VERSION     AK153729.1  GI:74148962
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636

REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159

REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861

REFERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
CONSRTM RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
PUBMED 11217851

REFERENCE 5
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
CONSRTM FANTOM Consortium
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420 (6915), 563-573 (2002)
PUBMED 12466851

REFERENCE 6
AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.
CONSRTM FANTOM Consortium
TITLE The transcriptional landscape of the mammalian genome
JOURNAL Science 309 (5740), 1559-1563 (2005)
PUBMED 16141072

REFERENCE 7
AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.
CONSRTM RIKEN Genome Exploration Research Group
TITLE Antisense transcription in the mammalian transcriptome
JOURNAL Science 309 (5740), 1564-1566 (2005)
PUBMED 16141073

REFERENCE 8 (bases 1 to 1299)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.

```
  TITLE     Direct Submission
  JOURNAL   Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM_DB:A630064E02"
                     /db_xref="taxon:10090"
                     /clone="A630064E02"
                     /tissue_type="thymus"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="3 days neonate"
     misc_feature    1. .1299
                     /note="interleukin 12a (MGD|MGI:96539 GB|NM_008351,
                     evidence: BLASTN, 100%, match=776)
                     putative"
ORIGIN

Alignment Scores:
Pred. No.:              8.47e-43        Length:         1299
Score:                  460.00          Matches:        103
Percent Similarity:     57.0%           Conservative:   27
Best Local Similarity:  45.2%           Mismatches:     43
Query Match:            46.0%           Indels:         55
DB:                     6               Gaps:           2

US-10-821-670A-36 (1-197) x AK153729 (1-1299)

Qy         25 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 44
              :::   |||            :::||||||:::   |||:::   |||||||||||:::
Db        118 AGCTTCTCCTTATGTTTTTCCCAGGCCAGAGAAAAACTGAAACATTATTCCTGCACTGCT 177

Qy         45 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeu 64
              |||:::||||||||||||||||||||:::|||:::|||||||||::::::   ||||||
Db        178 GAAGACATCGATCATGAAGACATCACACGGGACCAAACCAGCACATTGAAGACCTGTTTA 237

Qy         65 ProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSer--------- 81
              ||||||||||||      ||||||||||||||||||:::||||||   |||
Db        238 CCACTGGAACTACACAAGAACGAGAGTTGCCTGGCTACTAGAGAGACTTCTTCCACAACA 297

Qy         81 ------------------------------------------------------------ 81

Db        298 GTAAGTAAGCACTCTAAGGGTTCCTTCCCCATGACGGATTCATAACACTGATGCCTGGTC 357

Qy         82 ---Leu-IleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThr----- 98
                 ||| :::      ||||||||||||      :::|||||||||   |||
Db        358 ATTCTTTCTCTAGAGAGGGAGCTGCCTGCCCCCACAGAAGACGTCTTTGATGATGGTAAG 417

Qy         98 ------------------------------------------------------------ 98

Db        418 CCACATCACTTTTCTGAAATGCAGCAGGGTCCTGTAGTTCCAGCCCATCTCAATGATTCC 477

Qy         99 -------------------------ThrLeuCysLeuSerSerIleTyrGluAspLeuLy 110
                                       ||||||||||||   ||||||||||||||||||||
Db        478 TTGCCCATTGTGTCCTGCGCTCTAGACCCTGTGCCTTGGTAGCATCTATGAGGACTTGAA 537

Qy        110 sMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGl 130
              ||||||||||   ||||||:::|||:::||||||   |||                :::||

Db        538 GATGTACCAGACAGAGTTCCAGGCCATCAACGCAGCACTTCAGAATCACAACCATCAGCA 597

Qy        130 nIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVa 150
              ||||   ||||||:::   ||||||   ||||||||||||||||:::|||:::||||||
Db        598 GATCATTCTAGACAAGGGCATGCTGGTGGCCATCGATGAGCTGATGCAGTCTCTGAATCA 657

Qy        150 lAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLy 170
              |||      |||:::   |||         :::   |||   |||   |||:::   ||
Db        658 TAATGGCGAGACTCTGCGCCAGAAACCTCCTGTGGGAGAAGCAGACCCTTACAGAGTGAA 717

Qy        170 sIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMe 190
              |:::||||||||||||||||||||||||||      |||   |||||||||||||||::
Db        718 AATGAAGCTCTGCATCCTGCTTCACGCCTTCAGCACCCGCGTCGTGACCATCAACAGGGT 777

Qy        190 tMetSerTyrLeuAsnAlaSer 197
              :|||   |||||:::::::::
Db        778 GATGGGCTATCTGAGCTCCGCC 799

RESULT 8
BU698113
LOCUS       BU698113                563 bp    mRNA    linear   EST 09-OCT-2002
DEFINITION  LL2in12067T7 Hematopoietic Stem Cell Subtracted Library Mus
            musculus cDNA 5' similar to interleukin 12 p35 subunit, mRNA
            sequence.
ACCESSION   BU698113
VERSION     BU698113.1  GI:23610620
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 563)
  AUTHORS   Phillips,R.L., Ernst,R.E., Brunk,B.P., Ivanova,N., Mahan,M.A.,
            Deanehan,J.K., Moore,K.A., Overton,G.C. and Lemischka,I.R.
  TITLE     The genetic program of hematopoietic stem cells
  JOURNAL   Science 288 (5471), 1635-1640 (2000)
   PUBMED   10834841
COMMENT     Contact: Lemischka, Ihor R.
            Department of Molecular Biology
            Princeton University
            Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544, USA
            Tel: 609 258 2838
            Fax: 609 258 2759
            Email: ilemischka@molbio.princeton.edu
            These ESTs are derived from a subtracted cDNA library enriched for
            gene products expressed in day 14-14.5 fetal liver hematopoietic
            stem cells defined as Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E
            (Sca-1)pos
            Seq primer: M13Reverse or T7.
FEATURES             Location/Qualifiers
     source          1. .563
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /tissue_type="Hematopoietic"
                     /cell_type="Stem Cells; Lineageneg/lo, AA4.1pos, cKitpos,
                     Ly6A/E (Sca-1)pos"
                     /dev_stage="Embryonic day 14-14.5"
                     /lab_host="DH10B"
                     /clone_lib="Hematopoietic Stem Cell Subtracted Library"
                     /note="Organ: Fetal Liver; Vector: Sport 1; Site_1: Sal I;
                     Site_2: Not I; Two directionally cloned cDNA libraries
                     were made from fetal liver  hematopoietic stem cells
                     enriched to be Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E
                     (Sca-1)pos called Scapos and from AA4.1neg fetal liver
                     cells. Subtractive hybridization was  performed by
                     hybridization of the target, Scapos, single stranded cDNA
                     library in pSport1 to  biotinylated RNA transcribed from
                     the driver, AA4.1neg cDNA library in pSport2 with  inserts
                     cloned in the complementary orientation. For detailed
                     protocols and additional  information please see our
```

website at http://stemcell.princeton.edu."
ORIGIN

Alignment Scores:

Pred. No.:	1.95e-38	Length:	563
Score:	418.50	Matches:	88
Percent Similarity:	72.5%	Conservative:	23
Best Local Similarity:	57.5%	Mismatches:	40
Query Match:	41.8%	Indels:	2
DB:	3	Gaps:	1

US-10-821-670A-36 (1-197) x BU698113 (1-563)

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Qy         25 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 44
              :::   |||          :::||||||:::   |||:::   |||||||||||:::
Db         78 AGCTTCTCCTTATGTTTTCCCAGGCCAGAGAAAAACTGAAACATTATTCCTGCACTGCT 137

Qy         45 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeu 64
              |||:::|||||||||||||||||||:::||:::||||||||::::::   ||||||
Db        138 GAAGACATCGATCATGAAGACATCACACGGGACCAAACCAGCACATTGAAGACCTGTTTA 197

Qy         65 ProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThr 84
              ||||||||||||      ||||||||||||||||||:::||||||   |||      |||
Db        198 CCACTGGAACTACACAAGAACGAGAGTTGCCTGGCTACTAGAGAGACTTCTTCCACAACA 257

Qy         85 AsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSer 104
                ||||||||||||      :::|||||||||   |||   ||||||||||||   |||
Db        258 AGAGGGAGCTGCCTGCCCCCACAGAAGACGTCTTTGATGATGACCCTGTGCCTTGGTAGC 317

Qy        105 IleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeu 124
              |||||||||||||||||||||||||||   ||||||:::|||:::||||||   |||
Db        318 ATCTATGAGGACTTGAAGATGTACCAGACAGAGTTCCAGGCCATCAACGCAGCACTTCAG 377

Qy        125 MetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 144
                    :::||||||   ||||||:::   ||||||   ||||||||||||||||
Db        378 AATCACAACCATCAGCAGATCATTCTAGACAAGGGCATGCTGGTGGCCATCGATGAGCTG 437

Qy        145 LeuGlnAlaLeuAsnValAsnSerVal-ThrVal---ProGlnAsnSerSerLeuGluGl 163
              :::|||:::||||||   |||       |||:::   |||:::            |||::
Db        438 ATGCAGTCTCTGAATCATAATGGGNGAGACTCTTGCGCCAGAAACCTTCCTGTGGGAGAA 497

Qy        163 uProAspPheTyrLysThrLysIleLysLeuCysIle 175
              :   |||   |||:::   |||:::||||||   |||
Db        498 GCAGGACCCTTACAGAGTGAAAATGAAGCTCTTGATT 534
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RESULT 9
BG702253
LOCUS BG702253 812 bp mRNA linear EST 07-MAY-2001
DEFINITION 602683459F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4816118 5', mRNA sequence.
ACCESSION BG702253
VERSION BG702253.1 GI:13973409
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 812)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10714 row: e column: 15
High quality sequence stop: 804.
FEATURES Location/Qualifiers
source 1. .812
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4816118"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_95"
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:

Pred. No.:	1.66e-37	Length:	812
Score:	412.50	Matches:	92
Percent Similarity:	85.5%	Conservative:	2
Best Local Similarity:	83.6%	Mismatches:	16
Query Match:	41.2%	Indels:	3
DB:	2	Gaps:	0

US-10-821-670A-36 (1-197) x BG702253 (1-812)

```
Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||      ||||||   ||||||||||||   ||||||:::||||||||
Db        483 AGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 542

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||:::||||||   ||||||||||||||||||||||||||||||||||||
Db        543 AACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTTTAC 602

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 CCTTGCACTTCTGAAGAGATCGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 662

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||   ||||||||||||      |||||||||
Db        663 GAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCT--AAATCCAGAGAGACC 720

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              |||   ||||||||||||||||||||   ||||||||||||||||||||||      |||
Db        721 TCTTTCATAACTAATGGGAGTTGCCTGGC-TCCAGAAAGACCTCTTTTATGATGTGCCTG 779

Qy        101 CysLeuSerSerIleTyrGluAspLeuLys 110
              ||||||||||||  ||||||||||||||||
Db        780 TGCCTTAGTAGTAT-TATGAAGACTTGAAA 808
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RESULT 10
AI050362
LOCUS AI050362 589 bp mRNA linear EST 09-JUL-1998
DEFINITION ub30a07.r1 Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:1379220 5' similar to gb:M65291 INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (HUMAN); gb:M86672 Mus musculus interleukin 12 p35 subunit, complete cds (MOUSE);, mRNA sequence.
ACCESSION AI050362
VERSION AI050362.1 GI:3299479
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 589)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

```
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:901688
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 60.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:10090"
                     /clone="IMAGE:1379220"
                     /sex="male"
                     /tissue_type="Thymus"
                     /dev_stage="4 weeks"
                     /lab_host="DH10B"
                     /clone_lib="Soares_thymus_2NbMT"
                     /note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI;
                     1st strand cDNA was primed with a Not I - oligo(dT) primer
                     [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGTTTTTTTTTTTTTTTTTTTTTTTT
                     3']; double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. RNA
                     provided by Dr. Bertrand Jordan. Library went through two
                     rounds of normalization, and was constructed by Bento
                     Soares and M.Fatima Bonaldo."
ORIGIN

Alignment Scores:
Pred. No.:              1.05e-36        Length:         589
Score:                  404.00          Matches:        94
Percent Similarity:     68.8%           Conservative:   23
Best Local Similarity:  55.3%           Mismatches:     46
Query Match:            40.4%           Indels:         8
DB:                     1               Gaps:           3

US-10-821-670A-36 (1-197) x AI050362 (1-589)

Qy          25 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 44
               :::   |||            :::||||||:::   |||:::   |||||||||||:::
Db          87 AGCTTCTCCTTATGTTTTTCCCAGGCCAGAGAAAAACTGAAACATTATTCCTGCACTGCT 146

Qy          45 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeu 64
               |||:::|||||||||||||||||||:::|||:::|||||||||::::::   ||||||
Db         147 GAAGACATCGATCATGAAGACATCACACGGGACCAAACCAGCACATTGAAGACCTGTTTA 206

Qy          65 ProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThr 84
               ||||||||||||      |||||||||||||||||:::||||||   |||      |||
Db         207 CCACTGGAACTACACAAGAACGAGAGTTGCCTGGCTACTAGAGAGACTTCTTCCACAACA 266

Qy          85 AsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSer 104
               ||||||||||||      :::|||||||||   |||   ||||||||||||   |||
Db         267 AGAGGGAGCTGCCTGCCCCCACAGAAGACGTCTTTGATGATGACCCTGTGCCTTGGTAGC 326

Qy         105 IleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeu 124
               ||||||||||||||||||||||||||   ||||||:::|||:::||||||   |||
Db         327 ATCTATGAGGACTTGAAGATGTACCAGACAGAGTTCCAGGCCATCAACGCAGCACTTCAG 386

Qy         125 MetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 144
                        :::||||||   ||||||:::   ||||||      ||||||||||||
Db         387 AATCACAACCATCAGCAGATCATTCTAGACAAGGGCATGCTGGGTGGCATCGATGAGCTG 446

Qy         145 LeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeu------Glu 162
               :::|||:::||||||   |||       |||:::   |||   :::||||||      |||
Db         447 ATGCAGTCTCTGAATCATAATGGCGAGACTCTGCGCCAGAA-ACCTCCCTGTGGGGAGAA 505

Qy         163 GluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIle 182
                           :::   |||      :::   ||||||||         |||:::
Db         506 GCAGACCCCTTACAGGAGTGAAAATGAAGCGTCTGAATCCTGCTTTCA------CGCCTT 559

Qy         183 ArgAla---------ValThrIleAsnArg 189
                  |||         ||||||||||||||
Db         560 TCAGCACCCGGCGTCGTGACCATCAACAGG 589

RESULT 11
BI523344/c
LOCUS       BI523344               1099 bp    mRNA    linear   EST 29-AUG-2001
DEFINITION  603175938T1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 3',
            mRNA sequence.
ACCESSION   BI523344
VERSION     BI523344.1  GI:15348136
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1099)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11605  row: 1  column: 09
            High quality sequence start: 40
            High quality sequence stop: 727.
FEATURES             Location/Qualifiers
     source          1. .1099
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240216"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_121"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 017. Note:
                     this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              7.5e-33         Length:         1099
Score:                  374.50          Matches:        90
Percent Similarity:     80.7%           Conservative:   6
Best Local Similarity:  75.6%           Mismatches:     15
Query Match:            37.4%           Indels:         9
DB:                     2               Gaps:           1

US-10-821-670A-36 (1-197) x BI523344 (1-1099)
```

```
Qy          82 LeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCys 101
               |||   |||       :::   |||   ||||||:::                  ||||||
Db         776 TTGGATACTTTCCGCAATCTGCTCATGTCACGTCAG--------------GCCCTGTGC 732

Qy         102 LeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAla 121
               ||||||||||||||||||   ||||||||||||||||||||||||   ||||||||
Db         731 TTTAGTAGTATTTATGAAGACTG-AAGATGTACCAGGTGGAGTTCAAGACCATGAATGCA 673

Qy         122 LysLeu-LeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIl 141
               |||||| ||||||||||||||||||||||||||||||||||||||||||||||      ||
Db         672 AAGCTTCCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCAGTTAT 613

Qy         141 eAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLe 161
               ||||||||||:::|||||||||||||   ||||||   ||||||||||||   ||||||||
Db         612 TGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCCCT 553

Qy         161 uGluGluProAsp--PheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
               |||||||||||||  |||   ||||||:::|||||||||||||||||||||||||||||
Db         552 TGAAGAACCGGATTGTTTATCAAAACTGAAATCAAGCTCTGCATACTTCTTCATGCTTTC 493

Qy         181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
               ||||||||||||||||||:::|||:::||||||||||||||||||||
Db         492 AGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTCC 442
```

RESULT 12
AJ820622/c
LOCUS AJ820622 778 bp mRNA linear EST 12-MAY-2005
DEFINITION AJ820622 KN206 Bos sp. cDNA clone C0006020h12, mRNA sequence.
ACCESSION AJ820622
VERSION AJ820622.1 GI:51888098
KEYWORDS EST.
SOURCE Bos sp.
ORGANISM Bos sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 778)
AUTHORS McGuire,K. and Glass,E.J.
TITLE The expanding role of microarrays in the investigation of macrophage responses to pathogens
JOURNAL Vet. Immunol. Immunopathol. 105 (3-4), 259-275 (2005)
COMMENT Contact: McGuire K
Genomics and Genetics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options. Vector:pBluescriptII(SK+) R. Site 1:EcoRV(lost) R. Site 2:NotI Seq Primer: T7 Normalised library constructed from pooled monocytes from Bos taurus (Holstein) and Bos indicus (Sahiwals) cattle subjected to various stimuli, including infection with the protozoan parasite Theileria annulata.
FEATURES Location/Qualifiers
source 1. .778
/organism="Bos sp."
/mol_type="mRNA"
/db_xref="taxon:29061"
/clone="C0006020h12"
/tissue_type="blood"
/cell_type="bovine monocyte"
/clone_lib="KN206"
/note="Vector: pBluescriptII(SK+); Site_1: EcoRV(lost); Site_2: NotI; Normalised library constructed from pooled monocytes from Bos taurus (Holstein) and Bos indicus (Sahiwals) cattle subjected to various stimuli, including infection with the protozoan parasite Theileria annulata"
ORIGIN

Alignment Scores:
Pred. No.: 8.99e-31 Length: 778
Score: 355.00 Matches: 71
Percent Similarity: 90.8% Conservative: 8
Best Local Similarity: 81.6% Mismatches: 8
Query Match: 35.5% Indels: 0
DB: 1 Gaps: 0

US-10-821-670A-36 (1-197) x AJ820622 (1-778)

```
Qy         111 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 130
               ||||||   |||||||||:::|||||||||||||||||||||||||||||||||||||||
Db         777 ATGTACCACGTGGAGTTCCAGGCCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAA 718

Qy         131 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 150
               ||||||||||||||||||||||||   ||||||   ||||||:::||||||||||||
Db         717 ATCTTTCTAGACCAGAACATGCTGGCAGCTATTGCTGAGCTGATGCAGGCCCTGAATTTC 658

Qy         151 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 170
               :::|||   ||||||||||||      ||||||:::|||   ||||||||||||||||||
Db         657 GACAGTGAGACTGTGCCACAGAAACCCTCCCTGAAAGAACTGGATTTTTACAAGACAAAA 598

Qy         171 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 190
               :::||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db         597 GTCAAGCTCTGCATCCTTCTTCACGCCTTCAGAATTCGTGCGGTGACCATCGACAGAATG 538

Qy         191 MetSerTyrLeuAsnAlaSer 197
               ||||||||||:::::|||
Db         537 ATGAGCTATCTGAGTTCTTCC 517
```

RESULT 13
BU699383
LOCUS BU699383 561 bp mRNA linear EST 09-OCT-2002
DEFINITION LL2in11573T7 Hematopoietic Stem Cell Subtracted Library Mus musculus cDNA 5' similar to interleukin 12 p35 subunit, mRNA sequence.
ACCESSION BU699383
VERSION BU699383.1 GI:23615967
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 561)
AUTHORS Phillips,R.L., Ernst,R.E., Brunk,B.P., Ivanova,N., Mahan,M.A., Deanehan,J.K., Moore,K.A., Overton,G.C. and Lemischka,I.R.
TITLE The genetic program of hematopoietic stem cells
JOURNAL Science 288 (5471), 1635-1640 (2000)
PUBMED 10834841
COMMENT Contact: Lemischka, Ihor R.
Department of Molecular Biology
Princeton University
Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544, USA
Tel: 609 258 2838
Fax: 609 258 2759
Email: ilemischka@molbio.princeton.edu
These ESTs are derived from a subtracted cDNA library enriched for gene products expressed in day 14-14.5 fetal liver hematopoietic stem cells defined as Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E (Sca-1)pos
Seq primer: M13Reverse or T7.
FEATURES Location/Qualifiers
source 1. .561
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/tissue_type="Hematopoietic"
/cell_type="Stem Cells; Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E (Sca-1)pos"
/dev_stage="Embryonic day 14-14.5"
/lab_host="DH10B"
/clone_lib="Hematopoietic Stem Cell Subtracted Library"
/note="Organ: Fetal Liver; Vector: Sport 1; Site_1: Sal I; Site_2: Not I; Two directionally cloned cDNA libraries were made from fetal liver hematopoietic stem cells

enriched to be Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E (Sca-1)pos called Scapos and from AA4.1neg fetal liver cells. Subtractive hybridization was performed by hybridization of the target, Scapos, single stranded cDNA library in pSport1 to biotinylated RNA transcribed from the driver, AA4.1neg cDNA library in pSport2 with inserts cloned in the complementary orientation. For detailed protocols and additional information please see our website at http://stemcell.princeton.edu."

ORIGIN

Alignment Scores:

Pred. No.:	2.5e-30	Length:	561
Score:	349.50	Matches:	76
Percent Similarity:	68.1%	Conservative:	22
Best Local Similarity:	52.8%	Mismatches:	45
Query Match:	34.9%	Indels:	2
DB:	3	Gaps:	1

US-10-821-670A-36 (1-197) x BU699383 (1-561)

```
Qy         47 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 66
              :::|||||||||||||||||||:::|||:::||||||||||:::::   ||||||||||||
Db        128 CTCGATCATGAAGACATCACACGGGACCAAACCAGCACATTGAAGACCTGTTTACCACTG 187

Qy         67 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 86
              ||||||      ||||||||||||||||||:::||||||   |||      |||   |||
Db        188 GAACTACACAAGAACGAGAGTTGCCTGGCTACTAGAGAGACTTCTTCCACAACAAGAGGG 247

Qy         87 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 106
              |||||||||      :::|||||||||   |||   ||||||||||||   |||||||||
Db        248 AGCTGCCTGCCCCCACAGAAGACGTCTTTGATGATGACCCTGTGCCTTGGTAGCATCTAT 307

Qy        107 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 126
              ||||||||||||||||||||   ||||||:::|||:::||||||   |||
Db        308 GAGGACTTGAAGATGTACCAGACAGAGTTCCAGGCCATCAACGCAGCACTTCAGAATCAC 367

Qy        127 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 146
                 :::||||||   ||||||:::   ||||||      |||||||||||:::|||
Db        368 AACCATCAGCAGATCATTCTAGACAAGGGCATGCTGGTGGGCATCGATGAGCTGATGCAG 427

Qy        147 AlaLeuAsnValAsnSer---ValThrValProGlnAsnSerSerLeuGluGluProAsp 165
              :::|||:::   |||       :::     :::   |||       :::
Db        428 TCTCTGGATCATAATGGGCGAGACTCTGCGGCAAAAANCTCCTGTNGGGNGAAGCAGANC 487

Qy        166 PheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaVal 185
                 |||:::   ::::::||||||      ||||||::   |||      |||
Db        488 CTTTACAGAGTGGAAATGAAGCTCTG-NATCTGCTTTACGGCTTTAGCANCCGGTTGTGA 546

Qy        186 ThrIleAsnArg 189
                 :::   |||
Db        547 NCATTAAANAGG 558
```

RESULT 14
BF552757

```
LOCUS       BF552757                373 bp    mRNA    linear   EST 12-DEC-2000
DEFINITION  UI-R-C0-iz-d-02-0-UI.r1 UI-R-C0 Rattus norvegicus cDNA clone
            UI-R-C0-iz-d-02-0-UI 5', mRNA sequence.
ACCESSION   BF552757
VERSION     BF552757.1  GI:11662487
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 373)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
   PUBMED   8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156  MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            cDNA Library Preparation: M.B. Soares Lab Clone distribution:
            clones will be available through Research Genetics (www.resgen.com)
            This clone is also available through the I.M.A.G.E. Consortium at
            LLNL (info@image.llnl.gov). IMAGE ID= 1782759
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .373
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="UI-R-C0-iz-d-02-0-UI"
                     /dev_stage="adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="UI-R-C0"
                     /note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI;
                     The UI-R-C0 library is a subtracted library derived from
                     the UI-R-A1 and UI-R-E1 libraries. The UI-R-A1 library
                     consisted of a mixture of individually tagged normalized
                     libraries constructed from rat placenta, adult lung,
                     brain, liver, kidney, heart, spleen, ovary, and muscle.
                     The UI-R-E1 library consisted of a mixture of
                     individually tagged normalized libraries constructed from
                     8, 12 and 18-day embryo. The tag is a string of 3-5
                     nucleotides present between the Not I site and the
                     oligo-dT track which allows identification of the library
                     of origin of a clone within the mixture. The subtracted
                     library (UI-R-C0) was constructed as follows: PCR
                     amplified cDNA inserts from a pool of UI-R-A1 and UI-R-E1
                     clones from which 3' ESTs had been derived was used as a
                     driver in a hybridization with the pooled UI-R-A1 and
                     UI-R-E1 library in the form of single-stranded circles.
                     The remaining single-stranded circles (subtracted library)
                     was purified by hydroxyapatite column chromatography,
                     converted to double-stranded circles and electroporated
                     into DH10B bacteria (Life Technologies) to generate the
                     UI-R-C0 library. This procedure has been previously
                     described (Bonaldo, Lennon and Soares, Genome Research 6:
                     791-806, 1996)"
ORIGIN
```

Alignment Scores:

Pred. No.:	4.72e-30	Length:	373
Score:	345.00	Matches:	70
Percent Similarity:	73.8%	Conservative:	20
Best Local Similarity:	57.4%	Mismatches:	32
Query Match:	34.5%	Indels:	0
DB:	7	Gaps:	0

US-10-821-670A-36 (1-197) x BF552757 (1-373)

```
Qy         74 CysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLys 93
              |||||||||:::::|||   |||   |||      ||||||||||      :::|||
Db          8 TGCCTGGCTACTAAAGAGACTTCTTCCATAATAAGAGGGAGCTGCCTGCCTCCACAAAAG 67

Qy         94 ThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGln 113
              ||||||   |||   ||||||||||||   ||||||||||||||||||||||||||||||
Db         68 ACTTCTTTGATGATGACCCTGTGCCTTGGTAGCATCTATGAGGACTTGAAGATGTACCAG 127

Qy        114 ValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeu 133
                 ||||||:::|||:::||||||   |||               :::||||||   |||
Db        128 TCAGAGTTCCAGGCCATAAATGCAGCACTTCAGAGCCACAATCATCAGCAGATCACTCTG 187

Qy        134 AspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerVal 153
              |||:::|||||||||   |||||||||||||||:::::::::||||||   :::
Db        188 GACAGAAACATGCTGATGGCTATTGATGAGCTAATGCGGTCTCTGAATCACAGCGGCGAG 247
```

```
Qy        154 ThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeu 173
Db        248 ATTCTGCACCAGAAAGCTCCCATGGGAGAAGCAGATCCTTACAGAGTGAAGATGAAGCTC 307

Qy        174 CysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyr 193
Db        308 TGTATCCTGCTCCATGCCTTCAGCACACGCGTCATGACTATCAACAGGGTGATGAACTAT 367

Qy        194 LeuAsn 195
Db        368 CTGAGC 373

RESULT 15
CJ137697
LOCUS       CJ137697                692 bp    mRNA    linear   EST 23-SEP-2005
DEFINITION  CJ137697 RIKEN full-length enriched mouse cDNA library, C57BL/6J
            thymus 3 days neonate Mus musculus cDNA clone A630064E02 5', mRNA
            sequence.
ACCESSION   CJ137697
VERSION     CJ137697.1  GI:76238025
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 692)
  AUTHORS   The FANTOM Consortium and RIKEN Genome Exploration Research Group
            and Genome Science Group (Genome Network Project Core Group).
  TITLE     The transcriptional landscape of the mammalian genome
  JOURNAL   Science 309 (5740), 1559-1563 (2005)
   PUBMED   16141072
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. Tissues were provided by Dr. John Todd (
            Dept. of Medical Genetics Wellcome Trust Centre for Molecular
            Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes
            Hospital Cambridge ) whose assistance we gratefully acknowledge.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/.
FEATURES             Location/Qualifiers
     source          1. .692
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="A630064E02"
                     /tissue_type="thymus"
                     /dev_stage="3 days neonate"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library,
                     C57BL/6J thymus 3 days neonate"
ORIGIN

Alignment Scores:
Pred. No.:              1.49e-29        Length:         692
Score:                  344.00          Matches:        80
Percent Similarity:     53.8%           Conservative:   20
Best Local Similarity:  43.0%           Mismatches:     31
Query Match:            34.4%           Indels:         55
DB:                     5               Gaps:           2

US-10-821-670A-36 (1-197) x CJ137697 (1-692)

Qy         25 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 44
Db        118 AGCTTCTCCTTATGTTTTTCCCAGGCCAGAGAAAAACTGAAACATTATTCCTGCACTGCT 177

Qy         45 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeu 64
Db        178 GAAGACATCGATCATGAAGACATCACACGGGACCAAACCAGCACATTGAAGACCTGTTTA 237

Qy         65 ProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSer--------- 81
Db        238 CCACTGGAACTACACAAGAACGAGAGTTGCCTGGCTACTAGAGAGACTTCTTCCACAACA 297

Qy         81 ------------------------------------------------------------ 81
Db        298 GTAAGTAAGCACTCTAAGGGTTCCTTCCCCATGACGGATTCATAACACTGATGTCTGGTC 357

Qy         82 ---Leu-IleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThr----- 98
Db        358 ATTCTTTCTCTAGAGAGGGAGCTGCCTGCCCCCACAGAAGACGTCTTTGATGATGGTAAG 417

Qy         98 ------------------------------------------------------------ 98
Db        418 CCACATCACTTTTCTGAAATGCAGCAGGGTCCTGTAGTTCCAGCCCATCTCAATGATTCC 477

Qy         99 ------------------------ThrLeuCysLeuSerSerIleTyrGluAspLeuLy 110
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Qy        110 sMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGl 130
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Qy        130 nIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVa 150
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Qy        150 lAsnSerValThrVal 155
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Job time : 2417.57 secs
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OM protein - nucleic search, using frame_plus_p2n model

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	2	1001	100.0	591	3	US-09-917-265A-37	Sequence 37, Appl
	3	1001	100.0	666	3	US-09-917-265A-32	Sequence 32, Appl
c	4	1001	100.0	666	3	US-09-917-265A-34	Sequence 34, Appl
	5	1001	100.0	1533	3	US-09-917-265A-43	Sequence 43, Appl
c	6	1001	100.0	1533	3	US-09-917-265A-45	Sequence 45, Appl
	7	1001	100.0	1599	3	US-09-917-265A-38	Sequence 38, Appl
c	8	1001	100.0	1599	3	US-09-917-265A-40	Sequence 40, Appl
	9	998	99.7	591	3	US-09-011-143-9	Sequence 9, Appli
	10	998	99.7	591	3	US-09-302-495-9	Sequence 9, Appli
	11	998	99.7	591	3	US-10-079-616-9	Sequence 9, Appli
	12	998	99.7	689	3	US-09-011-143-26	Sequence 26, Appl
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	15	998	99.7	1441	3	US-09-011-143-8	Sequence 8, Appli
	16	998	99.7	1441	3	US-09-302-495-8	Sequence 8, Appli
	17	998	99.7	1441	3	US-10-079-616-8	Sequence 8, Appli
	18	960	95.9	1533	3	US-09-917-265A-66	Sequence 66, Appl
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	20	960	95.9	1599	3	US-09-917-265A-61	Sequence 61, Appl
c	21	960	95.9	1599	3	US-09-917-265A-63	Sequence 63, Appl
	22	944	94.3	561	3	US-09-917-265A-101	Sequence 101, App
c	23	944	94.3	561	3	US-09-917-265A-103	Sequence 103, App
	24	929	92.8	591	3	US-09-917-265A-49	Sequence 49, Appl
c	25	929	92.8	591	3	US-09-917-265A-51	Sequence 51, Appl
	26	929	92.8	666	3	US-09-917-265A-46	Sequence 46, Appl
c	27	929	92.8	666	3	US-09-917-265A-48	Sequence 48, Appl
	28	929	92.8	669	3	US-09-079-984A-12	Sequence 12, Appl
	29	929	92.8	669	3	US-09-390-729-12	Sequence 12, Appl
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	35	883	88.2	660	2	US-08-640-386A-3	Sequence 3, Appli
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	37	883	88.2	762	3	US-09-826-025-21	Sequence 21, Appl
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	39	883	88.2	1019	3	US-09-949-016-2462	Sequence 2462, Ap
	40	883	88.2	1316	2	US-08-684-687-3	Sequence 3, Appli
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	44	883	88.2	1364	2	US-08-965-688-3	Sequence 3, Appli
	45	883	88.2	1364	3	US-09-260-173-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-917-265A-35
; Sequence 35, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(591)
US-09-917-265A-35

Alignment Scores:

Pred. No.:	2.65e-122	Length:	591
Score:	1001.00	Matches:	197
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-36 (1-197) x US-09-917-265A-35 (1-591)

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Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
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Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
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Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
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Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
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RESULT 2
US-09-917-265A-37/c
; Sequence 37, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265A-37

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Score:	1001.00	Matches:	197
Percent Similarity:	100.0%	Conservative:	0
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Query Match:	100.0%	Indels:	0
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US-10-821-670A-36 (1-197) x US-09-917-265A-37 (1-591)

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Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
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Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
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Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
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Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
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Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
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RESULT 3
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; Sequence 32, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(666)
US-09-917-265A-32

Alignment Scores:

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US-10-821-670A-36 (1-197) x US-09-917-265A-32 (1-666)

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Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
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Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
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Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
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Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
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Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
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Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

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Db        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
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Db        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
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Db        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666

RESULT 4
US-09-917-265A-34/c
; Sequence 34, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-34

Alignment Scores:
Pred. No.:              3.2e-122      Length:        666
Score:                  1001.00       Matches:       197
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
Query Match:            100.0%        Indels:        0
DB:                     3             Gaps:          0

US-10-821-670A-36 (1-197) x US-09-917-265A-34 (1-666)

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Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
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Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 5
US-09-917-265A-43
; Sequence 43, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-09-917-265A-43

Alignment Scores:
Pred. No.:              1.19e-121     Length:        1533
Score:                  1001.00       Matches:       197
Percent Similarity:     100.0%        Conservative:  0
Best Local Similarity:  100.0%        Mismatches:    0
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Query Match:            100.0%      Indels:        0
DB:                     3           Gaps:          0

US-10-821-670A-36 (1-197) x US-09-917-265A-43 (1-1533)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        943 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1002

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1003 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1062

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1122

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1123 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1182

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1183 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1242

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1243 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1302

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1303 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1362

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1363 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1422

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1423 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1482

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1483 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533

RESULT 6
US-09-917-265A-45/c
; Sequence 45, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-45

Alignment Scores:
Pred. No.:              1.19e-121       Length:        1533
Score:                  1001.00         Matches:       197
Percent Similarity:     100.0%          Conservative:  0
Best Local Similarity:  100.0%          Mismatches:    0
Query Match:            100.0%          Indels:        0
DB:                     3               Gaps:          0

US-10-821-670A-36 (1-197) x US-09-917-265A-45 (1-1533)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 7
US-09-917-265A-38
; Sequence 38, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-09-917-265A-38

Alignment Scores:
Pred. No.:              1.27e-121       Length:        1599
Score:                  1001.00         Matches:       197
Percent Similarity:     100.0%          Conservative:  0
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Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-36 (1-197) x US-09-917-265A-38 (1-1599)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1009 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1068

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1069 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1128

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1129 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1188

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1189 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1248

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1249 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1308

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1309 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1368

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1369 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1428

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1429 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1488

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1489 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1548

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1549 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599

RESULT 8
US-09-917-265A-40/c
; Sequence 40, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-40

Alignment Scores:
Pred. No.:              1.27e-121       Length:         1599
Score:                  1001.00         Matches:        197
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-36 (1-197) x US-09-917-265A-40 (1-1599)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 9
US-09-011-143-9
; Sequence 9, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
```

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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  591 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-9

Alignment Scores:
Pred. No.:              6.6e-122      Length:         591
Score:                  998.00        Matches:        196
Percent Similarity:     100.0%        Conservative:   1
Best Local Similarity:  99.5%         Mismatches:     0
Query Match:            99.7%         Indels:         0
DB:                     3             Gaps:           0

US-10-821-670A-36 (1-197) x US-09-011-143-9 (1-591)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
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Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||:::|||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 591

RESULT 10
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US-09-302-495-9
; Sequence 9, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 591 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-302-495-9

Alignment Scores:
Pred. No.:              6.6e-122      Length:         591
Score:                  998.00        Matches:        196
Percent Similarity:     100.0%        Conservative:   1
Best Local Similarity:  99.5%         Mismatches:     0
Query Match:            99.7%         Indels:         0
DB:                     3             Gaps:           0

US-10-821-670A-36 (1-197) x US-09-302-495-9 (1-591)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180
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Qy          61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy          81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy         101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy         121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy         141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy         161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy         181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
               |||||||||||||||||||||||||||||||||||||||||||:::|||
Db         541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 591

RESULT 11
US-10-079-616-9
; Sequence 9, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 591 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-079-616-9

Alignment Scores:
Pred. No.:              6.6e-122        Length:         591
Score:                  998.00          Matches:        196
Percent Similarity:     100.0%          Conservative:   1
Best Local Similarity:  99.5%           Mismatches:     0
Query Match:            99.7%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-36 (1-197) x US-10-079-616-9 (1-591)

Qy           1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy          21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy          41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy          61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy          81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy         101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy         121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy         141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy         161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy         181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
               |||||||||||||||||||||||||||||||||||||||||||:::|||
Db         541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 591

RESULT 12
US-09-011-143-26
; Sequence 26, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
```

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;       STATE:  D.C.
;       COUNTRY:  USA
;       ZIP:  20004
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/011,143
;       FILING DATE:  04-FEB-1998
;       CLASSIFICATION:  536
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/JP97/01824
;       FILING DATE:  29-MAY-1997
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 165249/1996
;       FILING DATE:  04-JUN-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  BROWDY, Roger L.
;       REGISTRATION NUMBER:  25,618
;       REFERENCE/DOCKET NUMBER:  IMAMURA=1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-628-5197
;       TELEFAX:  202-737-3528
;   INFORMATION FOR SEQ ID NO:  26:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  689 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-09-011-143-26

Alignment Scores:
Pred. No.:              8.4e-122        Length:         689
Score:                  998.00          Matches:        196
Percent Similarity:     100.0%          Conservative:   1
Best Local Similarity:  99.5%           Mismatches:     0
Query Match:            99.7%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-36 (1-197) x US-09-011-143-26 (1-689)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 141

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 201

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 261

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        262 GAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 321

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 381

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 441

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 GCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 501

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        502 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 561

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        562 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 621

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||:::|||
Db        622 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 672

RESULT 13
US-09-302-495-26
; Sequence 26, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/302,495
;            FILING DATE: 30-Apr-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 26:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 689 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-302-495-26

Alignment Scores:
Pred. No.:              8.4e-122        Length:         689
Score:                  998.00          Matches:        196
Percent Similarity:     100.0%          Conservative:   1
Best Local Similarity:  99.5%           Mismatches:     0
Query Match:            99.7%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-36 (1-197) x US-09-302-495-26 (1-689)
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Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 141

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 201

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 261

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        262 GAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 321

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 381

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 441

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 GCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 501

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        502 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 561

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        562 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 621

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||:::|||
Db        622 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 672

RESULT 14
US-10-079-616-26
; Sequence 26, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 26:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 689 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-079-616-26

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Query Match:            99.7%           Indels:         0
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US-10-821-670A-36 (1-197) x US-10-079-616-26 (1-689)

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Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
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Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
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Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
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; Sequence 8, Application US/09011143
; Patent No. 6472509
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;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1441 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-8

Alignment Scores:
Pred. No.:              2.69e-121      Length:         1441
Score:                  998.00         Matches:        196
Percent Similarity:     100.0%         Conservative:   1
Best Local Similarity:  99.5%          Mismatches:     0
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GenCore version 5.1.9
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Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 2	1001	100.0	591	3	US-09-917-265-37	Sequence 37, Appl
3	1001	100.0	591	9	US-10-821-670-35	Sequence 35, Appl
c 4	1001	100.0	591	9	US-10-821-670-37	Sequence 37, Appl
5	1001	100.0	666	3	US-09-917-265-32	Sequence 32, Appl
c 6	1001	100.0	666	3	US-09-917-265-34	Sequence 34, Appl
7	1001	100.0	666	9	US-10-821-670-32	Sequence 32, Appl
c 8	1001	100.0	666	9	US-10-821-670-34	Sequence 34, Appl
9	1001	100.0	1533	3	US-09-917-265-43	Sequence 43, Appl
c 10	1001	100.0	1533	3	US-09-917-265-45	Sequence 45, Appl
11	1001	100.0	1533	9	US-10-821-670-43	Sequence 43, Appl
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13	1001	100.0	1599	3	US-09-917-265-38	Sequence 38, Appl
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18	998	99.7	689	6	US-10-079-616-26	Sequence 26, Appl
19	998	99.7	1441	6	US-10-079-616-8	Sequence 8, Appli
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27	960	95.9	1599	9	US-10-821-670-61	Sequence 61, Appl
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31	944	94.3	561	9	US-10-821-670-101	Sequence 101, App
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c 42	929	92.8	1455	3	US-09-917-265-106	Sequence 106, App
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45	883	88.2	762	3	US-09-826-025-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-09-917-265-35
; Sequence 35, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(591)
; OTHER INFORMATION:
US-09-917-265-35

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Alignment Scores:
Pred. No.:              5.63e-123       Length:         591
Score:                  1001.00         Matches:        197
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
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US-10-821-670A-36 (1-197) x US-09-917-265-35 (1-591)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
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Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
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Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
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Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
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RESULT 2
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; Sequence 37, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
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US-09-917-265-37

Alignment Scores:
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DB:                     3               Gaps:           0

US-10-821-670A-36 (1-197) x US-09-917-265-37 (1-591)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 3
US-10-821-670-35
; Sequence 35, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(591)
US-10-821-670-35
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Alignment Scores:
Pred. No.:                5.63e-123       Length:         591
Score:                    1001.00         Matches:        197
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              100.0%          Indels:         0
DB:                       9               Gaps:           0

US-10-821-670A-36 (1-197) x US-10-821-670-35 (1-591)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591

RESULT 4
US-10-821-670-37/c
; Sequence 37, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-37

Alignment Scores:
Pred. No.:                5.63e-123       Length:         591
Score:                    1001.00         Matches:        197
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              100.0%          Indels:         0
DB:                       9               Gaps:           0

US-10-821-670A-36 (1-197) x US-10-821-670-37 (1-591)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 5
US-09-917-265-32
; Sequence 32, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
;   OTHER INFORMATION:
US-09-917-265-32
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Alignment Scores:
Pred. No.:                6.85e-123       Length:         666
Score:                    1001.00         Matches:        197
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              100.0%          Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-36 (1-197) x US-09-917-265-32 (1-666)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666

RESULT 6
US-09-917-265-34/c
; Sequence 34, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-34

Alignment Scores:
Pred. No.:                6.85e-123       Length:         666
Score:                    1001.00         Matches:        197
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              100.0%          Indels:         0
DB:                       3               Gaps:           0

US-10-821-670A-36 (1-197) x US-09-917-265-34 (1-666)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 7
US-10-821-670-32
; Sequence 32, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
US-10-821-670-32
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Alignment Scores:
Pred. No.:                6.85e-123       Length:         666
Score:                    1001.00         Matches:        197
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              100.0%          Indels:         0
DB:                       9               Gaps:           0

US-10-821-670A-36 (1-197) x US-10-821-670-32 (1-666)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666

RESULT 8
US-10-821-670-34/c
; Sequence 34, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-34
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Alignment Scores:
Pred. No.:                6.85e-123       Length:         666
Score:                    1001.00         Matches:        197
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              100.0%          Indels:         0
DB:                       9               Gaps:           0

US-10-821-670A-36 (1-197) x US-10-821-670-34 (1-666)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 9
US-09-917-265-43
; Sequence 43, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
;   OTHER INFORMATION:
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US-09-917-265-43

Alignment Scores:
Pred. No.: 2.69e-122 Length: 1533
Score: 1001.00 Matches: 197
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-821-670A-36 (1-197) x US-09-917-265-43 (1-1533)

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Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        943 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1002

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1003 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1062

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1122

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1123 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1182

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1183 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1242

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1243 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1302

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1303 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1362

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1363 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1422

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1423 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1482

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1483 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
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RESULT 10
US-09-917-265-45/c
; Sequence 45, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265-45

Alignment Scores:
Pred. No.: 2.69e-122 Length: 1533
Score: 1001.00 Matches: 197
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-821-670A-36 (1-197) x US-09-917-265-45 (1-1533)

```
Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
```

RESULT 11
US-10-821-670-43
; Sequence 43, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)

US-10-821-670-43

Alignment Scores:

Pred. No.:	2.69e-122	Length:	1533
Score:	1001.00	Matches:	197
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	9	Gaps:	0

US-10-821-670A-36 (1-197) x US-10-821-670-43 (1-1533)

```
Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        943 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1002

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1003 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1062

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1122

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1123 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1182

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1183 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1242

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1243 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1302

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1303 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1362

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1363 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1422

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1423 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1482

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1483 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533
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RESULT 12
US-10-821-670-45/c
; Sequence 45, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
US-10-821-670-45

Alignment Scores:

Pred. No.:	2.69e-122	Length:	1533
Score:	1001.00	Matches:	197
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	9	Gaps:	0

US-10-821-670A-36 (1-197) x US-10-821-670-45 (1-1533)

```
Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
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RESULT 13
US-09-917-265-38
; Sequence 38, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1599)

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;   OTHER INFORMATION:
US-09-917-265-38

Alignment Scores:
Pred. No.:              2.89e-122       Length:         1599
Score:                  1001.00         Matches:        197
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-36 (1-197) x US-09-917-265-38 (1-1599)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1009 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1068

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1069 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1128

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1129 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1188

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1189 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1248

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
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Db       1249 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1308

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1309 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1368

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1369 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1428

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1429 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 1488

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
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Db       1489 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1548

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1549 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599

RESULT 14
US-09-917-265-40/c
; Sequence 40, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-40

Alignment Scores:
Pred. No.:              2.89e-122       Length:         1599
Score:                  1001.00         Matches:        197
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-36 (1-197) x US-09-917-265-40 (1-1599)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
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Db        591 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
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Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1

RESULT 15
US-10-821-670-38
; Sequence 38, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
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; LOCATION: (1)..(1599)
US-10-821-670-38

Alignment Scores:

Pred. No.:	2.89e-122	Length:	1599
Score:	1001.00	Matches:	197
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
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US-10-821-670A-36 (1-197) x US-10-821-670-38 (1-1599)

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Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
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Db       1009 AGAAACTTGCCAACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAA 1068

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40
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Db       1069 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 1128

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1129 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 1188

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
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Db       1189 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 1248

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1249 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 1308

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1309 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 1368

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1369 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 1428

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 160
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Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
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Db       1489 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 1548

Qy        181 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
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Job time : 775.817 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 10, 2006, 01:18:36 ; Search time 10.2494 Seconds
(without alignments)
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Title: US-10-821-670A-36
Perfect score: 1001
Sequence: 1 RNLPTPTPSPGMFQCLNHSQ.....HAFRIRAVTINRMMSYLNAS 197

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Searched: 253354 seqs, 63461778 residues

Total number of hits satisfying chosen parameters: 506708

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	92.5	9.2	2366	7	US-11-293-697-1960	Sequence 1960, Ap
	2	90	9.0	2480	6	US-10-953-349-35629	Sequence 35629, A
	3	87.5	8.7	1751	7	US-11-293-697-1794	Sequence 1794, Ap
	4	85	8.5	1875	7	US-11-217-529-174200	Sequence 174200,
	5	84	8.4	990	7	US-11-217-529-79916	Sequence 79916, A
c	6	83	8.3	1647	6	US-10-953-349-3750	Sequence 3750, Ap
	7	82	8.2	2406	7	US-11-217-529-76395	Sequence 76395, A
	8	81	8.1	2310	7	US-11-217-529-4722	Sequence 4722, Ap
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	10	79	7.9	762	7	US-11-217-529-166587	Sequence 166587,
	11	79	7.9	1836	7	US-11-217-529-2301	Sequence 2301, Ap
	12	79	7.9	2244	7	US-11-217-529-78602	Sequence 78602, A
	13	79	7.9	3405	7	US-11-217-529-77844	Sequence 77844, A
	14	79	7.9	6429	7	US-11-217-529-4027	Sequence 4027, Ap
	15	78.5	7.8	5198	6	US-10-505-928-342	Sequence 342, App
	16	77.5	7.7	1374	6	US-10-953-349-13043	Sequence 13043, A
	17	77.5	7.7	2463	7	US-11-217-529-79273	Sequence 79273, A
	18	77	7.7	1473	7	US-11-217-529-81075	Sequence 81075, A
c	19	77	7.7	1542	7	US-11-217-529-4965	Sequence 4965, Ap
	20	76.5	7.6	2583	7	US-11-217-529-5733	Sequence 5733, Ap
	21	76	7.6	28605	6	US-10-471-571A-4495	Sequence 4495, Ap
	22	75.5	7.5	1567	6	US-10-953-349-2350	Sequence 2350, Ap
	23	75.5	7.5	1902	7	US-11-217-529-78885	Sequence 78885, A
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	25	75	7.5	2619	7	US-11-217-529-78771	Sequence 78771, A
	26	75	7.5	9588	6	US-10-505-928-101	Sequence 101, App
	27	74.5	7.4	1155	6	US-10-953-349-6668	Sequence 6668, Ap
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	34	73.5	7.3	1433	6	US-10-953-349-19986	Sequence 19986, A
c	35	73.5	7.3	3403	7	US-11-145-307A-74	Sequence 74, Appl
	36	73	7.3	1905	7	US-11-217-529-81904	Sequence 81904, A
	37	73	7.3	3369	7	US-11-217-529-76775	Sequence 76775, A
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	40	72.5	7.2	1371	7	US-11-264-784-37	Sequence 37, Appl
	41	72.5	7.2	1371	7	US-11-264-737-42	Sequence 42, Appl
	42	72.5	7.2	1371	7	US-11-265-761-37	Sequence 37, Appl
	43	72.5	7.2	2723	7	US-11-293-697-823	Sequence 823, App
	44	72.5	7.2	3015	7	US-11-217-529-76510	Sequence 76510, A
	45	72.5	7.2	3189	7	US-11-293-697-748	Sequence 748, App

ALIGNMENTS

RESULT 1
US-11-293-697-1960
; Sequence 1960, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1960
; LENGTH: 2366
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-1960

Alignment Scores:

Pred. No.:	0.0776	Length:	2366
Score:	92.50	Matches:	47
Percent Similarity:	38.7%	Conservative:	30
Best Local Similarity:	23.6%	Mismatches:	85
Query Match:	9.2%	Indels:	37
DB:	7	Gaps:	9

US-10-821-670A-36 (1-197) x US-11-293-697-1960 (1-2366)

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Qy          4 ProThrProThrProSerProGlyMetPheGlnCysLeuAsn------HisSerGlnThr 21
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Qy         22 LeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSer 41
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Db        943 TTGATGAACCCATTGAGTGACTCTCTTAGTTCCATATCAATACCTTTGAATTCCTGGTCG 1002

Qy         42 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 61
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Qy         62 AlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSer 81
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Db       1039 GATGCATTGCCAGCTGAGTTATTGGAAGCCCTGAACACATTGTCAGAAGCCAAGGTGGAA 1098

Qy         82 LeuIleThrAsn-----------GlySerCysLeuAlaSerArgLysThrSerPheMet 97
                |||   :::           ||||||   |||   :::|||
Db       1099 ACCATCTGTCACAGAAAAGAGGGAGGTAGCAGTCTCATTGCCAGAAATGAATGTTTAGAA 1158

Qy         98 ThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLys 117
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Qy        118 AlaMetAsnAlaLysLeuLeuMetAspProLys---------ArgGlnIlePheLeuAsp 134
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Qy        135 GlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThr 154
              ||||||   :::|||:::   :::   |||           |||   ||||||||||||
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Db       1312 ---------AATAGCTCTGATCAGGAA-----------------------ACTGCGTGT 1338

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RESULT 2
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; Sequence 35629, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35629
;   LENGTH: 2480
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (601)..(601)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (603)..(603)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (621)..(621)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-35629

Alignment Scores:
Pred. No.:              0.17          Length:         2480
Score:                  90.00         Matches:        38
Percent Similarity:     43.3%         Conservative:   33
Best Local Similarity:  23.2%         Mismatches:     60
Query Match:            9.0%          Indels:         34
DB:                     6             Gaps:           6

US-10-821-670A-36 (1-197) x US-10-953-349-35629 (1-2480)

Qy         40 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 59
                |||   |||   ::::::|||       |||   ::::::            :::
Db       1328 TATCTTTGCTTGACCAAGGAAGCAACGCACAACAATCTATTGTTGCACTTGAGCAGGAAA 1387

Qy         60 ValGluAlaCysLeuProLeu--------------------------GluLeuThrMet 70
                :::   :::   :::   |||                                |||||||||
Db       1388 TTGCACTCCTCAGTCAGTTTGAACATGAAAATATAGTCCAGTATTATGGAACTGACAAG- 1446

Qy         71 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 90
                ||||||   |||           |||   |||:::|||   ||||||
Db       1447 GAAGAATCCAAACTCTATATT---TTTATTGAGCTTGTCACGCAAGGATCT--------- 1494

Qy         91 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 110
                                          |||||||||:::|||:::      |||
Db       1495 -------------------------------CTTTCATCCCTCTACCAAAAGTATAAA 1521

Qy        111 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 130
                :::   :::   :::       |||         ::::::|||
Db       1522 CTACGAGAATCACAAGTCTCTGCATACACAAGGCAGATTCTT---------AACGGATTG 1572

Qy        131 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 150
                ::::::|||   :::       :::           |||                :::
Db       1573 GTTTACCTGCATGAGAGAAATGTGGTCCACAGAGAT--------------ATCAAGTGT 1617

Qy        151 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 170
                  ::::::   |||       |||   |||::::::       ||||||         |||
Db       1618 GCCAATATATTGGTGCATGCAAATGGATCTGTAAAGCTTGCAGATTTTGGATTGGCAAAG 1677

Qy        171 ---IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArg 189
                   :::   ||||||:::   :::|||   |||   :::|||:::|||   ::::::
Db       1678 GAGGTTACCCTTTGTCTTTCTGTTCATTATTTCCATGTTCGCAGTGTCAAATTGTCTTAT 1737

Qy        190 MetMetSerTyr 193
                |||:::
Db       1738 GGTTGTAGTTTT 1749

RESULT 3
US-11-293-697-1794
; Sequence 1794, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1794
;   LENGTH: 1751
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1794

Alignment Scores:
Pred. No.:              0.205         Length:         1751
Score:                  87.50         Matches:        43
Percent Similarity:     35.1%         Conservative:   29
Best Local Similarity:  21.0%         Mismatches:     80
Query Match:            8.7%          Indels:         53
DB:                     7             Gaps:           8

US-10-821-670A-36 (1-197) x US-11-293-697-1794 (1-1751)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20
              |||:::||||||         |||   ||||||:::         :::   |||
```

```
Db        291 AGAGACTTACCA---------CCCAAGCCTGGGCTG---------GTGGGACACCGAGGG 332

Qy         21 ThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyr 40

Db        333 GCCCCCATGCTGGCTCCCGAGAACACCCTGATGTCCTTGCGGAAGACAGCTGAA---TGC 389

Qy         41 SerCysThrSerGluGluIleAsp--------------------------------His 49

Db        390 GGAGCTACTGTGTTTGAGACTGATGTGATGGTCAGCTCCGATGGGGTCCCCTTCCTCATG 449

Qy         50 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThr 69

Db        450 CATGATGAGCACCTCAGCAGGACCACGAATGTAGCCTCTGTATTCCCAACCCGAATCACA 509

Qy         70 MetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeu 89

Db        510 GCCCACAGCAGTGACTTCTCCTGGACTGAACTGAAGAGACTCAATGCTGGATCCTGGTTC 569

Qy         90 AlaSerArgLys-----------------------------------------------Thr 94

Db        570 CTAGAGAGGCGACCCTTCTGGGGGGCCAAACCGCTGGCAGGCCCTGATCAGAAAGAGGCT 629

Qy         95 SerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnVal 114

Db        630 GAGAGTCAGACGGTACCAGCATTAGAAGAGCTATTGGAG---------------------- 668

Qy        115 GluPheLysAlaMetAsnAlaLysLeuLeuMetAsp------------ProLysArgGln 130

Db        669 GAAGCTGCAGCCCTCAACCTTTCCATCATGTTCGACTTGCGCCGACCCCCACAGAACCAC 728

Qy        131 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 150

Db        729 ACATACTATGACACTTTTGTGATCCAGACATTGGAGACTGTGCTGAATGCAAGGGTGCCC 788

Qy        151 AsnSerVal---------------------------ThrValProGlnAsnSerSerLeu 161

Db        789 CAAGCCATGGTGATGTTGCCAGGACCCCCTCTCCCCACCCTGCCTTCCCTAGGCCATGAT 848

Qy        162 GluGluProAspPhe 166

Db        849 GATGAGGATGATTTT 863

RESULT 4
US-11-217-529-174200
; Sequence 174200, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174200
;   LENGTH: 1875
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-174200

Alignment Scores:
Pred. No.:              0.466          Length:        1875
Score:                  85.00          Matches:       43
Percent Similarity:     40.0%          Conservative:  33
Best Local Similarity:  22.6%          Mismatches:    65
Query Match:            8.5%           Indels:        49

DB:                     7              Gaps:          9

US-10-821-670A-36 (1-197) x US-11-217-529-174200 (1-1875)

Qy          1 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 20

Db        178 AGATTTATCATGACACCTTTATATTCCAGTGGCTCACAGGAACTT------CACTCAGAT 231

Qy         21 ThrLeuLeuArgAlaIle---------SerAsnThrLeuGlnLysAlaArgGlnThrLeu 37

Db        232 TTTTTGGTTAAAAGCATCCAAGATCTTACGAATTCGATGTTACAATTTAGTGATCCATTG 291

Qy         38 GluPheTyrSerCysThrSerGlu---GluIleAspHisGluAspIleThrLysAspLys 56

Db        292 ACCACATATAATAGGTACAAAGAAGATGACATTAGCTCTTCAGACAGTAGTAGTGATCTC 351

Qy         57 ThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAla 76

Db        352 AACTCTAATATAGAAGCTTCAAAACCA------------------------------- 378

Qy         77 SerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPhe 96

Db        379 -----------------GCCGCAAATGGTTCTTATACTCTTCAAAATATGCGGAACAAG 420

Qy         97 MetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPhe 116

Db        421 GCCCTTAATGTAGCCTTAGCGAAATTG--------------------AAAATAGCATTA 459

Qy        117 LysAlaMetAsnAlaLysLeuLeuMet---------AspProLysArg---------Gln 130

Db        460 AAGGACGTTACCATACGTTTAATAGTAAATGATAGAGATCCTTCCGATAACATCGTGGAG 519

Qy        131 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 150

Db        520 GTTCATCTAGAAAGCATACAACTTATTACTACAGACGCAAATTTACGACATATAAACATT 579

Qy        151 AsnSerValThrVal-ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLy 170

Db        580 GAAAATATCACCATTTCCTCAA--------------------------TACAAAAACAA 612

Qy        170 sIle---------LysLeuCysIleLeu 176

Db        613 GCTGTACCCGACTCTCCTGTGCATCCTT 640

RESULT 5
US-11-217-529-79916
; Sequence 79916, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79916
;   LENGTH: 990
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-79916

Alignment Scores:
Pred. No.:              0.235          Length:        990
Score:                  84.00          Matches:       46
Percent Similarity:     41.1%          Conservative:  32
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Best Local Similarity:  24.2%          Mismatches:    68
Query Match:            8.4%           Indels:        44
DB:                     7              Gaps:          8

US-10-821-670A-36 (1-197) x US-11-217-529-79916 (1-990)

Qy         17 AsnHisSerGlnThrLeuLeuArgAlaIleSer------AsnThrLeuGlnLysAlaArg 34
              |||   |||::::::|||||   |||         |||   :::|||||
Db         40 AATACCTCTGAATCGTTATTAGTTGATATTCAAGAATACAATCAAATTCAAAAACAAATT 99

Qy         35 GlnThrLeuGluPhe---TyrSerCysThrSerGluGluIleAspHisGluAspIleThr 53
              :::|||::::::        :::      :::||||||:::      :::       |||
Db        100 GAGACCATTCAGGCTGATCTCAACCATGTAACGGAAGAGCTACAGACGCAATATGCTACA 159

Qy         54 LysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu--------------- 68
                |||||   |||:::::::::   |||   |||   |||
Db        160 TCGCAAAAAACAAAGACCATTCAAAGTGATTTAAATCTCTCGTTGCATAAATTGGATTTG 219

Qy         69 --------------------ThrMetAsnGluSerCysLeuAlaSerArgGluIleSer 81
                                   :::      :::|||     |||
Db        220 GCTAAGCGTAATCTCGACGCGAATCCATCTTCCCAAATAATTGCGAGGAATGAAGAAATT 279

Qy         82 LeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThr---ThrLeu 100
              |||       |||   |||             ||||||      |||:::
Db        280 TTGAGGGACATTGGAGAATGTGAGAATGAAATCAAAACCAAGCAAATGAGCTTAAAGAAA 339

Qy        101 Cys---------LeuSerSerIleTyrGluAspLeuLysMetTyr--------------- 112
              |||         :::|||:::|||   :::|||:::|||   |||
Db        340 TGTCAAGAAGAAGTTTCGACCATTGAAAAAGACATGAAGGAGTACGATAGCGATAAAGGA 399

Qy        113 ------------------GlnValGluPheLysAlaMetAsnAlaLysLeu--------- 123
                               :::   |||   |||   :::       :::|||
Db        400 TCCAAGTTAAATGAATTAAAGAAGGAATTGAAACTATTGGCGAAAGAGCTGGAGGAGCAG 459

Qy        124 LeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGlu 143
                  :::   :::|||:::      |||   ||||||:::             ::::::
Db        460 GAATCGGAGTCAGAACGTAAATATGACTTGTTTCAAAACTTGGAATTAGAAACAGAGCAA 519

Qy        144 LeuLeuGlnAlaLeuAsnValAsnSerValThrValPro--------------------- 156
              |||         |||:::   |||         :::
Db        520 TTGAGCTCAGAACTAGATTCTAATAAGACGCTATTGCAAAACCATTTGAAATCTATTGAA 579

Qy        157 ------------GlnAsnSerSerLeuGlu 162
                          :::||||||   ||||||
Db        580 AGTTTGAAATTGGAAAATTCTGATTTGGAG 609

RESULT 6
US-10-953-349-3750/c
; Sequence 3750, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3750
;   LENGTH: 1647
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-3750

Alignment Scores:
Pred. No.:              0.677          Length:        1647
Score:                  83.00          Matches:       31
Percent Similarity:     44.8%          Conservative:  12
Best Local Similarity:  32.3%          Mismatches:    31
Query Match:            8.3%           Indels:        22
DB:                     6              Gaps:          5

US-10-821-670A-36 (1-197) x US-10-953-349-3750 (1-1647)

Qy         42 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 61
              |||         |||         |||||||||   ||||||            :::|||
Db       1098 TGCCTCCTTAGTGAATGTTTTTGGGAAGATATCCTTAAGGAT------------ATTGAG 1051

Qy         62 AlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu------ 79
              |||   :::|||       |||:::      :::||||||:::|||   :::
Db       1050 GCTACTGTCCCATCTTGGCTGAGTCAGATAGATAGTTGTGTCGCTGGCAAATCCAAGCTT 991

Qy         80 ---------------------IleSerLeuIleThrAsnGlySerCysLeuAlaSerArg 92
                                   :::|||::::::|||         ||||||
Db        990 TCTCAAGAATAAAGCAATCTCTTGAGCGTTGTAACA---------TGTCTTGGACCCTAC 940

Qy         93 LysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyr 112
                |||||   |||             |||         |||   |||   |||:::|||
Db        939 TACACCAGTTGTATGGCAATTTTTCTTCTCAAG------TATGTCGATTCTAAGGTCTAC 886

Qy        113 GlnValGlu------------PheLysAlaMetAsnAlaLysLeuLeu 124
                  |||             |||   ||||||:::   :::   |||
Db        885 TGCTATGAAACGGCCACCGGATTTACGGCTATGAGTCCTCAACCGCTC 838

RESULT 7
US-11-217-529-76395
; Sequence 76395, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76395
;   LENGTH: 2406
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-76395

Alignment Scores:
Pred. No.:              1.6            Length:        2406
Score:                  82.00          Matches:       36
Percent Similarity:     42.1%          Conservative:  25
Best Local Similarity:  24.8%          Mismatches:    48
Query Match:            8.2%           Indels:        36
DB:                     7              Gaps:          6

US-10-821-670A-36 (1-197) x US-11-217-529-76395 (1-2406)

Qy         46 GluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuPro 65
              :::||||||         :::      |||:::|||      |||
Db        277 AAGATAGACGAGTATAAAGTTGTTCTGGATCAAACACGCCAGGTTAATGAT--------- 327

Qy         66 LeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsn 85
                        ::::::   |||             |||:::||||||      |||
Db        328 ---------CAATTGGATAGTTCCATCAAGAAATTTCGGAAAATCTCTCAGGATACT--- 375

Qy         86 GlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIle 105
              |||:::   :::       ||||||   :::                 ||||||::::::
Db        376 GGAGCTTTCATTGAGGAAACGAAGACGATCTATGAAAAGCAGTCTAAATTAAGCAATCTA 435

Qy        106 TyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMet 125
                 |||   :::                 ||||||::::::         ::::::
Db        436 ACTGAGTCAATCCCT----------------AAAGCTCTCCATTATTTTGAAGTTTTG 477
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Qy        126 AspPro-------------------------------------------LysArgGlnIle 131
              ||||||                                           |||:::
Db        478 GACCCTATAATGCGTCGCTTGAACCATGCCACTTCTCCCGCTATTGTCAAGAAGAGCTCC 537

Qy        132 PheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsn 151
              |||             ||||||      |||||||||   |||:::   |||:::
Db        538 TTT------ACGACGATGTTGGCGACTATCGACGAGTCTTTACGTTTTTTGGAT------ 585

Qy        152 SerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIle 171
                          :::||||||   |||::::::        |||:::  |||
Db        586 --------------GAGAATAGTGACCTCAAGGATGCAGCAGCGTACAGAATCAAGTTC 630

Qy        172 LysLeuCysIleLeu 176
              |||   |||::::::
Db        631 AAGCAATGCTTGATC 645

RESULT 8
US-11-217-529-4722
; Sequence 4722, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4722
;   LENGTH: 2310
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-4722

Alignment Scores:
Pred. No.:              2           Length:         2310
Score:                  81.00       Matches:        43
Percent Similarity:     40.6%       Conservative:   39
Best Local Similarity:  21.3%       Mismatches:     76
Query Match:            8.1%        Indels:         44
DB:                     7           Gaps:           9

US-10-821-670A-36 (1-197) x US-11-217-529-4722 (1-2310)

Qy          4 ProThrPro---ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeu 22
              |||:::|||   :::|||||||||   :::         |||:::   |||   :::
Db       1051 CCCTCCCCATCTTCACCTTCACCAACATTAACTGCAGTCTTATCCCCATCTCCATCGAAT 1110

Qy         23 LeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCys 42
                 :::::::::|||:::|||            :::||||||           |||
Db       1111 ACTAAATCTGTTTCTCATACCGCTTCGCCAGTTAAGCAGACTAATAACGACATCAGT--- 1167

Qy         43 ThrSerGluGluIleAspHisGluAsp------IleThrLysAspLysThrSerThrVal 60
                    |||:::   |||   |||      ||||||   ::::::|||:::
Db       1168 AATGAACCAGAACTGCAACACAATGATCAACCTATAACGAATGAACAAACAACAAGAACA 1227

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              :::                        |||      :::   ::::::|||   |||:::
Db       1228 AAG--------------------ATGATGGCGGCGGCAACAGTATCATCTGAAGAATTG 1266

Qy         81 SerLeuIleThrAsn--------------GlySerCysLeuAlaSerArgLysThrSer 95
              |||          :::                  ||||||
Db       1267 AGTTTCGCTGATGATCTCGTTGAAAAAGTTTTCAGCTGCAATGATAAGCTATCAGATAAG 1326

Qy         96 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 115
              :::   |||   :::      :::               |||      |||::::::|||

Db       1327 TACAATACTCAAATATCGGCCAATATAGAACCTCCATTGCTGACATCATACAAGTTAGAA 1386

Qy         116 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 135
               |||      :::          |||      |||          |||
Db       1387 TTCCCCAATATTCCGAGAAGTGCACTC------CCGGCAGAA---------ACGGATGCG 1431

Qy         136 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 155
               ::::::::::::::::::::   |||                              :::
Db       1432 GACGTTATATCATCTTTAGAGTCGTTGTACCAC----------------------ATC 1467

Qy         156 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 175
                     ||||||      |||        |||   ||||||
Db       1468 CATTGCAACTCCGTTTATGAAAGCATCAAATTTTTGAAAACCGAT--------------- 1512

Qy         176 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 195
                                          ||||||:::      :::|||:::   |||
Db       1513 ----------------------------ACTATATCAAATGCTTTATCTTTCTCCAAC 1542

Qy         196 AlaSer 197
               ::::::
Db       1543 TCCAAT 1548

RESULT 9
US-10-953-349-5587/c
; Sequence 5587, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5587
;   LENGTH: 1798
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-5587

Alignment Scores:
Pred. No.:              1.82        Length:         1798
Score:                  80.00       Matches:        34
Percent Similarity:     42.0%       Conservative:   26
Best Local Similarity:  23.8%       Mismatches:     57
Query Match:            8.0%        Indels:         26
DB:                     6           Gaps:           5

US-10-821-670A-36 (1-197) x US-10-953-349-5587 (1-1798)

Qy          58 SerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAla--- 76
               |||:::          ||||||||||||   :::                  |||:::
Db       1271 TCCTCTGCTGCCTTTTGCCTACCACTCTCAGTTTTGTTCCGCGCCTGCGAGCTGAGTCTG 1212

Qy          77 ----------------------------------------SerArgGluIleSerLeu 82
                                                      :::|||   ||||||
Db       1211 TATCGTCCTACTAAGTCGATGTAATATGGAATTAGCGCCACCAACCGGACAATATCATCC 1152

Qy          83 IleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThr------Leu 100
               |||            ||||||||||||   |||   :::    :::          |||
Db       1151 ATA-----------TGTTTAGCATCAGGTAAAGAAAACTTGAAAAGCATCATCTTCTTG 1104

Qy          101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 120
                ||||||         :::   |||:::   :::              |||      ::::::
Db       1103 TGCTTGCCAGGGTGTTGGTCAGATATATGCATCGACATGAAATTCTTCCCATACTTATCC 1044

Qy          121 AlaLysLeuLeuMetAspProLys---------ArgGlnIlePheLeuAspGlnAsnMet 137
                |||          ||||||          |||   :::   :::   ::::::
Db       1043 ACAGCCTTG------TCACCAAAAACCTGATCAAGAACAGTGTCAGTGATCAAATCCGCA 990

Qy          138 LeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGln 157
                   |||::::::|||      ::::::|||   :::   ::::::      :::|||
```

```
Db        989 GCAACTTCCTTGGATTCAGAGATCAAGGCGAACTCCTCCGACACCCATTTCCTTCCAGCA 930

Qy        158 AsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeu 177

Db        929 GGAGGAGACACAATCCCAGCAAATCTTTGCAAATCCCTCATCTCCTTTTGCATAGTTTTT 870

Qy        178 HisAlaPhe 180

Db        869 GCAGCCTTC 861
```

RESULT 10
US-11-217-529-166587
; Sequence 166587, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 166587
; LENGTH: 762
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-166587

Alignment Scores:

Pred. No.:	0.661	Length:	762
Score:	79.00	Matches:	46
Percent Similarity:	36.6%	Conservative:	18
Best Local Similarity:	26.3%	Mismatches:	66
Query Match:	7.9%	Indels:	45
DB:	7	Gaps:	7

US-10-821-670A-36 (1-197) x US-11-217-529-166587 (1-762)

```
Qy         23 LeuArgAla---IleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSer 41

Db         48 TTACGTGCTACCATTTCTAATCGGATTAGTGAAGCACAAGGACGTTTGCGC------TCT 101

Qy         42 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 61

Db        102 TGCCGGTCTGGACCCTAT------------------------------CCGATTATA 128

Qy         62 AlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSer 81

Db        129 CGCTGGCTTGGGCTACATGCCAATCAGAAAAAATCATGTTGCCAGAATCGTCGAATATGT 188

Qy         82 LeuIleThrAsnGlySerCysLeuAla---------SerArgLysThrSerPheMetThr 98

Db        189 CTGTTCTTCGGATGTAGTTCTATCGTCGAACCAAACCAAACTGCAACTAGCTTTTATCCA 248

Qy         99 ThrLeu------------------------------------------------------ 100

Db        249 ACACTTCCTGTCAGCAGAATTACTTCAACTAACTGAAGAAGAAAAAAATAAAATCTTGGA 308

Qy        101 ---Cys-LeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMe 119

Db        309 ATTTGTTGTGAGCAACCTGTATAACGAA---------CAATTTGTGGAAGTAAGAGTGCG 359

Qy        119 tAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuTh 139

Db        360 TGCTGCAGCCATACTGTCTGATATCGTTCACAACTGGAAGGAAGACCAAGCATTGTTGGA 419
```

```
Qy        139 rAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSe 159

Db        420 CCTGATCGACAGGTTTGCAAAGGGGCTTGACGCCAACAAATACACT---------- 465

Qy        159 rSerLeuGluGluProAspPheTyrLysThrLysIleLysLeu 173

Db        466 -TCGAAGGAAAAGCAAAAGTTATCAAAGACAGATATCAAAATC 507
```

RESULT 11
US-11-217-529-2301
; Sequence 2301, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2301
; LENGTH: 1836
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-2301

Alignment Scores:

Pred. No.:	2.51	Length:	1836
Score:	79.00	Matches:	39
Percent Similarity:	35.8%	Conservative:	30
Best Local Similarity:	20.2%	Mismatches:	93
Query Match:	7.9%	Indels:	31
DB:	7	Gaps:	3

US-10-821-670A-36 (1-197) x US-11-217-529-2301 (1-1836)

```
Qy          2 AsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThr 21

Db        355 AATATCAAGGAACCGCAGAGAGACCCAGCGGGAAGCCAA---------- 393

Qy         22 LeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSer 41

Db        394 ------AGATCAAAAAACAATGCCCTTTCCTTACCAACACAGACAACTTCTTCGTCCACC 447

Qy         42 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 61

Db        448 TCCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTATGATTCTGTAAGAAGGACTGAT 507

Qy         62 AlaCysLeuProLeuGluLeuThr----------MetAsnGluSerCysLeuAlaSer 77

Db        508 AATAGCGTTAGAATGCAAAAGAATAAACACTCCAGATTCAACAAGGAATTACCCCGCAGC 567

Qy         78 ArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMet 97

Db        568 AGGGAAAGCTCAAATATGAATTCTGGATCTATCATCAGTCAATACAATGTCGATACTCAG 627

Qy         98 ThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLys 117

Db        628 GCAACCGCTATAATGAGCGATATGCAAAAACAATATGAGTCGCAGCAACTGCCTTCGTTG 687

Qy        118 AlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIle---------- 131

Db        688 TTTATAAACGAGACTTTACTGATTGATCCAAATGGTAAAGTTTCAGAGGTTATAAAGTTG 747

Qy        132 --------------------------------PheLeuAspGlnAsnMetLeuThrAla 140
```

```
Db        748 ATATTTGAAGAAGTCGGCTACAAATTTGATGATTTTAGTGATATTTCCGTTTTCCAACTG 807

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSer-ValThrValProGlnAsnSerSe 160
              :::   |||:::   |||   :::      :::||| |||          ||||||
Db        808 ATGCAAGAAATGTATCAATTAATTAAGAAGGATTCTAGTAATAAAAAGTCAAAATTAACT 867

Qy        160 rLeuGluGluProAspPheTyrLysThrLysIleLys 172
               |||      |||         |||   |||   |||
Db        868 ACTTTTGCCTCCAAAGTAAAAGAAAAAGAAATGCAAG 904

RESULT 12
US-11-217-529-78602
; Sequence 78602, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78602
;   LENGTH: 2244
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-78602

Alignment Scores:
Pred. No.:              3.4          Length:        2244
Score:                  79.00        Matches:       48
Percent Similarity:     40.1%        Conservative:  31
Best Local Similarity:  24.4%        Mismatches:    74
Query Match:            7.9%         Indels:        44
DB:                     7            Gaps:          9

US-10-821-670A-36 (1-197) x US-11-217-529-78602 (1-2244)

Qy         18 HisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeu 37
              ||||||   :::|||       :::|||      |||:::|||:::          |||
Db        220 CATAGTGTTTCATTGAGTTTAAAGTTGTCT---GCCTTGAAGAAGTCAAATAGTGATTTG 276

Qy         38 GluPheTyr------SerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 55
              |||             |||   |||   |||      ::::::|||      ||||||
Db        277 GAGAAACAAGGAAAATCAGTGACATTAGAAAGCAAAGAAAACGAACTCCCTACCAAAAGG 336

Qy         56 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 75
              |||:::                    :::|||   :::   ||||||
Db        337 AAATCGCCTGATGAT-----------------AAACTCAACTTAGAAGAGTCATGGAAG 378

Qy         76 AlaSerArgGluIleSer---------LeuIleThrAsnGlySerCys------------ 88
              |||   :::||||||:::            :::   |||      |||
Db        379 GCTATTAAAGAAATAAACCATTACTGTTTCTTGAAAAACGATCCATGCATAAATCAAACC 438

Qy         89 -------------------------LeuAlaSerArgLysThrSerPheMetThrThr 99
                                       :::      :::|||   |||      |||:::
Db        439 GACGATTTTGCGTTCACAAACTTTATCATAAAAGATAAAAAAAACTCGTTGAGTACATCA 498

Qy        100 LeuCysLeuSer---------SerIleTyrGluAspLeuLysMetTyrGlnValGluPhe 116
              :::   ||||||         |||   :::      ||||||   :::      |||
Db        499 ATACCGCTATCGTCGCAGAATTCATCATTTCCGCCCTTAAAAAAGCATAACAATGAGCTC 558

Qy        117 LysAlaMet-------------------------AsnAlaLysLeuLeuMetAsp--- 126
                 :::                                 |||:::   ::::::
Db        559 CTTGGTATTTTTGTGCCTTGTAACCTGCCGAAAACAACTCGTAAAGTAGCCATTGAGAAT 618

Qy        127 ---------ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGlu 143
                       |||                :::             |||   |||   :::|||
Db        619 TTCAATAGACCAAGTCCTGATGATATAATACAATCGGCCCAACTTAATGCTTTCAATGAA 678

Qy        144 LeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeuGluGlu 163
              |||:::   ||||||:::   ||||||                :::      :::|||
Db        679 AAATTAGAAAACTTAAATATCAAATCTGTG---------CCCAAGGCCGAAAAAAAGGAA 729

Qy        164 ProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              |||         :::|||                |||   :::|||:::|||
Db        730 CCAATTAACCTTCAAACACCACCTACTGAGTCGATTGATATTCATTCATTC 780

RESULT 13
US-11-217-529-77844
; Sequence 77844, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77844
;   LENGTH: 3405
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-77844

Alignment Scores:
Pred. No.:              6.39         Length:        3405
Score:                  79.00        Matches:       41
Percent Similarity:     36.0%        Conservative:  21
Best Local Similarity:  23.8%        Mismatches:    48
Query Match:            7.9%         Indels:        62
DB:                     7            Gaps:          9

US-10-821-670A-36 (1-197) x US-11-217-529-77844 (1-3405)

Qy         45 GluGluIleAspHis-----------GluAspIleThrLysAsp------LysThrSer 58
              |||   :::||||||               |||   |||:::      |||::::::
Db        655 GAAAATGTGGATCATTCTATTGATTTACACTCTATAGTCAAAAATTTTGTCAAATCCAAT 714

Qy         59 ThrValGluAlaCysLeuProLeuGlu-----------------------------Leu 68
              |||:::|||:::       :::|||
Db        715 ACTCTGGAAAGTGCCTACTTAATTGAAGGAGGGAAGAGCGATGATTCAAAAGATGTAGAG 774

Qy         69 ThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCys 88
              |||   |||   |||   |||            ||||||   :::|||   |||   |||
Db        775 ACTAAAAATCTATCCATTCTA-----------ATAAGCTTTCTAACCAAAGGCGACTGT 822

Qy         89 LeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAsp 108
              |||                                          :::   |||   :::
Db        823 TTG-----------------------------------------AACTTTTACAATAAC 840

Qy        109 LeuLysMetTyrGlnValGluPheLys-----------------AlaMetAsnAlaLys 122
              :::            ||||||||                 |||:::|||   |||
Db        841 ATTTTACAAAGGTTATCTGAATTCAAAACATTTTTGAAATCTGAAGCACTAAATCTGAAA 900

Qy        123 ---------LeuLeuMetAspProLys---ArgGlnIlePheLeuAspGlnAsnMetLeu 138
                       |||      |||||||||            |||::::::         |||
Db        901 TTTGTTTGTCTAAACTATGATCCCAAATGCCTCCCTACCTTTATTGAGAGTGAAGCGTTA 960

Qy        139 ThrAlaIleAspGluLeuLeuGlnAlaLeuAsn-------------------------- 149
              |||         |||               |||
```

```
Db        961 ACAGAAAACGCTGAAGAAGCCGACATTACCAATGGTTCAACAATGATCAGTGCTTCGCTG 1020

Qy        150 --------------------------ValAsnSerValThrValProGlnAsnSerSer 160
                                        |||:::   :::         |||
Db       1021 CATCATAATATAGCGAACAAAGATGCTACAAGGTCGATTATAATTGAATTCAAAAGCCCC 1080

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLys 172
               :::|||:::   |||   :::|||   |||::::::
Db       1081 GTGGAGAAAAGCGATTTATTCAAAAAGAAATTACAA 1116

RESULT 14
US-11-217-529-4027
; Sequence 4027, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4027
;   LENGTH: 6429
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-4027

Alignment Scores:
Pred. No.:              16.7          Length:        6429
Score:                  79.00         Matches:       46
Percent Similarity:     36.6%         Conservative:  18
Best Local Similarity:  26.3%         Mismatches:    66
Query Match:            7.9%          Indels:        45
DB:                     7             Gaps:          7

US-10-821-670A-36 (1-197) x US-11-217-529-4027 (1-6429)

Qy         23 LeuArgAla---IleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSer 41
              |||||||||   |||||||||   :::   :::|||:::      |||         |||
Db       5712 TTACGTGCTACCATTTCTAATCGGATTAGTGAAGCACAAGGACGTTTGCGC------TCT 5765

Qy         42 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 61
              |||   |||                                              :::
Db       5766 TGCCGGTCTGGACCCTAT------------------------------CCGATTATA 5792

Qy         62 AlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSer 81
                    |||   |||                 :::||||||      :::|||   |||
Db       5793 CGCTGGCTTGGGCTACATGCCAATCAGAAAAAATCATGTTGCCAGAATCGTCGAATATGT 5852

Qy         82 LeuIleThrAsnGlySerCysLeuAla---------SerArgLysThrSerPheMetThr 98
              |||           |||   :::                         |||||||||
Db       5853 CTGTTCTTCGGATGTAGTTCTATCGTCGAACCAAACCAAACTGCAACTAGCTTTTATCCA 5912

Qy         99 ThrLeu------------------------------------------------------ 100
              ||||||
Db       5913 ACACTTCCTGTCAGCAGAATTACTTCAACTAACTGAAGAAGAAAAAAATAAAATCTTGGA 5972

Qy        101 ---Cys-LeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMe 119
                 ||| :::|||::::::|||   :::               ||||||   :::
Db       5973 ATTTGTTGTGAGCAACCTGTATAACGAA---------CAATTTGTGGAAGTAAGAGTGCG 6023

Qy        119 tAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuTh 139
               |||   :::|||   |||                 ||||||   :::|||
Db       6024 TGCTGCAGCCATACTGTCTGATATCGTTCACAACTGGAAGGAAGACCAAGCATTGTTGGA 6083

Qy        139 rAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSe 159
                 |||||          :::   |||:::   |||       |||
Db       6084 CCTGATCGACAGGTTTGCAAAGGGGCTTGACGCCAACAAATACACT------------- 6129

Qy        159 rSerLeuGluGluProAspPheTyrLysThrLysIleLysLeu 173
               |||   |||:::          ||||||   ||||||:::
Db       6130 -TCGAAGGAAAAGCAAAAGTTATCAAAGACAGATATCAAAATC 6171

RESULT 15
US-10-505-928-342
; Sequence 342, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
;  APPLICANT: Ludwig Institute for Cancer Research et al.
;  TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
;  FILE REFERENCE: 28967/39178
;  CURRENT APPLICATION NUMBER: US/10/505,928
;  CURRENT FILING DATE:  2004-08-27
;  PRIOR APPLICATION NUMBER: US 60/363,019
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: PatentIn 3.2
; SEQ ID NO 342
;   LENGTH: 5198
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-505-928-342

Alignment Scores:
Pred. No.:              14            Length:        5198
Score:                  78.50         Matches:       54
Percent Similarity:     39.7%         Conservative:  40
Best Local Similarity:  22.8%         Mismatches:    81
Query Match:            7.8%          Indels:        62
DB:                     6             Gaps:          13

US-10-821-670A-36 (1-197) x US-10-505-928-342 (1-5198)

Qy          1 ArgAsnLeuPro--------------ThrProThrProSer---ProGlyMetPhe--- 13
              |||   :::|||               |||||||||   |||   ||||||   |||
Db        690 CGAGAAGTACCTGAATGCCTAGAAATAACCCCTACTGCTTCTCTTCCTGGGGACTTTTTG 749

Qy         14 ---GlnCysLeuAsnHisSerGlnThrLeu-----------------LeuArgAlaIle 26
                  |||       |||:::|||   |||                 :::   ::::::
Db        750 ATTCCATGCAAAGTTCATACTCAAGAACTTTGTTCAAGAGAAATGATAGTTCACAGTGTA 809

Qy         27 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 46
                 :::           |||   :::   |||:::   :::   |||:::   :::
Db        810 GATGAC---TTCAGTTCAGCTTTAAAGGCTCTACAGTGCCATATATGTAGCAAAGATTCC 866

Qy         47 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 66
              :::|||       :::                                  |||   :::
Db        867 TTGGACTGTGGTAAGCTGCTTTCC-------------------------CTAAGAGTT 899

Qy         67 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu--------------------- 79
                 :::|||      ||||||   |||   |||   |||
Db        900 CATATCACTTCCAGGGAGAGT---TTGGACAGTGTGGAATTTGACTTGCATTGGGCAGCA 956

Qy         80 IleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThr 99
              ::::::|||      |||      |||         :::           :::   |||
Db        957 GTAACTCTAGCAAATAACTTTAAATGCACACCTGTGAAGCCCATCCCCATTATTCCAACA 1016

Qy        100 LeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMet 119
                     ::::::      :::|||   :::   ||||||:::
Db       1017 GCTCTGGCAAGAAACTTGAGCAGTAATCTGAATATTTCTCAAGTTCAAGGGACTTATAAA 1076

Qy        120 AsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThr 139
                   |||   ||||||      |||::::::   |||           |||
Db       1077 TATGGATATCTTACCATGGATGAAACACGCAAATTGTTACTT-----------TTGTTG 1124

Qy        140 AlaIleAspGluLeuLeuGlnAlaLeu----------------------AsnValAsn 151
                    |||      :::   :::|||                          :::
Db       1125 GAATCTGATCCCAAGGTTTATTCTCTACCATTGGTGGGAATTTGGCTGTCTGGAATTACA 1184
```

```
Qy        152 SerValThrValProGln----------------------------AsnSerSerLeu 161
                 :::      ||||||                            |||||||||::: 
Db       1185 CATATCTATAGTCCTCAGGTATGGGCTTGCTGTTTGCGATACATATTCAATTCTTCTGTT 1244

Qy        162 GluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe-Ar 181
               :::|||      |||   ::::::              |||:::|||::::::   
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2006, 22:44:33 ; Search time 151.409 Seconds
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1403666 seqs, 935554401 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
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Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        661 GCTTCC 666
              ||||||
Db        661 GCTTCC 666
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RESULT 2
US-09-917-265A-34/c
; Sequence 34, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-34

  Query Match           100.0%;  Score 666;  DB 3;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  666;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 607

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        606 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 547

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 427

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 307

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 247

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 187

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 127

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 7

Qy        661 GCTTCC 666
              ||||||
Db          6 GCTTCC 1
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RESULT 3
US-09-011-143-8
; Sequence 8, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
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;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1441 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-8

  Query Match             90.4%;  Score 602;  DB 3;  Length 1441;
  Best Local Similarity   99.8%;  Pred. No. 1.6e-300;
  Matches  652;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTA 653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTA 795


RESULT 4
US-09-302-495-8
; Sequence 8, Application US/09302495
; Patent No. 6518045

;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1441 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-302-495-8

  Query Match             90.4%;  Score 602;  DB 3;  Length 1441;
  Best Local Similarity   99.8%;  Pred. No. 1.6e-300;
  Matches  652;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
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Db        623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
                |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTA 653
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTA 795


RESULT 5
US-10-079-616-8
; Sequence 8, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1441 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA

;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-079-616-8

  Query Match             90.4%;  Score 602;  DB 3;  Length 1441;
  Best Local Similarity   99.8%;  Pred. No. 1.6e-300;
  Matches  652;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
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Db        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
                |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTA 653
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTA 795


RESULT 6
US-09-917-265A-101
; Sequence 101, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 101
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
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;   NAME/KEY: CDS
;   LOCATION: (1)..(561)
US-09-917-265A-101

  Query Match             83.8%;  Score 558;  DB 3;  Length 561;
  Best Local Similarity   100.0%;  Pred. No. 8e-278;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543

Qy        649 AGCTATCTGAATGCTTCC 666
              ||||||||||||||||||
Db        544 AGCTATCTGAATGCTTCC 561


RESULT 7
US-09-917-265A-103/c
; Sequence 103, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 103
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-103

  Query Match             83.8%;  Score 558;  DB 3;  Length 561;
  Best Local Similarity   100.0%;  Pred. No. 8e-278;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        649 AGCTATCTGAATGCTTCC 666
              ||||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1


RESULT 8
US-09-917-265A-35
; Sequence 35, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(591)
US-09-917-265A-35

  Query Match             81.1%;  Score 540;  DB 3;  Length 591;
  Best Local Similarity   99.8%;  Pred. No. 1.6e-268;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666
                 ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591


RESULT 9
US-09-917-265A-37/c
; Sequence 37, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-37

  Query Match             81.1%;  Score 540;  DB 3;  Length 591;
  Best Local Similarity   99.8%;  Pred. No. 1.6e-268;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666
                 ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1


RESULT 10
US-09-011-143-9
; Sequence 9, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
```

```
;       TELEPHONE:  202-628-5197
;       TELEFAX:  202-737-3528
;   INFORMATION FOR SEQ ID NO:  9:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  591 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-09-011-143-9

  Query Match             79.1%;  Score 527;  DB 3;  Length 591;
  Best Local Similarity   99.8%;  Pred. No. 8.1e-262;
  Matches  577;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTA 653
              |||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTA 578


RESULT 11
US-09-302-495-9
; Sequence 9, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/302,495
;            FILING DATE: 30-Apr-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 591 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-302-495-9

  Query Match             79.1%;  Score 527;  DB 3;  Length 591;
  Best Local Similarity   99.8%;  Pred. No. 8.1e-262;
  Matches  577;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTA 653
              |||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTA 578


RESULT 12
US-10-079-616-9
; Sequence 9, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 591 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-079-616-9

  Query Match             79.1%;  Score 527;  DB 3;  Length 591;
  Best Local Similarity   99.8%;  Pred. No. 8.1e-262;
  Matches  577;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTA 653
              |||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTA 578


RESULT 13
US-09-917-265A-43
; Sequence 43, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-09-917-265A-43

  Query Match             76.1%;  Score 507;  DB 3;  Length 1533;
  Best Local Similarity   99.8%;  Pred. No. 1.7e-251;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        976 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 1035

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1036 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 1095

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1096 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 1155

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1156 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 1215

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1216 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 1275

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1276 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 1335

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1336 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 1395

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
                ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1396 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 1455

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1456 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 1515

Qy        649 AGCTATCTGAATGCTTCC 666
                |||||||||||||||||
Db       1516 AGCTATCTGAATGCTTCC 1533


RESULT 14
US-09-917-265A-45/c
; Sequence 45, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-45

  Query Match             76.1%;  Score 507;  DB 3;  Length 1533;
  Best Local Similarity   99.8%;  Pred. No. 1.7e-251;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
                ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        649 AGCTATCTGAATGCTTCC 666
                |||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1


RESULT 15
US-09-917-265A-38
; Sequence 38, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-09-917-265A-38

  Query Match             76.1%;  Score 507;  DB 3;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 1.7e-251;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1042 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 1101

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1102 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 1161

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1162 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 1221

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1222 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 1281

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1282 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 1341

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1342 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 1401

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1402 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 1461

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1462 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 1521

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1522 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 1581

Qy        649 AGCTATCTGAATGCTTCC 666
              |||||||||||||||||
Db       1582 AGCTATCTGAATGCTTCC 1599


RESULT 16
US-09-917-265A-40/c
; Sequence 40, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-40

  Query Match             76.1%;  Score 507;  DB 3;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 1.7e-251;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        649 AGCTATCTGAATGCTTCC 666
              |||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1


RESULT 17
US-09-011-143-26
; Sequence 26, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  26:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  689 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-26

  Query Match             37.2%;  Score 248;  DB 3;  Length 689;
  Best Local Similarity   98.8%;  Pred. No. 8.7e-118;
  Matches  598;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         49 AACCACCTGGACCACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGA 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         55 AACCACCTGGACCACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGA 114

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        115 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 174

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 234

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              |||||||||||||||||||||||||||||||||| | ||||||||| | |||||||||
Db        235 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATGAAT 294

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 354

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 414

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              |||||||||||||||||||||||||||||||||| | ||||||||||||||||||||
Db        415 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATC 474

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 534

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        535 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATC 594

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 654

Qy        649 AGCTA 653
              |||||
Db        655 AGCTA 659


RESULT 18
US-09-302-495-26
; Sequence 26, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 26:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 689 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-302-495-26

  Query Match           37.2%;  Score 248;  DB 3;  Length 689;
  Best Local Similarity  98.8%;  Pred. No. 8.7e-118;
  Matches  598;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         49 AACCACCTGGACCACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGA 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         55 AACCACCTGGACCACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGA 114

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 174

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 234

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              |||||||||||||||||||||||||||||||||| | ||||||||| | |||||||||
Db        235 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATGAAT 294

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 354

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 414

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              |||||||||||||||||||||||||||||||||| | ||||||||||||||||||||
Db        415 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATC 474

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 534

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        535 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATC 594

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 654

Qy        649 AGCTA 653
              |||||
Db        655 AGCTA 659


RESULT 19
US-10-079-616-26
; Sequence 26, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
```

```
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 26:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 689 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-079-616-26

  Query Match             37.2%;  Score 248;  DB 3;  Length 689;
  Best Local Similarity   98.8%;  Pred. No. 8.7e-118;
  Matches  598;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          49 AACCACCTGGACCACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGA 108
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          55 AACCACCTGGACCACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGA 114

Qy         109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         115 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 174

Qy         169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         175 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 234

Qy         229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
               |||||||||||||||||||||||||||||||| | ||||||||| | |||||||||
Db         235 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATGAAT 294

Qy         289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         295 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 354

Qy         349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         355 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 414

Qy         409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
               |||||||||||||||||||||||||||||||||| | ||||||||||||||||||||
Db         415 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATC 474

Qy         469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         475 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 534

Qy         529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
               |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db         535 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATC 594

Qy         589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         595 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 654

Qy         649 AGCTA 653
               |||||
Db         655 AGCTA 659


RESULT 20
US-09-917-265A-49
; Sequence 49, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(591)
US-09-917-265A-49

  Query Match             12.2%;  Score 81;  DB 3;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222

Qy         298 CTGGCTTCCAGAGAGATCTCT 318
               |||||||||||||||||||||
Db         223 CTGGCTTCCAGAGAGATCTCT 243


RESULT 21
US-09-917-265A-51/c
; Sequence 51, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
```

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;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-51

  Query Match             12.2%;  Score 81;  DB 3;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 22
US-09-917-265A-46
; Sequence 46, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
US-09-917-265A-46

  Query Match             12.2%;  Score 81;  DB 3;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 23
US-09-917-265A-48/c
; Sequence 48, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-48

  Query Match             12.2%;  Score 81;  DB 3;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 24
US-09-079-984A-2
; Sequence 2, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,984A
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  669 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 666
;      IDENTIFICATION METHOD:  Similarity
US-09-079-984A-2

  Query Match             12.2%;  Score 81;  DB 3;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-31;
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  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 25
US-09-079-984A-12
; Sequence 12, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,984A
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  669 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 666
;      IDENTIFICATION METHOD:  Similarity
US-09-079-984A-12

  Query Match             12.2%;  Score 81;  DB 3;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 26
US-09-390-729-2
; Sequence 2, Application US/09390729
; Patent No. 6562334
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/390,729
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/079,984
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  669 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 666
;      IDENTIFICATION METHOD:  Similarity
US-09-390-729-2

  Query Match             12.2%;  Score 81;  DB 3;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 27
US-09-390-729-12
; Sequence 12, Application US/09390729
; Patent No. 6562334
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
```

```
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/390,729
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/079,984
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  669 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 666
;      IDENTIFICATION METHOD:  Similarity
US-09-390-729-12

  Query Match             12.2%;  Score 81;  DB 3;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 28
US-09-917-265A-104
; Sequence 104, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 104
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (232)..(897)
US-09-917-265A-104

  Query Match             12.2%;  Score 81;  DB 3;  Length 1455;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 528

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        529 CTGGCTTCCAGAGAGATCTCT 549


RESULT 29
US-09-917-265A-106/c
; Sequence 106, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 106
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-106

  Query Match             12.2%;  Score 81;  DB 3;  Length 1455;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-31;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 928

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        927 CTGGCTTCCAGAGAGATCTCT 907


RESULT 30
US-09-917-265A-66
; Sequence 66, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
```

; SEQ ID NO 66
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)
US-09-917-265A-66

Query Match 12.2%; Score 81; DB 3; Length 1533;
Best Local Similarity 100.0%; Pred. No. 1.4e-31;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1105 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1164

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db       1165 CTGGCTTCCAGAGAGATCTCT 1185
```

RESULT 31
US-09-917-265A-68/c
; Sequence 68, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-917-265A-68

Query Match 12.2%; Score 81; DB 3; Length 1533;
Best Local Similarity 100.0%; Pred. No. 1.4e-31;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349
```

RESULT 32
US-09-917-265A-61
; Sequence 61, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 61
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1599)
US-09-917-265A-61

Query Match 12.2%; Score 81; DB 3; Length 1599;
Best Local Similarity 100.0%; Pred. No. 1.4e-31;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1230

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db       1231 CTGGCTTCCAGAGAGATCTCT 1251
```

RESULT 33
US-09-917-265A-63/c
; Sequence 63, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-917-265A-63

Query Match 12.2%; Score 81; DB 3; Length 1599;
Best Local Similarity 100.0%; Pred. No. 1.4e-31;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349
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RESULT 34
US-09-949-016-20385
; Sequence 20385, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

```
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20385
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-20385

  Query Match             9.8%;  Score 65;  DB 3;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 159

Qy        619 ATTCG 623
              |||||
Db        160 ATTCG 164


RESULT 35
US-09-949-016-87352
; Sequence 87352, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 87352
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-87352

  Query Match             9.8%;  Score 65;  DB 3;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 159

Qy        619 ATTCG 623
              |||||
Db        160 ATTCG 164


RESULT 36
US-08-186-529-3
; Sequence 3, Application US/08186529
; Patent No. 5573764
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,529
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McDaniels, Patricia A.
;      REGISTRATION NUMBER:  33,194
;      REFERENCE/DOCKET NUMBER:  GI 5225
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8401
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  660 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Lymphoblast
;      CELL LINE:  RPMI 8866
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..660
US-08-186-529-3

  Query Match             9.8%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        619 ATTCG 623
              |||||
Db        610 ATTCG 614


RESULT 37
US-08-640-386A-3
; Sequence 3, Application US/08640386A
; Patent No. 5756085
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/640,386A
```

```
;       FILING DATE:
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Brown, Scott A.
;       REGISTRATION NUMBER:  32,724
;       REFERENCE/DOCKET NUMBER:  GI 5225A
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-498-8224
;       TELEFAX:  617-876-5851
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  660 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     ORIGINAL SOURCE:
;       ORGANISM:  Homo sapiens
;       CELL TYPE:  Lymphoblast
;       CELL LINE:  RPMI 8866
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..660
US-08-640-386A-3

  Query Match             9.8%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        619 ATTCG 623
              |||||
Db        610 ATTCG 614


RESULT 38
US-08-184-009-199
; Sequence 199, Application US/08184009
; Patent No. 5833975
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/184,009
;      FILING DATE:  19-JAN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  199:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  721 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-184-009-199

  Query Match             9.8%;  Score 65;  DB 2;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy        619 ATTCG 623
              |||||
Db        671 ATTCG 675


RESULT 39
US-08-458-356-199
; Sequence 199, Application US/08458356
; Patent No. 5942235
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,356
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  199:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  721 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-458-356-199

  Query Match             9.8%;  Score 65;  DB 2;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
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Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy        619 ATTCG 623
              |||||
Db        671 ATTCG 675


RESULT 40
US-08-460-736-199
; Sequence 199, Application US/08460736
; Patent No. 6265189
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,736
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  199:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  721 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-460-736-199

  Query Match             9.8%;  Score 65;  DB 3;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy        619 ATTCG 623
              |||||
Db        671 ATTCG 675


RESULT 41
US-09-535-370-199
; Sequence 199, Application US/09535370
; Patent No. 6537594
;   GENERAL INFORMATION:
;        APPLICANT: Paoletti, Enzo
;                   Tartaglia, James
;                   Cox, William I.
;        TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
;        NUMBER OF SEQUENCES: 217
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Curtis, Morris & Safford
;             STREET: 530 Fifth Avenue
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10036
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/535,370
;             FILING DATE: 24-Mar-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/460,736
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Frommer, William S.
;             REGISTRATION NUMBER: 25,506
;             REFERENCE/DOCKET NUMBER: 454310-2530
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 840-3333
;             TELEFAX: (212) 840-0712
;             TELEX: 425066CURTMS
;   INFORMATION FOR SEQ ID NO: 199:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 721 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 199:
US-09-535-370-199

  Query Match             9.8%;  Score 65;  DB 3;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy        619 ATTCG 623
              |||||
Db        671 ATTCG 675


RESULT 42
US-09-663-667-199
; Sequence 199, Application US/09663667
; Patent No. 6780407
;   GENERAL INFORMATION:
;        APPLICANT: Paoletti, Enzo
;                   Tartaglia, James
;                   Cox, William I.
;        TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
;        NUMBER OF SEQUENCES: 217
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Curtis, Morris & Safford
;             STREET: 530 Fifth Avenue
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10036
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
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;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.25
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/663,667
;              FILING DATE: 15-Sep-2000
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: US/08/184,009
;              FILING DATE: <Unknown>
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Frommer, William S.
;              REGISTRATION NUMBER: 25,506
;              REFERENCE/DOCKET NUMBER: 454310-2530
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (212) 840-3333
;              TELEFAX: (212) 840-0712
;              TELEX: 425066CURTMS
;    INFORMATION FOR SEQ ID NO: 199:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 721 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;         MOLECULE TYPE: cDNA
;         SEQUENCE DESCRIPTION: SEQ ID NO: 199:
US-09-663-667-199

  Query Match             9.8%;  Score 65;  DB 3;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy        619 ATTCG 623
              |||||
Db        671 ATTCG 675


RESULT 43
US-08-848-760B-21
; Sequence 21, Application US/08848760B
; Patent No. 6248721
;   GENERAL INFORMATION:
;         APPLICANT: Chang, Lung-Ji
;         TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
;         NUMBER OF SEQUENCES: 33
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
;              STREET: 2421 N.W. 41st Street, Suite A-1
;              CITY: Gainesville
;              STATE: Florida
;              COUNTRY: United States of America
;              ZIP: 32606
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/08/848,760B
;              FILING DATE: 25-Jan-2001
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: 08/838,702
;              FILING DATE: 09-APR-1997
;         ATTORNEY/AGENT INFORMATION:
;              NAME: PACE, DORAN R.
;              REGISTRATION NUMBER: 38,261
;              REFERENCE/DOCKET NUMBER: CNG-100C1
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (352) 375-8100
;              TELEFAX: (352) 372-5800
;    INFORMATION FOR SEQ ID NO: 21:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 762 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: double
;              TOPOLOGY: linear
;         MOLECULE TYPE: other nucleic acid
;              DESCRIPTION: /desc = "DNA"
;         SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-08-848-760B-21

  Query Match             9.8%;  Score 65;  DB 3;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
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Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        619 ATTCG 623
              |||||
Db        712 ATTCG 716


RESULT 44
US-09-826-025-21
; Sequence 21, Application US/09826025
; Patent No. 6730512
;   GENERAL INFORMATION:
;         APPLICANT: Chang, Lung-Ji
;         TITLE OF INVENTION: Combination Immunogene Therapy
;         NUMBER OF SEQUENCES: 25
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: Medlen & Carroll, LLP
;              STREET: 220 Montgomery Street, Suite 2200
;              CITY: San Francisco
;              STATE: California
;              COUNTRY: United States of America
;              ZIP: 94104
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/826,025
;              FILING DATE: 04-Apr-2001
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: 08/838,702
;              FILING DATE: <Unknown>
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Ingolia, Diane E.
;              REGISTRATION NUMBER: 40,027
;              REFERENCE/DOCKET NUMBER: CHANG-02687
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (415) 705-8410
;              TELEFAX: (415) 397-8338
;    INFORMATION FOR SEQ ID NO: 21:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 762 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: double
;              TOPOLOGY: linear
;         MOLECULE TYPE: other nucleic acid
;              DESCRIPTION: /desc = "DNA"
;         SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-826-025-21

  Query Match             9.8%;  Score 65;  DB 3;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        619 ATTCG 623
              |||||
Db        712 ATTCG 716


RESULT 45
US-09-543-679A-2890
; Sequence 2890, Application US/09543679A
; Patent No. 7034007
;  GENERAL INFORMATION:
;       APPLICANT: NYCE, Jonathan W.
;       TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                           COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                           OF AIRWAY DISORDERS ASSOCIATED WITH
;                           BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;       NUMBER OF SEQUENCES: 3111
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;            STREET: 7 Clarke Drive
;            CITY: Cranbury
;            STATE: NJ
;            COUNTRY: USA
;            ZIP: 08512
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD-R
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: N/A
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/543,679A
;            FILING DATE: 13-Apr-2000
;            CLASSIFICATION: UNKNOWN
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/127,958
;            FILING DATE: 1998-08-03
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Amzel, Viviana
;            REGISTRATION NUMBER: 30,930
;            REFERENCE/DOCKET NUMBER: EPI-0067191b
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 609-409-3035
;            TELEFAX: 413-254-9245
;            TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2890:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 762 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2890:
US-09-543-679A-2890

  Query Match             9.8%;  Score 65;  DB 5;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        619 ATTCG 623
              |||||
Db        712 ATTCG 716


RESULT 46
US-09-949-016-2462
; Sequence 2462, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2462
;   LENGTH: 1019
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-2462

  Query Match             9.8%;  Score 65;  DB 3;  Length 1019;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        712 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 771

Qy        619 ATTCG 623
              |||||
Db        772 ATTCG 776


RESULT 47
US-08-751-767A-1
; Sequence 1, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1026 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  170..826
US-08-751-767A-1

  Query Match             9.8%;  Score 65;  DB 2;  Length 1026;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 778

Qy        619 ATTCG 623
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Db        779 ATTCG 783


RESULT 48
US-09-023-655-1041
; Sequence 1041, Application US/09023655
; Patent No. 6607879
;  GENERAL INFORMATION:
;    APPLICANT:  Cocks, Benjamin G.
;    APPLICANT:  Susan G. Stuart
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1508
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/023,655
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0001 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  1041:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1026 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GENBANK
;      CLONE:  g180623
US-09-023-655-1041

  Query Match             9.8%;  Score 65;  DB 3;  Length 1026;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 778

Qy        619 ATTCG 623
              |||||
Db        779 ATTCG 783


RESULT 49
US-09-949-016-130
; Sequence 130, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 130
;   LENGTH: 1026
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-130

  Query Match             9.8%;  Score 65;  DB 3;  Length 1026;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 778

Qy        619 ATTCG 623
              |||||
Db        779 ATTCG 783


RESULT 50
US-09-634-368-6
; Sequence 6, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 1287
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: human Fc-p35
;   OTHER INFORMATION: fusion protein coding sequence
US-09-634-368-6

  Query Match             9.8%;  Score 65;  DB 3;  Length 1287;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
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  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1177 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1236

Qy        619 ATTCG 623
              |||||
Db       1237 ATTCG 1241


RESULT 51
US-08-684-687-3
; Sequence 3, Application US/08684687
; Patent No. 5830451
;  GENERAL INFORMATION:
;    APPLICANT:  KIEFF, ELLIOTT D.
;    APPLICANT:  DEVERGNE, ODILE
;    TITLE OF INVENTION:  A NOVEL HAEMATOPOIETIC CYTOKINE AND USES
;    TITLE OF INVENTION:  THEREFOR
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  WOLF, GREENFIELD & SACKS, P.C.
;      STREET:  600 ATLANTIC AVENUE
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/684,687
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,092
;      FILING DATE:  11-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  GATES, EDWARD R.
;      REGISTRATION NUMBER:  31,616
;      REFERENCE/DOCKET NUMBER:  B0801/7051
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1316 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  HOMO SAPIENS
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  102..863
US-08-684-687-3

  Query Match             9.8%;  Score 65;  DB 2;  Length 1316;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 812

Qy        619 ATTCG 623
              |||||
Db        813 ATTCG 817


RESULT 52
US-09-851-520-3
; Sequence 3, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
;   LENGTH: 1316
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (102)...(863)
US-09-851-520-3

  Query Match             9.8%;  Score 65;  DB 3;  Length 1316;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 812

Qy        619 ATTCG 623
              |||||
Db        813 ATTCG 817


RESULT 53
US-08-265-087-3
; Sequence 3, Application US/08265087
; Patent No. 5571515
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/265,087
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
```

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;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1364 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  101..859
US-08-265-087-3

  Query Match             9.8%;  Score 65;  DB 2;  Length 1364;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 811

Qy        619 ATTCG 623
              |||||
Db        812 ATTCG 816


RESULT 54
US-08-621-493-3
; Sequence 3, Application US/08621493
; Patent No. 5723127
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/621,493
;      FILING DATE:  25-MAR-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1364 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  101..859
US-08-621-493-3

  Query Match             9.8%;  Score 65;  DB 2;  Length 1364;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 811

Qy        619 ATTCG 623
              |||||
Db        812 ATTCG 816


RESULT 55
US-08-965-688-3
; Sequence 3, Application US/08965688
; Patent No. 5976539
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/965,688
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/621,493
;      FILING DATE:  25-MAR-1996
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1364 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  101..859
US-08-965-688-3

  Query Match             9.8%;  Score 65;  DB 2;  Length 1364;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        752 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 811

Qy        619 ATTCG 623
              |||||
Db        812 ATTCG 816


RESULT 56
US-09-260-173-3
; Sequence 3, Application US/09260173
; Patent No. 6168923
;  GENERAL INFORMATION:
;       APPLICANT: Scott, Phillip
;                  Trinchieri, Giorgio
;       TITLE OF INVENTION: Compositions and Methods for Use of
;                           IL-12 as an Adjuvant
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Howson and Howson
;            STREET: Spring House Corporate Center, PO Box 457
;            CITY: Spring House
;            STATE: Pennsylvania
;            COUNTRY: USA
;            ZIP: 19477
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/260,173
;            FILING DATE: 01-Mar-1999
;            CLASSIFICATION: <Unknown>
;                            17-JUN-1994
;                            18-APR-1994
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/965,688
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: 08/265,087
;            FILING DATE: 17-JUN-1994
;            APPLICATION NUMBER: US 08/229,282
;            FILING DATE: 18-APR-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Bak, Mary E.
;            REGISTRATION NUMBER: 31,215
;            REFERENCE/DOCKET NUMBER: WST51AUSA
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 215-540-9206
;            TELEFAX: 215-540-5818
;   INFORMATION FOR SEQ ID NO: 3:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1364 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: unknown
;       MOLECULE TYPE: cDNA
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  101..859
;       SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-260-173-3

  Query Match             9.8%;  Score 65;  DB 3;  Length 1364;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 811

Qy        619 ATTCG 623
              |||||
Db        812 ATTCG 816


RESULT 57
US-09-924-703-5
; Sequence 5, Application US/09924703
; Patent No. 6555658
; GENERAL INFORMATION:
;  APPLICANT: TRINCHIERI, GIORGIO
;  APPLICANT:  PERUSSIA, BICE
;  APPLICANT:  CLARK, STEVEN C.
;  APPLICANT:  WONG, GORDON G.
;  APPLICANT:  HEWICK, RODNEY
;  APPLICANT:  KOBAYASHI, MICHIKO
;  TITLE OF INVENTION: ANTIBODIES TO NATURAL KILLER STIMULATORY FACTOR
;  FILE REFERENCE: 01142.0142.0100
;  CURRENT APPLICATION NUMBER: US/09/924,703
;  CURRENT FILING DATE:  2001-08-09
;  PRIOR APPLICATION NUMBER: 09/325,958
;  PRIOR FILING DATE: 1999-06-04
;  PRIOR APPLICATION NUMBER: 08/858,000
;  PRIOR FILING DATE: 1997-05-16
;  PRIOR APPLICATION NUMBER: 08/403,013
;  PRIOR FILING DATE: 1995-03-13
;  PRIOR APPLICATION NUMBER: 07/584,941
;  PRIOR FILING DATE: 1990-09-18
;  PRIOR APPLICATION NUMBER: 07/307,817
;  PRIOR FILING DATE: 1989-02-07
;  PRIOR APPLICATION NUMBER: 07/269,945
;  PRIOR FILING DATE: 1988-11-10
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 1395
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
;   OTHER INFORMATION: sequence of the 30 kD subunit of NKSF
;   NAME/KEY: CDS
;   LOCATION: (114)..(872)
US-09-924-703-5

  Query Match             9.8%;  Score 65;  DB 3;  Length 1395;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        765 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 824

Qy        619 ATTCG 623
              |||||
Db        825 ATTCG 829


RESULT 58
US-08-751-767A-11
; Sequence 11, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
```

```
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/751,767A
;       FILING DATE:  08-NOV-1996
;       CLASSIFICATION:  536
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  SADOFF, B.J.
;       REGISTRATION NUMBER:  36,663
;       REFERENCE/DOCKET NUMBER:  117-221
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  7038164091
;       TELEFAX:  7038164100
;   INFORMATION FOR SEQ ID NO:  11:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1560 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..1557
US-08-751-767A-11

  Query Match             9.8%;  Score 65;  DB 2;  Length 1560;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1450 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1509

Qy        619 ATTCG 623
              |||||
Db       1510 ATTCG 1514


RESULT 59
US-08-751-767A-9
; Sequence 9, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1623 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1620
US-08-751-767A-9

  Query Match             9.8%;  Score 65;  DB 2;  Length 1623;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1513 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1572

Qy        619 ATTCG 623
              |||||
Db       1573 ATTCG 1577


RESULT 60
US-09-310-842-2
; Sequence 2, Application US/09310842A
; Patent No. 6451593
; GENERAL INFORMATION:
;  APPLICANT: Wittig, Prof. Burghardt
;  APPLICANT: Junghans, Claas
;  TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
;  TITLE OF INVENTION: Therapy
;  FILE REFERENCE: XI 597/99
;  CURRENT APPLICATION NUMBER: US/09/310,842A
;  CURRENT FILING DATE: 1999-05-12
;  EARLIER APPLICATION NUMBER: DE 196 48 625.4
;  EARLIER FILING DATE: 1996-11-13
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 1645
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (1)..(1645)
;   OTHER INFORMATION: Interleukin-12 (IL-12, p35-subunit); Oligo DNA
;   OTHER INFORMATION: Dumbbell
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1)..(2)
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at
;   OTHER INFORMATION: position 1 to 2  can be modified with amino or caroxy
;   OTHER INFORMATION: features
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1644)..(1645)
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1644
;   OTHER INFORMATION: to 1645  can be modified with amino or caroxy features
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Strandness: both;  nucleic
;   OTHER INFORMATION: acid (linear),  hypothetical: No. 6451593 anti-sense: No
US-09-310-842-2

  Query Match             9.8%;  Score 65;  DB 3;  Length 1645;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1284 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1343
```

```
Qy        619 ATTCG 623
              |||||
Db       1344 ATTCG 1348


RESULT 61
US-09-543-679A-2893
; Sequence 2893, Application US/09543679A
; Patent No. 7034007
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
;        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                            OF AIRWAY DISORDERS ASSOCIATED WITH
;                            BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;        NUMBER OF SEQUENCES: 3111
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 Clarke Drive
;             CITY: Cranbury
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: N/A
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/543,679A
;             FILING DATE: 13-Apr-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/127,958
;             FILING DATE: 1998-08-03
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-0067191b
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2893:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 4521 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2893:
US-09-543-679A-2893

  Query Match             9.8%;  Score 65;  DB 5;  Length 4521;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        619 ATTCG 623
              |||||
Db        712 ATTCG 716


RESULT 62
US-08-751-767A-7
; Sequence 7, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6139 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3222..4841
US-08-751-767A-7

  Query Match             9.8%;  Score 65;  DB 2;  Length 6139;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4734 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 4793

Qy        619 ATTCG 623
              |||||
Db       4794 ATTCG 4798


RESULT 63
US-09-949-016-11872
; Sequence 11872, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11872
;   LENGTH: 10764
;   TYPE: DNA
```

```
;   ORGANISM: Human
US-09-949-016-11872

  Query Match             9.8%;  Score 65;  DB 3;  Length 10764;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8457 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 8516

Qy        619 ATTCG 623
              |||||
Db       8517 ATTCG 8521


RESULT 64
US-09-949-016-14204
; Sequence 14204, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14204
;   LENGTH: 10765
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-14204

  Query Match             9.8%;  Score 65;  DB 3;  Length 10765;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8457 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 8516

Qy        619 ATTCG 623
              |||||
Db       8517 ATTCG 8521


RESULT 65
US-09-949-016-20381
; Sequence 20381, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20381
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-20381

  Query Match             8.4%;  Score 56;  DB 3;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-18;
  Matches   56;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        208 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 263
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 199


RESULT 66
US-09-949-016-87348
; Sequence 87348, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 87348
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-87348

  Query Match             8.4%;  Score 56;  DB 3;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-18;
  Matches   56;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        208 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 263
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 199


RESULT 67
US-09-011-143-24
; Sequence 24, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
```

```
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  79 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-24

  Query Match             6.5%;  Score 43;  DB 3;  Length 79;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-12;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        222 TGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGC 264
              |||||||||||||||||||||||||||||||||||||||||||
Db          1 TGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGC 43


RESULT 68
US-09-302-495-24
; Sequence 24, Application US/09302495
; Patent No. 6518045
;  GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/302,495
;            FILING DATE: 30-Apr-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;  INFORMATION FOR SEQ ID NO: 24:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 79 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-302-495-24

  Query Match             6.5%;  Score 43;  DB 3;  Length 79;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-12;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        222 TGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGC 264
              |||||||||||||||||||||||||||||||||||||||||||
Db          1 TGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGC 43


RESULT 69
US-10-079-616-24
; Sequence 24, Application US/10079616
; Patent No. 6566097
;  GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;  INFORMATION FOR SEQ ID NO: 24:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 79 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 24:
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US-10-079-616-24

  Query Match             6.5%;  Score 43;  DB 3;  Length 79;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-12;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        222 TGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGC 264
              |||||||||||||||||||||||||||||||||||||||||||
Db          1 TGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGC 43


RESULT 70
US-09-917-265A-91
; Sequence 91, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91
;   LENGTH: 39
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-917-265A-91

  Query Match             4.1%;  Score 27;  DB 3;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 0.0011;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAA 135
              |||||||||||||||||||||||||||
Db         13 ATGTTCCAGTGCCTCAACCACTCCCAA 39


RESULT 71
US-09-634-368-1
; Sequence 1, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 582
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine p35
;   OTHER INFORMATION: coding sequence for mature protein
US-09-634-368-1

  Query Match             4.1%;  Score 27;  DB 3;  Length 582;
  Best Local Similarity   100.0%;  Pred. No. 0.0011;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        388 ATCTATGAGGACTTGAAGATGTACCAG 414
              ||||||||||||||||||||||||||||
Db        301 ATCTATGAGGACTTGAAGATGTACCAG 327


RESULT 72
US-08-385-335A-10
; Sequence 10, Application US/08385335A
; Patent No. 5891680
;  GENERAL INFORMATION:
;    APPLICANT:  Lieschke, Graham J.
;    APPLICANT:  Mulligan, Richard C.
;    TITLE OF INVENTION:  Bioactive Fusion Proteins
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/385,335A
;      FILING DATE:  08-FEB-1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  WHI95-01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-861-6240
;      TELEFAX:  617-861-9540
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  713 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-08-385-335A-10

  Query Match             4.1%;  Score 27;  DB 2;  Length 713;
  Best Local Similarity   100.0%;  Pred. No. 0.0011;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        388 ATCTATGAGGACTTGAAGATGTACCAG 414
              ||||||||||||||||||||||||||||
Db        413 ATCTATGAGGACTTGAAGATGTACCAG 439


RESULT 73
US-09-634-368-5
; Sequence 5, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 1278
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
```

```
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: Fc-p35 fusion protein coding sequence
US-09-634-368-5

  Query Match             4.1%;  Score 27;  DB 3;  Length 1278;
  Best Local Similarity   100.0%;  Pred. No. 0.0011;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        388 ATCTATGAGGACTTGAAGATGTACCAG 414
              |||||||||||||||||||||||||||
Db        997 ATCTATGAGGACTTGAAGATGTACCAG 1023


RESULT 74
US-09-634-368-12
; Sequence 12, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 1569
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p35-linker-p40 fusion protein coding sequence
US-09-634-368-12

  Query Match             4.1%;  Score 27;  DB 3;  Length 1569;
  Best Local Similarity   100.0%;  Pred. No. 0.0011;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        388 ATCTATGAGGACTTGAAGATGTACCAG 414
              |||||||||||||||||||||||||||
Db        301 ATCTATGAGGACTTGAAGATGTACCAG 327


RESULT 75
US-09-634-368-11
; Sequence 11, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 2013
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p35-linker-p40-IL-2 fusion protein coding sequence
US-09-634-368-11

  Query Match             4.1%;  Score 27;  DB 3;  Length 2013;
  Best Local Similarity   100.0%;  Pred. No. 0.0011;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        388 ATCTATGAGGACTTGAAGATGTACCAG 414
              |||||||||||||||||||||||||||
Db        301 ATCTATGAGGACTTGAAGATGTACCAG 327


RESULT 76
US-09-634-368-13
; Sequence 13, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 13
;   LENGTH: 2709
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: Fc-p35-linker-p40-IL-2 fusion protein coding
;   OTHER INFORMATION: sequence
US-09-634-368-13

  Query Match             4.1%;  Score 27;  DB 3;  Length 2709;
  Best Local Similarity   100.0%;  Pred. No. 0.0011;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        388 ATCTATGAGGACTTGAAGATGTACCAG 414
              |||||||||||||||||||||||||||
Db        997 ATCTATGAGGACTTGAAGATGTACCAG 1023


RESULT 77
US-08-659-206A-4
; Sequence 4, Application US/08659206A
; Patent No. 5922685
;  GENERAL INFORMATION:
;    APPLICANT:  Rakhmilevich, Alexander
;    TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/659,206A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  110229.91144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  4:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6295 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "plasmid pWRG3196"
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(955..1260, 1334..1675)
;      OTHER INFORMATION:  /product= "p35 gene product"
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2377..3384
;      OTHER INFORMATION:  /product= "p40 gene product"
US-08-659-206A-4

  Query Match             4.1%;  Score 27;  DB 2;  Length 6295;
  Best Local Similarity   100.0%;  Pred. No. 0.0011;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        388 ATCTATGAGGACTTGAAGATGTACCAG 414
              |||||||||||||||||||||||||||
Db       1394 ATCTATGAGGACTTGAAGATGTACCAG 1420


RESULT 78
US-08-659-206A-1
; Sequence 1, Application US/08659206A
; Patent No. 5922685
;  GENERAL INFORMATION:
;    APPLICANT:  Rakhmilevich, Alexander
;    TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/659,206A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  110229.91144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7287 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Plasmid DNA"
;    IMMEDIATE SOURCE:
;      CLONE:  pWRG3169
;    FEATURE:
;      NAME/KEY:  promoter
;      LOCATION:  1..628
;    FEATURE:
;      NAME/KEY:  iDNA
;      LOCATION:  629..810
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(953..1258, 1332..1673)
;      OTHER INFORMATION:  /product= "p35 gene product"
;    FEATURE:
;      NAME/KEY:  polyA_site
;      LOCATION:  1797..2024
;    FEATURE:
;      NAME/KEY:  promoter
;      LOCATION:  2110..2737
;    FEATURE:
;      NAME/KEY:  iDNA
;      LOCATION:  2738..2919
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2983..3990
;      OTHER INFORMATION:  /product= "p40 gene product"
;    FEATURE:
;      NAME/KEY:  polyA_site
;      LOCATION:  4075..4306
US-08-659-206A-1

  Query Match             4.1%;  Score 27;  DB 2;  Length 7287;
  Best Local Similarity   100.0%;  Pred. No. 0.0011;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        388 ATCTATGAGGACTTGAAGATGTACCAG 414
              |||||||||||||||||||||||||||
Db       1392 ATCTATGAGGACTTGAAGATGTACCAG 1418


RESULT 79
US-09-917-265A-90/c
; Sequence 90, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90
;   LENGTH: 27
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-917-265A-90

  Query Match             3.6%;  Score 24;  DB 3;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.037;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        643 ATGATGAGCTATCTGAATGCTTCC 666
              ||||||||||||||||||||||||
Db         27 ATGATGAGCTATCTGAATGCTTCC 4


RESULT 80
US-09-011-143-25/c
; Sequence 25, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
```

```
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  36 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-25

  Query Match             3.6%;  Score 24;  DB 3;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 0.037;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        421 TTCAAGGCCATGAATGCAAAGCTG 444
              ||||||||||||||||||||||||
Db         36 TTCAAGGCCATGAATGCAAAGCTG 13


RESULT 81
US-09-302-495-25/c
; Sequence 25, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;    INFORMATION FOR SEQ ID NO: 25:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 36 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-302-495-25

  Query Match             3.6%;  Score 24;  DB 3;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 0.037;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        421 TTCAAGGCCATGAATGCAAAGCTG 444
              ||||||||||||||||||||||||
Db         36 TTCAAGGCCATGAATGCAAAGCTG 13


RESULT 82
US-10-079-616-25/c
; Sequence 25, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
```

```
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 25:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 36 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-10-079-616-25

  Query Match             3.6%;  Score 24;  DB 3;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 0.037;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        421 TTCAAGGCCATGAATGCAAAGCTG 444
              ||||||||||||||||||||||||
Db         36 TTCAAGGCCATGAATGCAAAGCTG 13


RESULT 83
US-09-917-265A-92/c
; Sequence 92, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92
;   LENGTH: 41
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-917-265A-92

  Query Match             3.6%;  Score 24;  DB 3;  Length 41;
  Best Local Similarity   100.0%;  Pred. No. 0.037;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        643 ATGATGAGCTATCTGAATGCTTCC 666
              ||||||||||||||||||||||||
Db         41 ATGATGAGCTATCTGAATGCTTCC 18


RESULT 84
US-08-859-998-383
; Sequence 383, Application US/08859998
; Patent No. 5994076
;  GENERAL INFORMATION:
;    APPLICANT:  Chenchik, Alex
;    APPLICANT:  Jokhadze, George
;    APPLICANT:  Bibilashvilli, Robert
;    TITLE OF INVENTION:  METHOD OF ASSAYING DIFFERENTIAL
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1375
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  2200 Sand Hill Road, Suite 100
;      CITY:  Menlo Park
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,998
;      FILING DATE:  21-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Field, Bret E.
;      REGISTRATION NUMBER:  37,620
;      REFERENCE/DOCKET NUMBER:. 09096/002001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-322-5070
;      TELEFAX:  415-854-0875
;  INFORMATION FOR SEQ ID NO:  383:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      OTHER INFORMATION:  oligonucleotide primer
US-08-859-998-383

  Query Match             3.2%;  Score 21;  DB 2;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        406 ATGTACCAGGTGGAGTTCAAG 426
              |||||||||||||||||||||
Db          1 ATGTACCAGGTGGAGTTCAAG 21


RESULT 85
US-09-225-928-383
; Sequence 383, Application US/09225928
; Patent No. 6352829
;  GENERAL INFORMATION:
;       APPLICANT: Chenchik, Alex
;                  Jokhadze, George
;                  Bibilashvilli, Robert
;       TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
;                           EXPRESSION
;       NUMBER OF SEQUENCES: 1375
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Fish & Richardson, P.C.
;            STREET: 2200 Sand Hill Road, Suite 100
;            CITY: Menlo Park
;            STATE: CA
;            COUNTRY: US
;            ZIP: 94025
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: Windows95
;            SOFTWARE: FastSEQ for Windows Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/225,928
;            FILING DATE: 05-Jan-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/859,998
;            FILING DATE: 21-MAY-1997
```

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;       ATTORNEY/AGENT INFORMATION:
;            NAME: Field, Bret E.
;            REGISTRATION NUMBER: 37,620
;            REFERENCE/DOCKET NUMBER: 09096/002001
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 415-322-5070
;            TELEFAX: 415-854-0875
;   INFORMATION FOR SEQ ID NO: 383:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 32 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       FEATURE:
;            OTHER INFORMATION:  oligonucleotide primer
;       SEQUENCE DESCRIPTION: SEQ ID NO: 383:
US-09-225-928-383

  Query Match             3.2%;  Score 21;  DB 3;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        406 ATGTACCAGGTGGAGTTCAAG 426
              |||||||||||||||||||||
Db          1 ATGTACCAGGTGGAGTTCAAG 21


RESULT 86
US-09-225-201B-383
; Sequence 383, Application US/09225201B
; Patent No. 6489455
;  GENERAL INFORMATION:
;       APPLICANT: Chenchik, Alex
;                  Jokhadze, George
;                  Bibilashvilli, Robert
;       TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
;                           EXPRESSION
;       NUMBER OF SEQUENCES: 1375
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Fish & Richardson, P.C.
;            STREET: 2200 Sand Hill Road, Suite 100
;            CITY: Menlo Park
;            STATE: CA
;            COUNTRY: US
;            ZIP: 94025
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: Windows95
;            SOFTWARE: FastSEQ for Windows Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/225,201B
;            FILING DATE: 05-Jan-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/859,998
;            FILING DATE: 21-MAY-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Field, Bret E.
;            REGISTRATION NUMBER: 37,620
;            REFERENCE/DOCKET NUMBER: 09096/002001
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 415-322-5070
;            TELEFAX: 415-854-0875
;   INFORMATION FOR SEQ ID NO: 383:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 32 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       FEATURE:
;            OTHER INFORMATION:  oligonucleotide primer
;       SEQUENCE DESCRIPTION: SEQ ID NO: 383:
US-09-225-201B-383

  Query Match             3.2%;  Score 21;  DB 3;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        406 ATGTACCAGGTGGAGTTCAAG 426
              |||||||||||||||||||||
Db          1 ATGTACCAGGTGGAGTTCAAG 21


RESULT 87
US-09-011-143-22
; Sequence 22, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  95 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-22

  Query Match             3.2%;  Score 21;  DB 3;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         49 AACCACCTGGACCACCTCAGT 69
              |||||||||||||||||||||
Db         75 AACCACCTGGACCACCTCAGT 95


RESULT 88
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US-09-302-495-22
; Sequence 22, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 22:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 95 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-302-495-22

  Query Match             3.2%;  Score 21;  DB 3;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         49 AACCACCTGGACCACCTCAGT 69
              |||||||||||||||||||||
Db         75 AACCACCTGGACCACCTCAGT 95


RESULT 89
US-10-079-616-22
; Sequence 22, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 22:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 95 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-10-079-616-22

  Query Match             3.2%;  Score 21;  DB 3;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         49 AACCACCTGGACCACCTCAGT 69
              |||||||||||||||||||||
Db         75 AACCACCTGGACCACCTCAGT 95


RESULT 90
US-08-012-543-13
; Sequence 13, Application US/08012543
; Patent No. 5596072
;  GENERAL INFORMATION:
;    APPLICANT:  Culpepper, Janice
;    APPLICANT:  McKenzie, Andrew
;    APPLICANT:  Dang, Warren
;    APPLICANT:  de Waal Malefyt, Rene
;    APPLICANT:  Heath, Andrew
;    APPLICANT:  Aversa, Gregorio
;    APPLICANT:  Briere, Francine
;    APPLICANT:  Banchereau, Jacques
;    APPLICANT:  de Vries, Jan
;    APPLICANT:  Zurawski, Gerard
;    TITLE OF INVENTION:  Human Interleukin-13
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DNAX Research Institute
;      STREET:  901 California Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
```

```
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/012,543
;      FILING DATE:  01-FEB-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/933,416
;      FILING DATE:  21-AUG-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  DX0302K1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-852-9196
;      TELEFAX:  415-496-1200
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-012-543-13

  Query Match             3.0%;  Score 20;  DB 2;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        328 AATGGGAGTTGCCTGGCCTC 347
              ||||||||||||||||||||
Db          1 AATGGGAGTTGCCTGGCCTC 20


RESULT 91
US-08-621-841-19
; Sequence 19, Application US/08621841
; Patent No. 6096869
;  GENERAL INFORMATION:
;    APPLICANT:  Stanley, Margaret A.
;    APPLICANT:  Scarpini, Cinzia G.
;    TITLE OF INVENTION:  TREATMENT OF PAPILLOMAVIRUS-ASSOCIATED
;    TITLE OF INVENTION:  LESIONS
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/621,841
;      FILING DATE:  22-MAR-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9505784.0
;      FILING DATE:  22-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dreger, Walter H.
;      REGISTRATION NUMBER:  24,190
;      REFERENCE/DOCKET NUMBER:  A-63316
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 781-1989
;      TELEFAX:  (415) 398-3249
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-621-841-19

  Query Match             3.0%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        324 AACTAATGGGAGTTGCCTGG 343
              ||||||||||||||||||||
Db          1 AACTAATGGGAGTTGCCTGG 20


RESULT 92
US-08-621-841-52/c
; Sequence 52, Application US/08621841
; Patent No. 6096869
;  GENERAL INFORMATION:
;    APPLICANT:  Stanley, Margaret A.
;    APPLICANT:  Scarpini, Cinzia G.
;    TITLE OF INVENTION:  TREATMENT OF PAPILLOMAVIRUS-ASSOCIATED
;    TITLE OF INVENTION:  LESIONS
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/621,841
;      FILING DATE:  22-MAR-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9505784.0
;      FILING DATE:  22-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dreger, Walter H.
;      REGISTRATION NUMBER:  24,190
;      REFERENCE/DOCKET NUMBER:  A-63316
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 781-1989
;      TELEFAX:  (415) 398-3249
;  INFORMATION FOR SEQ ID NO:  52:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-621-841-52

  Query Match             3.0%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        588 CAAGCTCTGCATACTTCTTC 607
              ||||||||||||||||||||
Db         20 CAAGCTCTGCATACTTCTTC 1
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```
RESULT 93
US-09-851-520-28/c
; Sequence 28, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 28
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-520-28

  Query Match             3.0%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        168 GAAGGCCAGACAAACTCTAG 187
              ||||||||||||||||||||
Db         20 GAAGGCCAGACAAACTCTAG 1


RESULT 94
US-09-851-520-31/c
; Sequence 31, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 31
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-520-31

  Query Match             3.0%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        241 AAAACCAGCACAGTGGAGGC 260
              ||||||||||||||||||||
Db         20 AAAACCAGCACAGTGGAGGC 1


RESULT 95
US-09-851-520-39/c
; Sequence 39, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 39
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-520-39

  Query Match             3.0%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        328 AATGGGAGTTGCCTGGCCTC 347
              ||||||||||||||||||||
Db         20 AATGGGAGTTGCCTGGCCTC 1


RESULT 96
US-09-851-520-40/c
; Sequence 40, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 40
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-520-40

  Query Match             3.0%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        335 GTTGCCTGGCCTCCAGAAAG 354
              ||||||||||||||||||||
Db         20 GTTGCCTGGCCTCCAGAAAG 1


RESULT 97
US-09-851-520-41/c
; Sequence 41, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 41
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-520-41

  Query Match             3.0%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        341 TGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||
Db         20 TGGCCTCCAGAAAGACCTCT 1


RESULT 98
```

```
US-09-851-520-42/c
; Sequence 42, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 42
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-520-42

  Query Match             3.0%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        346 TCCAGAAAGACCTCTTTTAT 365
              ||||||||||||||||||||
Db         20 TCCAGAAAGACCTCTTTTAT 1


RESULT 99
US-09-851-520-45/c
; Sequence 45, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 45
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-520-45

  Query Match             3.0%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        404 AGATGTACCAGGTGGAGTTC 423
              ||||||||||||||||||||
Db         20 AGATGTACCAGGTGGAGTTC 1


RESULT 100
US-09-851-520-57/c
; Sequence 57, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 57
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-520-57

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2006, 23:31:05 ; Search time 1119.52 Seconds
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 18892170 seqs, 6143817638 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
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Db        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        661 GCTTCC 666
               ||||||
Db        661 GCTTCC 666
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RESULT 2
US-09-917-265-34/c
; Sequence 34, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-34

  Query Match            100.0%;  Score 666;  DB 3;  Length 666;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  666;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 607

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 547

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 427

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 307

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 247

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 187

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 127

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 7

Qy        661 GCTTCC 666
               ||||||
Db          6 GCTTCC 1
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```
RESULT 3
US-10-821-670-32
; Sequence 32, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
US-10-821-670-32
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  Query Match             100.0%;  Score 666;  DB 9;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  666;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        661 GCTTCC 666
              ||||||
Db        661 GCTTCC 666


RESULT 4
US-10-821-670-34/c
; Sequence 34, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
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US-10-821-670-34

  Query Match             100.0%;  Score 666;  DB 9;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  666;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 607

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 547

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 427

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 307

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 247

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 187

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 127

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 7

Qy        661 GCTTCC 666
              ||||||
Db          6 GCTTCC 1


RESULT 5
US-10-079-616-8
; Sequence 8, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
```

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;           ZIP: 20004
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/10/079,616
;           FILING DATE: 22-Feb-2002
;           CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: 09/011,143
;           FILING DATE: 04-FEB-1998
;           APPLICATION NUMBER: PCT/JP97/01824
;           FILING DATE: 29-MAY-1997
;           APPLICATION NUMBER: JP 165249/1996
;           FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;           NAME: BROWDY, Roger L.
;           REGISTRATION NUMBER: 25,618
;           REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: 202-628-5197
;           TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 1441 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-079-616-8

  Query Match             90.4%;  Score 602;  DB 6;  Length 1441;
  Best Local Similarity   99.8%;  Pred. No. 2.4e-311;
  Matches  652;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTA 653
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTA 795


RESULT 6
US-09-917-265-101
; Sequence 101, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(561)
;   OTHER INFORMATION:
US-09-917-265-101

  Query Match             83.8%;  Score 558;  DB 3;  Length 561;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-288;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
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Db        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543

Qy        649 AGCTATCTGAATGCTTCC 666
              |||||||||||||||||
Db        544 AGCTATCTGAATGCTTCC 561


RESULT 7
US-09-917-265-103/c
; Sequence 103, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 103
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-103

  Query Match             83.8%;  Score 558;  DB 3;  Length 561;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-288;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        649 AGCTATCTGAATGCTTCC 666
              |||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1


RESULT 8
US-10-821-670-101
; Sequence 101, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 101
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(561)
US-10-821-670-101

  Query Match             83.8%;  Score 558;  DB 9;  Length 561;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-288;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543

Qy        649 AGCTATCTGAATGCTTCC 666
              |||||||||||||||||
Db        544 AGCTATCTGAATGCTTCC 561


RESULT 9
US-10-821-670-103/c
; Sequence 103, Application US/10821670
```

```
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 103
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-103

  Query Match             83.8%;  Score 558;  DB 9;  Length 561;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-288;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        649 AGCTATCTGAATGCTTCC 666
              |||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1


RESULT 10
US-09-917-265-35
; Sequence 35, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(591)
;   OTHER INFORMATION:
US-09-917-265-35

  Query Match             81.1%;  Score 540;  DB 3;  Length 591;
  Best Local Similarity   99.8%;  Pred. No. 3.9e-278;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591


RESULT 11
US-09-917-265-37/c
; Sequence 37, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
```

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;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-37

  Query Match             81.1%;  Score 540;  DB 3;  Length 591;
  Best Local Similarity   99.8%;  Pred. No. 3.9e-278;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1


RESULT 12
US-10-821-670-35
; Sequence 35, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(591)
US-10-821-670-35

  Query Match             81.1%;  Score 540;  DB 9;  Length 591;
  Best Local Similarity   99.8%;  Pred. No. 3.9e-278;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591


RESULT 13
US-10-821-670-37/c
; Sequence 37, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-37
```

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  Query Match             81.1%;  Score 540;  DB 9;  Length 591;
  Best Local Similarity   99.8%;  Pred. No. 3.9e-278;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy         136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy         196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy         256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy         316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy         376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy         436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy         496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy         556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy         616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1


RESULT 14
US-10-079-616-9
; Sequence 9, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 591 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-079-616-9

  Query Match             79.1%;  Score 527;  DB 6;  Length 591;
  Best Local Similarity   99.8%;  Pred. No. 3.6e-271;
  Matches  577;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy         196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy         256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy         316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy         376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy         436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy         496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy         556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615
               |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy         616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTA 653
               |||||||||||||||||||||||||||||||||||||
Db         541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTA 578


RESULT 15
US-09-917-265-43
; Sequence 43, Application US/09917265
; Patent No. US20020052030A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
;   OTHER INFORMATION:
US-09-917-265-43

  Query Match             76.1%;  Score 507;  DB 3;  Length 1533;
  Best Local Similarity   99.8%;  Pred. No. 1.9e-260;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        976 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 1035

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1036 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 1095

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1096 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 1155

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1156 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 1215

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1216 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 1275

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1276 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 1335

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1336 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 1395

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1396 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 1455

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1456 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 1515

Qy        649 AGCTATCTGAATGCTTCC 666
              |||||||||||||||||
Db       1516 AGCTATCTGAATGCTTCC 1533


RESULT 16
US-09-917-265-45/c
; Sequence 45, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-45

  Query Match             76.1%;  Score 507;  DB 3;  Length 1533;
  Best Local Similarity   99.8%;  Pred. No. 1.9e-260;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        649 AGCTATCTGAATGCTTCC 666
              |||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1


RESULT 17
US-10-821-670-43
; Sequence 43, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
```

```
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-10-821-670-43

  Query Match             76.1%;  Score 507;  DB 9;  Length 1533;
  Best Local Similarity   99.8%;  Pred. No. 1.9e-260;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        976 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 1035

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1036 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 1095

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1096 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 1155

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1156 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 1215

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1216 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 1275

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1276 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 1335

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1336 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 1395

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1396 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 1455

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1456 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 1515

Qy        649 AGCTATCTGAATGCTTCC 666
              ||||||||||||||||||
Db       1516 AGCTATCTGAATGCTTCC 1533


RESULT 18
US-10-821-670-45/c
; Sequence 45, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-45

  Query Match             76.1%;  Score 507;  DB 9;  Length 1533;
  Best Local Similarity   99.8%;  Pred. No. 1.9e-260;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        649 AGCTATCTGAATGCTTCC 666
              ||||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1


RESULT 19
US-09-917-265-38
; Sequence 38, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
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US-09-917-265-38

  Query Match             76.1%;  Score 507;  DB 3;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 1.9e-260;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1042 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 1101

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1102 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 1161

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1162 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 1221

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1222 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 1281

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1282 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 1341

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1342 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 1401

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1402 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 1461

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db       1462 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 1521

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1522 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 1581

Qy        649 AGCTATCTGAATGCTTCC 666
              ||||||||||||||||||
Db       1582 AGCTATCTGAATGCTTCC 1599


RESULT 20
US-09-917-265-40/c
; Sequence 40, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-40

  Query Match             76.1%;  Score 507;  DB 3;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 1.9e-260;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db       138 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        649 AGCTATCTGAATGCTTCC 666
              ||||||||||||||||||
Db        18 AGCTATCTGAATGCTTCC 1


RESULT 21
US-10-821-670-38
; Sequence 38, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-10-821-670-38

  Query Match             76.1%;  Score 507;  DB 9;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 1.9e-260;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1042 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 1101
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Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1102 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 1161

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1162 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 1221

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1222 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 1281

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1282 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 1341

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1342 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 1401

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1402 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 1461

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db       1462 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 1521

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1522 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 1581

Qy        649 AGCTATCTGAATGCTTCC 666
              ||||||||||||||||||
Db       1582 AGCTATCTGAATGCTTCC 1599
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RESULT 22
US-10-821-670-40/c
; Sequence 40, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
US-10-821-670-40

Query Match 76.1%; Score 507; DB 9; Length 1599;
Best Local Similarity 99.8%; Pred. No. 1.9e-260;
Matches 557; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        649 AGCTATCTGAATGCTTCC 666
              ||||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1
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RESULT 23
US-10-041-672C-2
; Sequence 2, Application US/10041672C
; Publication No. US20030157059A1
; GENERAL INFORMATION:
; APPLICANT: Mologen Forschungs-, Entwicklungs- und Vetriebs GmbH
; APPLICANT: Universitat Zurich
; TITLE OF INVENTION: FELINE INTERLEUKIN-12 AS IMMUNOSTIMULANT
; FILE REFERENCE: NHL-NP-36
; CURRENT APPLICATION NUMBER: US/10/041,672C
; CURRENT FILING DATE: 2002-01-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 669
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: feline IL-12 p35
US-10-041-672C-2

Query Match 45.5%; Score 303; DB 7; Length 669;
Best Local Similarity 99.2%; Pred. No. 3.9e-151;
Matches 503; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
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              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              |||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTG 507
              |||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTG 507


RESULT 24
US-10-079-616-26
; Sequence 26, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 26:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 689 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-079-616-26

  Query Match             37.2%;  Score 248;  DB 6;  Length 689;
  Best Local Similarity   98.8%;  Pred. No. 1.1e-121;
  Matches  598;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         49 AACCACCTGGACCACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGA 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         55 AACCACCTGGACCACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGA 114

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 174

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 234

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              |||||||||||||||||||||||||||||||||||| | ||||||||| | ||||||||||
Db        235 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATGAAT 294

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 354

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 414

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              |||||||||||||||||||||||||||||||||| | ||||||||||||||||||||||
Db        415 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATC 474

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 534

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        535 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATC 594

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 654

Qy        649 AGCTA 653
              |||||
Db        655 AGCTA 659


RESULT 25
US-09-917-265-49
; Sequence 49, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(591)
;   OTHER INFORMATION:
US-09-917-265-49
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  Query Match             12.2%;  Score 81;  DB 3;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        223 CTGGCTTCCAGAGAGATCTCT 243


RESULT 26
US-09-917-265-51/c
; Sequence 51, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-51

  Query Match             12.2%;  Score 81;  DB 3;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 27
US-10-821-670-49
; Sequence 49, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(591)
US-10-821-670-49

  Query Match             12.2%;  Score 81;  DB 9;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        223 CTGGCTTCCAGAGAGATCTCT 243


RESULT 28
US-10-821-670-51/c
; Sequence 51, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-51

  Query Match             12.2%;  Score 81;  DB 9;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 29
US-09-917-265-46
; Sequence 46, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
;   OTHER INFORMATION:
US-09-917-265-46

  Query Match             12.2%;  Score 81;  DB 3;  Length 666;
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  Best Local Similarity   100.0%;  Pred. No. 3.5e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 30
US-09-917-265-48/c
; Sequence 48, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-48

  Query Match             12.2%;  Score 81;  DB 3;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 31
US-10-821-670-46
; Sequence 46, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
US-10-821-670-46

  Query Match             12.2%;  Score 81;  DB 9;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 32
US-10-821-670-48/c
; Sequence 48, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-48

  Query Match             12.2%;  Score 81;  DB 9;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 33
US-09-917-265-104
; Sequence 104, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (232)..(897)
;   OTHER INFORMATION:
US-09-917-265-104

  Query Match             12.2%;  Score 81;  DB 3;  Length 1455;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-32;
```

```
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 528

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        529 CTGGCTTCCAGAGAGATCTCT 549


RESULT 34
US-09-917-265-106/c
; Sequence 106, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 106
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-106

  Query Match            12.2%;  Score 81;  DB 3;  Length 1455;
  Best Local Similarity  100.0%;  Pred. No. 3.5e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 928

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        927 CTGGCTTCCAGAGAGATCTCT 907


RESULT 35
US-10-821-670-104
; Sequence 104, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 104
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (232)..(897)
US-10-821-670-104

  Query Match            12.2%;  Score 81;  DB 9;  Length 1455;
  Best Local Similarity  100.0%;  Pred. No. 3.5e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 528

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        529 CTGGCTTCCAGAGAGATCTCT 549


RESULT 36
US-10-821-670-106/c
; Sequence 106, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 106
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-106

  Query Match            12.2%;  Score 81;  DB 9;  Length 1455;
  Best Local Similarity  100.0%;  Pred. No. 3.5e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 928

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        927 CTGGCTTCCAGAGAGATCTCT 907


RESULT 37
US-09-917-265-66
; Sequence 66, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
;   OTHER INFORMATION:
US-09-917-265-66

  Query Match            12.2%;  Score 81;  DB 3;  Length 1533;
  Best Local Similarity  100.0%;  Pred. No. 3.5e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1105 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1164

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db       1165 CTGGCTTCCAGAGAGATCTCT 1185
```

RESULT 38
US-09-917-265-68/c
; Sequence 68, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-917-265-68

Query Match 12.2%; Score 81; DB 3; Length 1533;
Best Local Similarity 100.0%; Pred. No. 3.5e-32;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349
```

RESULT 39
US-10-821-670-66
; Sequence 66, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)
US-10-821-670-66

Query Match 12.2%; Score 81; DB 9; Length 1533;
Best Local Similarity 100.0%; Pred. No. 3.5e-32;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1105 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1164

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db       1165 CTGGCTTCCAGAGAGATCTCT 1185
```

RESULT 40
US-10-821-670-68/c
; Sequence 68, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-821-670-68

Query Match 12.2%; Score 81; DB 9; Length 1533;
Best Local Similarity 100.0%; Pred. No. 3.5e-32;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349
```

RESULT 41
US-09-917-265-61
; Sequence 61, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1599)
; OTHER INFORMATION:
US-09-917-265-61

Query Match 12.2%; Score 81; DB 3; Length 1599;
Best Local Similarity 100.0%; Pred. No. 3.5e-32;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1230

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db       1231 CTGGCTTCCAGAGAGATCTCT 1251
```

RESULT 42
US-09-917-265-63/c
; Sequence 63, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-917-265-63

```
  Query Match             12.2%;  Score 81;  DB 3;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349
```

RESULT 43
US-10-821-670-61
; Sequence 61, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1599)
US-10-821-670-61

```
  Query Match             12.2%;  Score 81;  DB 9;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1230

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db       1231 CTGGCTTCCAGAGAGATCTCT 1251
```

RESULT 44
US-10-821-670-63/c
; Sequence 63, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-821-670-63

```
  Query Match             12.2%;  Score 81;  DB 9;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349
```

RESULT 45
US-10-041-672C-8
; Sequence 8, Application US/10041672C
; Publication No. US20030157059A1
; GENERAL INFORMATION:
; APPLICANT: Mologen Forschungs-, Entwicklungs- und Vetriebs GmbH
; APPLICANT: Universitat Zurich
; TITLE OF INVENTION: FELINE INTERLEUKIN-12 AS IMMUNOSTIMULANT
; FILE REFERENCE: NHL-NP-36
; CURRENT APPLICATION NUMBER: US/10/041,672C
; CURRENT FILING DATE: 2002-01-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 71
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer f12p35-1-lang
US-10-041-672C-8

```
  Query Match             10.7%;  Score 71;  DB 7;  Length 71;
  Best Local Similarity   100.0%;  Pred. No. 8e-27;
  Matches   71;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        485 TGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCAC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCAC 60

Qy        545 AGAACTCCTCC 555
```

```
              ||||||||||||
Db         61 AGAACTCCTCC 71


RESULT 46
US-10-741-601-946
; Sequence 946, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 946
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-946

  Query Match             9.8%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 72

Qy        619 ATTCG 623
              |||||
Db         73 ATTCG 77


RESULT 47
US-10-741-601-947
; Sequence 947, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 947
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-947

  Query Match             9.8%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 80

Qy        619 ATTCG 623
              |||||
Db         81 ATTCG 85


RESULT 48
US-10-741-601-951
; Sequence 951, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 951
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-951

  Query Match             9.8%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 181

Qy        619 ATTCG 623
              |||||
Db        182 ATTCG 186


RESULT 49
US-10-741-601-955
; Sequence 955, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 955
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-955

  Query Match             9.8%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 72

Qy        619 ATTCG 623
              |||||
Db         73 ATTCG 77


RESULT 50
US-10-741-601-957
; Sequence 957, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 957
```

```
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-957

  Query Match             9.8%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 80

Qy        619 ATTCG 623
              |||||
Db         81 ATTCG 85


RESULT 51
US-10-741-601-960
; Sequence 960, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 960
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-960

  Query Match             9.8%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 181

Qy        619 ATTCG 623
              |||||
Db        182 ATTCG 186


RESULT 52
US-10-741-601-7417
; Sequence 7417, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7417
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-7417

  Query Match             9.8%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 72

Qy        619 ATTCG 623
              |||||
Db         73 ATTCG 77


RESULT 53
US-10-741-601-7418
; Sequence 7418, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7418
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-7418

  Query Match             9.8%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 80

Qy        619 ATTCG 623
              |||||
Db         81 ATTCG 85


RESULT 54
US-10-741-601-7431
; Sequence 7431, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7431
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-7431

  Query Match             9.8%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 181

Qy        619 ATTCG 623
              |||||
Db        182 ATTCG 186
```

```
RESULT 55
US-10-741-601-11370/c
; Sequence 11370, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11370
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-11370

  Query Match             9.8%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 130

Qy        619 ATTCG 623
              |||||
Db        129 ATTCG 125


RESULT 56
US-10-741-601-11372/c
; Sequence 11372, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11372
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-11372

  Query Match             9.8%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 122

Qy        619 ATTCG 623
              |||||
Db        121 ATTCG 117


RESULT 57
US-10-741-601-11417/c
; Sequence 11417, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11417
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-11417

  Query Match             9.8%;  Score 65;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 21

Qy        619 ATTCG 623
              |||||
Db         20 ATTCG 16


RESULT 58
US-10-741-600-3487
; Sequence 3487, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3487
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-3487

  Query Match             9.8%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 72

Qy        619 ATTCG 623
              |||||
Db         73 ATTCG 77


RESULT 59
US-10-741-600-3488
; Sequence 3488, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3488
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-3488
```

```
  Query Match             9.8%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 80

Qy        619 ATTCG 623
              |||||
Db         81 ATTCG 85


RESULT 60
US-10-741-600-3492
; Sequence 3492, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3492
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-3492

  Query Match             9.8%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 181

Qy        619 ATTCG 623
              |||||
Db        182 ATTCG 186


RESULT 61
US-10-741-600-3496
; Sequence 3496, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3496
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-3496

  Query Match             9.8%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 72

Qy        619 ATTCG 623
              |||||
Db         73 ATTCG 77


RESULT 62
US-10-741-600-3498
; Sequence 3498, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3498
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-3498

  Query Match             9.8%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 80

Qy        619 ATTCG 623
              |||||
Db         81 ATTCG 85


RESULT 63
US-10-741-600-3501
; Sequence 3501, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3501
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-3501

  Query Match             9.8%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 181

Qy        619 ATTCG 623
              |||||
Db        182 ATTCG 186


RESULT 64
US-10-741-600-20963
; Sequence 20963, Application US/10741600
; Publication No. US20050026169A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20963
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-20963

  Query Match             9.8%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 72

Qy        619 ATTCG 623
              |||||
Db         73 ATTCG 77


RESULT 65
US-10-741-600-20964
; Sequence 20964, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20964
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-20964

  Query Match             9.8%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 80

Qy        619 ATTCG 623
              |||||
Db         81 ATTCG 85


RESULT 66
US-10-741-600-20992
; Sequence 20992, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20992
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-20992

  Query Match             9.8%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 181

Qy        619 ATTCG 623
              |||||
Db        182 ATTCG 186


RESULT 67
US-10-741-600-28831/c
; Sequence 28831, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28831
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-28831

  Query Match             9.8%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 130

Qy        619 ATTCG 623
              |||||
Db        129 ATTCG 125


RESULT 68
US-10-741-600-28833/c
; Sequence 28833, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28833
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-28833

  Query Match             9.8%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 122

Qy        619 ATTCG 623
              |||||
Db        121 ATTCG 117


RESULT 69
US-10-741-600-28877/c
; Sequence 28877, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28877
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-28877

  Query Match             9.8%;  Score 65;  DB 9;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 21

Qy        619 ATTCG 623
              |||||
Db         20 ATTCG 16


RESULT 70
US-10-995-561-1976
; Sequence 1976, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1976
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-1976

  Query Match             9.8%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 72

Qy        619 ATTCG 623
              |||||
Db         73 ATTCG 77


RESULT 71
US-10-995-561-1977
; Sequence 1977, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1977
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-1977

  Query Match             9.8%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 80

Qy        619 ATTCG 623
              |||||
Db         81 ATTCG 85


RESULT 72
US-10-995-561-1981
; Sequence 1981, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1981
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-1981

  Query Match             9.8%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 181

Qy        619 ATTCG 623
              |||||
Db        182 ATTCG 186


RESULT 73
US-10-995-561-1986
; Sequence 1986, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
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;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1986
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-1986

  Query Match             9.8%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 72

Qy        619 ATTCG 623
              |||||
Db         73 ATTCG 77


RESULT 74
US-10-995-561-1988
; Sequence 1988, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1988
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-1988

  Query Match             9.8%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 80

Qy        619 ATTCG 623
              |||||
Db         81 ATTCG 85


RESULT 75
US-10-995-561-1991
; Sequence 1991, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1991
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-1991

  Query Match             9.8%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 181

Qy        619 ATTCG 623
              |||||
Db        182 ATTCG 186


RESULT 76
US-10-995-561-18302
; Sequence 18302, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18302
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-18302

  Query Match             9.8%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 72

Qy        619 ATTCG 623
              |||||
Db         73 ATTCG 77


RESULT 77
US-10-995-561-18303
; Sequence 18303, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18303
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-18303
```

```
  Query Match             9.8%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 80

Qy        619 ATTCG 623
              |||||
Db         81 ATTCG 85


RESULT 78
US-10-995-561-18335
; Sequence 18335, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18335
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-18335

  Query Match             9.8%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 181

Qy        619 ATTCG 623
              |||||
Db        182 ATTCG 186


RESULT 79
US-10-995-561-26362/c
; Sequence 26362, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26362
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-26362

  Query Match             9.8%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 21

Qy        619 ATTCG 623
              |||||
Db         20 ATTCG 16


RESULT 80
US-10-995-561-26545/c
; Sequence 26545, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26545
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-26545

  Query Match             9.8%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 130

Qy        619 ATTCG 623
              |||||
Db        129 ATTCG 125


RESULT 81
US-10-995-561-26548/c
; Sequence 26548, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26548
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-26548

  Query Match             9.8%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 122

Qy        619 ATTCG 623
              |||||
Db        121 ATTCG 117
```

```
RESULT 82
US-10-995-561-73346/c
; Sequence 73346, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73346
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-73346

  Query Match             9.8%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 130

Qy        619 ATTCG 623
              |||||
Db        129 ATTCG 125


RESULT 83
US-10-995-561-73349/c
; Sequence 73349, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73349
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-73349

  Query Match             9.8%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 122

Qy        619 ATTCG 623
              |||||
Db        121 ATTCG 117


RESULT 84
US-10-995-561-73383/c
; Sequence 73383, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73383
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-73383

  Query Match             9.8%;  Score 65;  DB 10;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 21

Qy        619 ATTCG 623
              |||||
Db         20 ATTCG 16


RESULT 85
US-09-754-014-6
; Sequence 6, Application US/09754014
; Patent No. US20020119940A1
;   GENERAL INFORMATION:
;        APPLICANT: Jeff No. US20020119940A1dstrom
;                   Bruce Freimark
;                   Deepa Deshpande
;        TITLE OF INVENTION: GENE EXPRESSION AND DELIVERY SYTEMS
;                            AND USES
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                     Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 90071-2066
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                          storage
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: IBM P.C. DOS 5.0
;             SOFTWARE: FastSEQ for Windows 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/754,014
;             FILING DATE: 03-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/948,958
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Berkman, Charles S.
;             REGISTRATION NUMBER: 38,077
;             REFERENCE/DOCKET NUMBER: 226/284
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 660 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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US-09-754-014-6

  Query Match             9.8%;  Score 65;  DB 3;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        619 ATTCG 623
              |||||
Db        610 ATTCG 614


RESULT 86
US-09-836-866-4
; Sequence 4, Application US/09836866
; Patent No. US20020123473A1
;   GENERAL INFORMATION:
;        APPLICANT: No. US20020123473A1dstrom, Jeff
;                   Freimark, Bruce
;                   Deshpande, Deepa
;        TITLE OF INVENTION: IL-12 GENE EXPRESSION AND
;                            DELIVERY SYTEMS AND USES
;        NUMBER OF SEQUENCES: 8
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                     Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 90071-2066
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                          storage
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: IBM P.C. DOS 5.0
;             SOFTWARE: FastSEQ for Windows 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/836,866
;             FILING DATE: 16-Apr-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/949,160
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Warburg, Richard J.
;             REGISTRATION NUMBER: 32,327
;             REFERENCE/DOCKET NUMBER: 226/285
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 660 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-836-866-4

  Query Match             9.8%;  Score 65;  DB 3;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        619 ATTCG 623
              |||||
Db        610 ATTCG 614


RESULT 87
US-10-267-384-199
; Sequence 199, Application US/10267384
; Publication No. US20030198623A1
;   GENERAL INFORMATION:
;        APPLICANT: Paoletti, Enzo
;                   Tartaglia, James
;                   Cox, William I.
;        TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
;        NUMBER OF SEQUENCES: 217
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Curtis, Morris & Safford
;             STREET: 530 Fifth Avenue
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10036
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/267,384
;             FILING DATE: 09-Oct-2002
;             CLASSIFICATION: 435
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Frommer, William S.
;             REGISTRATION NUMBER: 25,506
;             REFERENCE/DOCKET NUMBER: 454310-2530
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 840-3333
;             TELEFAX: (212) 840-0712
;             TELEX: 425066CURTMS
;   INFORMATION FOR SEQ ID NO: 199:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 721 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 199:
US-10-267-384-199

  Query Match             9.8%;  Score 65;  DB 7;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy        619 ATTCG 623
              |||||
Db        671 ATTCG 675


RESULT 88
US-09-826-025-21
; Sequence 21, Application US/09826025
; Patent No. US20020162123A1
;   GENERAL INFORMATION:
;        APPLICANT: Chang, Lung-Ji
;        TITLE OF INVENTION: Combination Immunogene Therapy
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Medlen & Carroll, LLP
;             STREET: 220 Montgomery Street, Suite 2200
;             CITY: San Francisco
```

```
;            STATE: California
;            COUNTRY: United States of America
;            ZIP: 94104
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/826,025
;            FILING DATE: 04-Apr-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/838,702
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Ingolia, Diane E.
;            REGISTRATION NUMBER: 40,027
;            REFERENCE/DOCKET NUMBER: CHANG-02687
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 705-8410
;            TELEFAX: (415) 397-8338
;   INFORMATION FOR SEQ ID NO: 21:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 762 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: other nucleic acid
;            DESCRIPTION: /desc = "DNA"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-826-025-21

  Query Match             9.8%;  Score 65;  DB 3;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        619 ATTCG 623
              |||||
Db        712 ATTCG 716


RESULT 89
US-10-785-577-21
; Sequence 21, Application US/10785577
; Publication No. US20040237129A1
;  GENERAL INFORMATION:
;       APPLICANT: Chang, Lung-Ji
;       TITLE OF INVENTION: Combination Immunogene Therapy
;       NUMBER OF SEQUENCES: 25
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Medlen & Carroll, LLP
;            STREET: 220 Montgomery Street, Suite 2200
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: United States of America
;            ZIP: 94104
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/785,577
;            FILING DATE: 23-Feb-2004
;            CLASSIFICATION: 424
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/838,702
;            FILING DATE: 9-Apr-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Ingolia, Diane E.
;            REGISTRATION NUMBER: 40,027
;            REFERENCE/DOCKET NUMBER: CHANG-02687
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 705-8410
;            TELEFAX: (415) 397-8338
;   INFORMATION FOR SEQ ID NO: 21:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 762 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: other nucleic acid
;            DESCRIPTION: /desc = "DNA"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-10-785-577-21

  Query Match             9.8%;  Score 65;  DB 9;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        619 ATTCG 623
              |||||
Db        712 ATTCG 716


RESULT 90
US-10-688-845-57
; Sequence 57, Application US/10688845
; Publication No. US20040247578A1
; GENERAL INFORMATION:
;  APPLICANT: Lotze, Michael T
;  APPLICANT:  Tahara, Hideaki
;  TITLE OF INVENTION: Methods And Reagents For Inducing Immunity
;  FILE REFERENCE: UPT-004
;  CURRENT APPLICATION NUMBER: US/10/688,845
;  CURRENT FILING DATE:  2003-10-15
;  PRIOR APPLICATION NUMBER: 60/418,865
;  PRIOR FILING DATE: 2002-10-15
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
;   LENGTH: 762
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-688-845-57

  Query Match             9.8%;  Score 65;  DB 9;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        619 ATTCG 623
              |||||
Db        712 ATTCG 716


RESULT 91
US-10-373-456-19
; Sequence 19, Application US/10373456
; Publication No. US20040009146A1
; GENERAL INFORMATION:
;  APPLICANT: Podhajcer, Osvaldo
;  TITLE OF INVENTION: Anti-Tumor Vaccine and Method
;  FILE REFERENCE: 1423P-US/101141-14
```

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;  CURRENT APPLICATION NUMBER: US/10/373,456
;  CURRENT FILING DATE:  2003-02-25
;  PRIOR APPLICATION NUMBER: US 60/359,836
;  PRIOR FILING DATE: 2002-02-26
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 811
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-373-456-19

  Query Match             9.8%;  Score 65;  DB 7;  Length 811;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 557

Qy        619 ATTCG 623
              |||||
Db        558 ATTCG 562


RESULT 92
US-10-349-507-4
; Sequence 4, Application US/10349507
; Publication No. US20030199002A1
; GENERAL INFORMATION:
;  APPLICANT: Hekimi , Siegfried
;  APPLICANT:. Jiang , Ning
;  APPLICANT:  Benard, Claire
;  APPLICANT:  Kebir , Hania
;  APPLICANT:  McCright, Brenton
;  APPLICANT:  Lakowski , Bernard
;  TITLE OF INVENTION: CLK-2 NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
;  FILE REFERENCE: 11202-006-999
;  CURRENT APPLICATION NUMBER: US/10/349,507
;  CURRENT FILING DATE:  2003-01-22
;  PRIOR APPLICATION NUMBER: 10/312,187
;  PRIOR FILING DATE: 2002-12-20
;  PRIOR APPLICATION NUMBER: PCT/CA01/00913
;  PRIOR FILING DATE: 2001-06-20
;  PRIOR APPLICATION NUMBER: 60/213,174
;  PRIOR FILING DATE: 2000-06-22
;  PRIOR APPLICATION NUMBER: 60/254,932
;  PRIOR FILING DATE: 2000-12-13
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 856
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (170)...(826)
US-10-349-507-4

  Query Match             9.8%;  Score 65;  DB 7;  Length 856;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 778

Qy        619 ATTCG 623
              |||||
Db        779 ATTCG 783


RESULT 93
US-10-267-565-4
; Sequence 4, Application US/10267565
; Publication No. US20030204059A1
; GENERAL INFORMATION:
;  APPLICANT: Gately, Maurice
;  APPLICANT:  Gubler, Ulrich
;  APPLICANT:  Hulmes, Jeffery
;  APPLICANT:  Podlaski, Frank
;  APPLICANT:  Stern, Alvin
;  TITLE OF INVENTION: PURIFICATION AND CHARACTERIZATION OF CYTOTOXIC
;  TITLE OF INVENTION:  LYMPHOCYTE MATURATION FACTOR AND MONOCLONAL
;  TITLE OF INVENTION:  ANTIBODIES THERETO
;  FILE REFERENCE: 11126-005
;  CURRENT APPLICATION NUMBER: US/10/267,565
;  CURRENT FILING DATE:  2003-01-23
;  PRIOR APPLICATION NUMBER: 09/401,839
;  PRIOR FILING DATE: 1999-09-22
;  PRIOR APPLICATION NUMBER: 08/459,151
;  PRIOR FILING DATE: 1995-06-02
;  PRIOR APPLICATION NUMBER: 08/205,011
;  PRIOR FILING DATE: 1994-03-02
;  PRIOR APPLICATION NUMBER: 07/857,023
;  PRIOR FILING DATE: 1992-03-24
;  PRIOR APPLICATION NUMBER: 07/572,284
;  PRIOR FILING DATE: 1990-08-27
;  PRIOR APPLICATION NUMBER: 07/520,935
;  PRIOR FILING DATE: 1990-05-09
;  PRIOR APPLICATION NUMBER: 07/455,708
;  PRIOR FILING DATE: 1989-12-22
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 856
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (170)...(826)
US-10-267-565-4

  Query Match             9.8%;  Score 65;  DB 7;  Length 856;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 778

Qy        619 ATTCG 623
              |||||
Db        779 ATTCG 783


RESULT 94
US-10-373-456-17
; Sequence 17, Application US/10373456
; Publication No. US20040009146A1
; GENERAL INFORMATION:
;  APPLICANT: Podhajcer, Osvaldo
;  TITLE OF INVENTION: Anti-Tumor Vaccine and Method
;  FILE REFERENCE: 1423P-US/101141-14
;  CURRENT APPLICATION NUMBER: US/10/373,456
;  CURRENT FILING DATE:  2003-02-25
;  PRIOR APPLICATION NUMBER: US 60/359,836
;  PRIOR FILING DATE: 2002-02-26
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
;   LENGTH: 868
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-373-456-17
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  Query Match             9.8%;  Score 65;  DB 7;  Length 868;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 620

Qy        619 ATTCG 623
              |||||
Db        621 ATTCG 625


RESULT 95
US-10-172-399-5
; Sequence 5, Application US/10172399
; Publication No. US20030045495A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Chuan-Yuan
;  APPLICANT:  Dewhirst, Mark
;  APPLICANT:  Huang, Qian
;  TITLE OF INVENTION: A METHOD FOR SELECTIVE EXPRESSION OF THERAPEUTIC GENES BY HYPERTH
;  FILE REFERENCE: 180-129
;  CURRENT APPLICATION NUMBER: US/10/172,399
;  CURRENT FILING DATE:  2002-06-14
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 1026
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (170)..(829)
US-10-172-399-5

  Query Match             9.8%;  Score 65;  DB 6;  Length 1026;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 778

Qy        619 ATTCG 623
              |||||
Db        779 ATTCG 783


RESULT 96
US-10-641-643-1041
; Sequence 1041, Application US/10641643
; Publication No. US20040077003A1
;   GENERAL INFORMATION:
;        APPLICANT: Cocks, Benjamin G.
;                   Susan G. Stuart
;                   Jeffrey J. Seilhamer
;        TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
;                            GENE EXPRESSION
;        NUMBER OF SEQUENCES: 1508
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
;             STREET: 3174 PORTER DRIVE
;             CITY: PALO ALTO
;             STATE: CALIFORNIA
;             COUNTRY: USA
;             ZIP: 94304
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/641,643
;             FILING DATE: 14-Aug-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: <Unknown>
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Zeller, Karen J.
;             REGISTRATION NUMBER: 37,071
;             REFERENCE/DOCKET NUMBER: PA-0001 US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (650) 855-0555
;             TELEFAX: (650) 845-4166
;   INFORMATION FOR SEQ ID NO: 1041:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1026 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        IMMEDIATE SOURCE:
;             LIBRARY: GENBANK
;             CLONE: g180623
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1041 :
US-10-641-643-1041

  Query Match             9.8%;  Score 65;  DB 8;  Length 1026;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
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Db        719 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 778

Qy        619 ATTCG 623
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Db        779 ATTCG 783


RESULT 97
US-10-603-064-6
; Sequence 6, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
;  APPLICANT: Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION: Multiple Cytokine Protein Complexes
;  FILE REFERENCE: LEX-010
;  CURRENT APPLICATION NUMBER: US/10/603,064
;  CURRENT FILING DATE:  2003-06-24
;  PRIOR APPLICATION NUMBER: US/09/634,368
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: 60/147,924
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 1287
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: human Fc-p35
;   OTHER INFORMATION: fusion protein coding sequence
US-10-603-064-6

  Query Match             9.8%;  Score 65;  DB 8;  Length 1287;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1177 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1236

Qy        619 ATTCG 623
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              |||||
Db       1237 ATTCG 1241


RESULT 98
US-10-476-960-3
; Sequence 3, Application US/10476960
; Publication No. US20040248828A1
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Isis Pharmaceuticals, Inc.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTSP-0392
;  CURRENT APPLICATION NUMBER: US/10/476,960
;  CURRENT FILING DATE:  2003-11-05
;  PRIOR APPLICATION NUMBER: 09/851,520
;  PRIOR FILING DATE: 2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
;   LENGTH: 1316
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (102)...(863)
US-10-476-960-3

  Query Match             9.8%;  Score 65;  DB 9;  Length 1316;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 812

Qy        619 ATTCG 623
              |||||
Db        813 ATTCG 817


RESULT 99
US-11-089-191-3
; Sequence 3, Application US/11089191
; Publication No. US20050261228A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Susan Gregory
;  APPLICANT:  Ronnie C. Hanecak
;  APPLICANT:  Kevin P. Anderson
;  APPLICANT:  Ming-Yi Chiang
;  APPLICANT:  Vickie Brown-Driver
;  APPLICANT:  David J. Ecker
;  APPLICANT:  Timothy Vickers
;  APPLICANT:  Jacqueline Wyatt
;  APPLICANT:  Eric G. Marcusson
;  APPLICANT:  Nicholas M. Dean
;  APPLICANT:  Sanjay Bhanot
;  APPLICANT:  Elizabeth J. Ackermann
;  APPLICANT:  Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: BNDL-0021US.P1
;  CURRENT APPLICATION NUMBER: US/11/089,191
;  CURRENT FILING DATE:  2005-03-23
;  PRIOR APPLICATION NUMBER: 10/476,960
;  PRIOR FILING DATE: 2003-11-07
;  PRIOR APPLICATION NUMBER: PCT/US02/13871
;  PRIOR FILING DATE: 2002-05-01
;  PRIOR APPLICATION NUMBER: 09/851,520
;  PRIOR FILING DATE: 2001-05-07
;  PRIOR APPLICATION NUMBER: 10/67,236
;  PRIOR FILING DATE: 2003-09-17
;  PRIOR APPLICATION NUMBER: 10/038,335
;  PRIOR FILING DATE: 2002-01-02
;  PRIOR APPLICATION NUMBER: 09/299,058
;  PRIOR FILING DATE: 1999-04-23
;  PRIOR APPLICATION NUMBER: 08/403,888
;  PRIOR FILING DATE: 1995-06-12
;  PRIOR APPLICATION NUMBER: PCT/US93/09297
;  PRIOR FILING DATE: 1993-09-29
;  PRIOR APPLICATION NUMBER: 07/954,185
;  PRIOR FILING DATE: 1992-09-29
;  PRIOR APPLICATION NUMBER: 10/515,546
;  PRIOR FILING DATE: 2004-11-23
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
;   LENGTH: 1316
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (102)...(863)
US-11-089-191-3

  Query Match             9.8%;  Score 65;  DB 15;  Length 1316;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 812

Qy        619 ATTCG 623
              |||||
Db        813 ATTCG 817


RESULT 100
US-09-924-703-5
; Sequence 5, Application US/09924703
; Patent No. US20020137898A1
; GENERAL INFORMATION:
;  APPLICANT: TRINCHIERI, GIORGIO
;  APPLICANT:  PERUSSIA, BICE
;  APPLICANT:  CLARK, STEVEN C.
;  APPLICANT:  WONG, GORDON G.
;  APPLICANT:  HEWICK, RODNEY
;  APPLICANT:  KOBAYASHI, MICHIKO
;  TITLE OF INVENTION: ANTIBODIES TO NATURAL KILLER STIMULATORY FACTOR
;  FILE REFERENCE: 01142.0142.0100
;  CURRENT APPLICATION NUMBER: US/09/924,703
;  CURRENT FILING DATE:  2001-08-09
;  PRIOR APPLICATION NUMBER: 09/325,958
;  PRIOR FILING DATE: 1999-06-04
;  PRIOR APPLICATION NUMBER: 08/858,000
;  PRIOR FILING DATE: 1997-05-16
;  PRIOR APPLICATION NUMBER: 08/403,013
;  PRIOR FILING DATE: 1995-03-13
;  PRIOR APPLICATION NUMBER: 07/584,941
;  PRIOR FILING DATE: 1990-09-18
;  PRIOR APPLICATION NUMBER: 07/307,817
;  PRIOR FILING DATE: 1989-02-07
;  PRIOR APPLICATION NUMBER: 07/269,945
;  PRIOR FILING DATE: 1988-11-10
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 1395
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
;   OTHER INFORMATION: sequence of the 30 kD subunit of NKSF
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;   NAME/KEY: CDS
;   LOCATION: (114)..(872)
US-09-924-703-5

  Query Match             9.8%;  Score 65;  DB 3;  Length 1395;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-23;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        765 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 824

Qy        619 ATTCG 623
              |||||
Db        825 ATTCG 829


Search completed: June 10, 2006, 02:00:29
Job time : 1123.52 secs
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2006, 23:41:15 ; Search time 15.4095 Seconds
(without alignments)
5485.659 Million cell updates/sec

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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 253354 seqs, 63461778 residues

Word size : 1

Total number of hits satisfying chosen parameters: 506630

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 200 summaries

Database : Published_Applications_NA_New:*
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3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	18	2.7	2324	7	US-11-293-697-1624	Sequence 1624, Ap
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c	7	17	2.6	5298	7	US-11-217-529-1583	Sequence 1583, Ap
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	14	16	2.4	1159	6	US-10-953-349-19286	Sequence 19286, A
	15	16	2.4	1186	6	US-10-953-349-20117	Sequence 20117, A
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191	14	2.1	996	7	US-11-265-761-108	Sequence 108, App
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ALIGNMENTS

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RESULT 1
US-11-266-409-9
; Sequence 9, Application US/11266409
; Publication No. US20060093578A1
; GENERAL INFORMATION:
;  APPLICANT: SUZUMURA, AKIO
;  TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATING MULTIPLE SCLEROSIS
;  FILE REFERENCE: 279847US40
;  CURRENT APPLICATION NUMBER: US/11/266,409
;  CURRENT FILING DATE:  2005-11-04
;  PRIOR APPLICATION NUMBER: US 60/624,851
;  PRIOR FILING DATE: 2004-11-04
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA
US-11-266-409-9

  Query Match             2.7%;  Score 18;  DB 7;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.7;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        397 GACTTGAAGATGTACCAG 414
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Db          1 GACTTGAAGATGTACCAG 18


RESULT 2
US-11-293-697-1624
; Sequence 1624, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
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; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1624
; LENGTH: 2324
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-1624

Query Match 2.7%; Score 18; DB 7; Length 2324;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 170 AGTTGCCTGGCCTCCAGA 187

RESULT 3
US-11-217-529-3208/c
; Sequence 3208, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3208
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3208

Query Match 2.6%; Score 17; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 48 AAACCACCTGGACCACC 64
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RESULT 4
US-11-217-529-1610/c
; Sequence 1610, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1610
; LENGTH: 918
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1610

Query Match 2.6%; Score 17; DB 7; Length 918;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 219 TCATGAAGATATCACAA 235
|||||||||||||||||
Db 223 TCATGAAGATATCACAA 207

RESULT 5
US-11-293-697-1253/c
; Sequence 1253, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1253
; LENGTH: 2024
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-1253

Query Match 2.6%; Score 17; DB 7; Length 2024;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 515 CCCTGAATGTCAACAGT 531
|||||||||||||||||
Db 191 CCCTGAATGTCAACAGT 175

RESULT 6
US-10-839-442A-9/c
; Sequence 9, Application US/10839442A
; Publication No. US20060115896A1
; GENERAL INFORMATION:
; APPLICANT: WONG, SUSAN J.
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
; FILE REFERENCE: 454311-2232.2
; CURRENT APPLICATION NUMBER: US/10/839,442A
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: 10/699,550
; PRIOR FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: 60/476,513
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/422,755
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US03/34823
; PRIOR FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: PCT/US02/09036
; PRIOR FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 9
; LENGTH: 2697
; TYPE: DNA
; ORGANISM: Dengue virus type 1
US-10-839-442A-9

Query Match 2.6%; Score 17; DB 6; Length 2697;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         59 ACCACCTCAGTTTGGCC 75
              |||||||||||||||||
Db        193 ACCACCTCAGTTTGGCC 177
```

RESULT 7
US-11-217-529-1583/c
; Sequence 1583, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1583
; LENGTH: 5298
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1583

Query Match 2.6%; Score 17; DB 7; Length 5298;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        601 CTTCTTCATGCTTTCAG 617
              |||||||||||||||||
Db       1938 CTTCTTCATGCTTTCAG 1922
```

RESULT 8
US-10-839-442A-3/c
; Sequence 3, Application US/10839442A
; Publication No. US20060115896A1
; GENERAL INFORMATION:
; APPLICANT: WONG, SUSAN J.
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
; FILE REFERENCE: 454311-2232.2
; CURRENT APPLICATION NUMBER: US/10/839,442A
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: 10/699,550
; PRIOR FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: 60/476,513
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/422,755
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US03/34823
; PRIOR FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: PCT/US02/09036
; PRIOR FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 10735
; TYPE: DNA
; ORGANISM: Dengue virus type 1
US-10-839-442A-3

Query Match 2.6%; Score 17; DB 6; Length 10735;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         59 ACCACCTCAGTTTGGCC 75
              |||||||||||||||||
Db       7766 ACCACCTCAGTTTGGCC 7750
```

RESULT 9
US-10-488-619-237
; Sequence 237, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations W
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 237
; LENGTH: 360
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(444)
; OTHER INFORMATION: N IS G, C, A OR T
US-10-488-619-237

Query Match 2.4%; Score 16; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        208 GAAGAGATTGATCATG 223
              ||||||||||||||||
Db        248 GAAGAGATTGATCATG 263
```

RESULT 10
US-11-217-529-81513/c
; Sequence 81513, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81513
; LENGTH: 483
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-81513

Query Match 2.4%; Score 16; DB 7; Length 483;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         23 TCCTTGTAACCATCCT 38
              ||||||||||||||||
Db         48 TCCTTGTAACCATCCT 33
```

```
RESULT 11
US-10-488-619-2250
; Sequence 2250, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2250
;   LENGTH: 569
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-488-619-2250

  Query Match             2.4%;  Score 16;  DB 6;  Length 569;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        550 TCCTCCCTGGAAGAAC 565
              ||||||||||||||||
Db        379 TCCTCCCTGGAAGAAC 394


RESULT 12
US-10-488-619-2249/c
; Sequence 2249, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2249
;   LENGTH: 807
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-488-619-2249

  Query Match             2.4%;  Score 16;  DB 6;  Length 807;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        550 TCCTCCCTGGAAGAAC 565
              ||||||||||||||||
Db        420 TCCTCCCTGGAAGAAC 405


RESULT 13
US-11-217-529-585
; Sequence 585, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 585
;   LENGTH: 861
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-585

  Query Match             2.4%;  Score 16;  DB 7;  Length 861;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        396 GGACTTGAAGATGTAC 411
              ||||||||||||||||
Db        370 GGACTTGAAGATGTAC 385


RESULT 14
US-10-953-349-19286
; Sequence 19286, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19286
;   LENGTH: 1159
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-19286

  Query Match             2.4%;  Score 16;  DB 6;  Length 1159;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        396 GGACTTGAAGATGTAC 411
              ||||||||||||||||
Db        561 GGACTTGAAGATGTAC 576


RESULT 15
US-10-953-349-20117
; Sequence 20117, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20117
;   LENGTH: 1186
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-20117

  Query Match             2.4%;  Score 16;  DB 6;  Length 1186;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         85 CCCACACCCACACCAA 100
              ||||||||||||||||
Db        155 CCCACACCCACACCAA 170
```

```
RESULT 16
US-10-953-349-36627/c
; Sequence 36627, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36627
;   LENGTH: 1203
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-36627

  Query Match             2.4%;  Score 16;  DB 6;  Length 1203;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        597 CATACTTCTTCATGCT 612
              ||||||||||||||||
Db        531 CATACTTCTTCATGCT 516


RESULT 17
US-11-183-218-9/c
; Sequence 9, Application US/11183218
; Publication No. US20060088906A1
; GENERAL INFORMATION:
;  APPLICANT: Neose Technologies, Inc.
;  APPLICANT:  DeFrees, Shawn
;  APPLICANT:  Zopf, David
;  APPLICANT:  Bayer, Robert
;  APPLICANT:  Hakes, David
;  APPLICANT:  Chen, Xi
;  APPLICANT:  Bowe, Caryne
;  TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND
;  TITLE OF INVENTION: GLYCOCONJUGATION OF ERYTHROPOIETIN
;  FILE REFERENCE: 040853-01-5083-US02
;  CURRENT APPLICATION NUMBER: US/11/183,218
;  CURRENT FILING DATE:  2005-07-15
;  PRIOR APPLICATION NUMBER: US 10/410,945
;  PRIOR FILING DATE: 2003-04-09
;  PRIOR APPLICATION NUMBER: PCT/US02/32263
;  PRIOR FILING DATE: 2002-10-09
;  PRIOR APPLICATION NUMBER: US 60/407,527
;  PRIOR FILING DATE: 2002-08-28
;  PRIOR APPLICATION NUMBER: US 60/404,249
;  PRIOR FILING DATE: 2002-08-16
;  PRIOR APPLICATION NUMBER: US 60/396,594
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: US 60/391,777
;  PRIOR FILING DATE: 2002-06-25
;  PRIOR APPLICATION NUMBER: US 60/387,292
;  PRIOR FILING DATE: 2002-06-07
;  PRIOR APPLICATION NUMBER: US 60/344,692
;  PRIOR FILING DATE: 2001-11-19
;  PRIOR APPLICATION NUMBER: US 60/334,301
;  PRIOR FILING DATE: 2001-11-28
;  PRIOR APPLICATION NUMBER: US 60/334,233
;  PRIOR FILING DATE: 2001-11-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
;   LENGTH: 1437
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-183-218-9

  Query Match             2.4%;  Score 16;  DB 7;  Length 1437;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        452 ATCCTAAAAGGCAGAT 467
              ||||||||||||||||
Db         64 ATCCTAAAAGGCAGAT 49


RESULT 18
US-10-471-571A-2411
; Sequence 2411, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 2411
;   LENGTH: 1536
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-2411

  Query Match             2.4%;  Score 16;  DB 6;  Length 1536;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        575 ATAAAACTAAAATCAA 590
              ||||||||||||||||
Db        983 ATAAAACTAAAATCAA 998


RESULT 19
US-10-953-349-16963
; Sequence 16963, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16963
;   LENGTH: 1575
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-16963

  Query Match             2.4%;  Score 16;  DB 6;  Length 1575;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        419 AGTTCAAGGCCATGAA 434
              ||||||||||||||||
Db        613 AGTTCAAGGCCATGAA 628


RESULT 20
US-10-953-349-34653
; Sequence 34653, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
```

```
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34653
;   LENGTH: 1676
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-34653

  Query Match             2.4%;  Score 16;  DB 6;  Length 1676;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        219 TCATGAAGATATCACA 234
              ||||||||||||||||
Db       1426 TCATGAAGATATCACA 1441


RESULT 21
US-11-293-697-326
; Sequence 326, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 326
;   LENGTH: 1859
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-326

  Query Match             2.4%;  Score 16;  DB 7;  Length 1859;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        409 TACCAGGTGGAGTTCA 424
              ||||||||||||||||
Db        386 TACCAGGTGGAGTTCA 401


RESULT 22
US-11-217-529-78920/c
; Sequence 78920, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78920
;   LENGTH: 1944
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-78920

  Query Match             2.4%;  Score 16;  DB 7;  Length 1944;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        146 GAGCCATCAGCAACAC 161
              ||||||||||||||||
Db       1790 GAGCCATCAGCAACAC 1775


RESULT 23
US-10-370-959-6/c
; Sequence 6, Application US/10370959
; Publication No. US20060088907A1
; GENERAL INFORMATION:
;  APPLICANT: Millennium Pharmaceuticals, Inc
;  APPLICANT:  Meyers, Rachel E.
;  APPLICANT:  Williamson, Mark W.
;  APPLICANT:  Kapeller-Libermann, Rosana
;  APPLICANT:  MacBeth, Kyle J.
;  APPLICANT:  Hunter, John J.
;  APPLICANT:  Rudolph-Owen, Laura A.
;  APPLICANT:  Bandaru, Rajasekhar
;  APPLICANT:  Tsai, Fong-Ying
;  TITLE OF INVENTION: NOVEL 13237, 18480, 2245, 16228, 7677,
;  TITLE OF INVENTION:  26320, 46619, 33166, 16836, 46867, 21617, 55562, 39228,
;  TITLE OF INVENTION:  62088, 46745, 23155, 21657, 42755, 32229, 22325, 46863 AND
;  TITLE OF INVENTION:  32252 MOLECULES AND USES THEREFOR
;  FILE REFERENCE: MPI03-017OMNIM
;  CURRENT APPLICATION NUMBER: US/10/370,959
;  CURRENT FILING DATE:  2003-02-20
;  PRIOR APPLICATION NUMBER: US 09/910,150
;  PRIOR FILING DATE: 2001-07-18
;  PRIOR APPLICATION NUMBER: US 60/219,028
;  PRIOR FILING DATE: 2000-07-18
;  PRIOR APPLICATION NUMBER: US 10/251,507
;  PRIOR FILING DATE: 2002-09-20
;  PRIOR APPLICATION NUMBER: US 09/715,479
;  PRIOR FILING DATE: 2000-11-17
;  PRIOR APPLICATION NUMBER: US 60/218,053
;  PRIOR FILING DATE: 2000-07-13
;  PRIOR APPLICATION NUMBER: US 09/644,929
;  PRIOR FILING DATE: 2000-08-23
;  PRIOR APPLICATION NUMBER: US 60/212,439
;  PRIOR FILING DATE: 2000-06-16
;  PRIOR APPLICATION NUMBER: US 09/892,870
;  PRIOR FILING DATE: 2001-06-26
;  PRIOR APPLICATION NUMBER: US 60/214,174
;  PRIOR FILING DATE: 2000-06-26
;  PRIOR APPLICATION NUMBER: US 09/775,117
;  PRIOR FILING DATE: 2001-02-01
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 156
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 2079
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(2079)
US-10-370-959-6

  Query Match             2.4%;  Score 16;  DB 6;  Length 2079;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         51 CCACCTGGACCACCTC 66
              ||||||||||||||||
Db       1012 CCACCTGGACCACCTC 997
```

```
RESULT 24
US-10-511-937-2883/c
; Sequence 2883, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
;  APPLICANT: EXPRESSION DIAGNOSTICS, INC.
;  APPLICANT:  Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  APPLICANT:  Prentice, James
;  APPLICANT:  Morris, MacDonald
;  APPLICANT:  Rosenberg, Steven
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
;  TITLE OF INVENTION:  AND MONITORING TRANSPLANT REJECTION
;  FILE REFERENCE: 506612000104
;  CURRENT APPLICATION NUMBER: US/10/511,937
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: PCT/US2003/012946
;  PRIOR FILING DATE: 2003-04-24
;  PRIOR APPLICATION NUMBER: US 10/131,831
;  PRIOR FILING DATE: 2002-04-24
;  PRIOR APPLICATION NUMBER: US 10/325,899
;  PRIOR FILING DATE: 2002-12-20
;  NUMBER OF SEQ ID NOS: 3117
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2883
;   LENGTH: 2243
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (39)..(39)
;   OTHER INFORMATION: n is a, c, g, t or u
US-10-511-937-2883

  Query Match             2.4%;  Score 16;  DB 6;  Length 2243;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        283 ATGAATGAGAGTTGCC 298
              ||||||||||||||||
Db        560 ATGAATGAGAGTTGCC 545


RESULT 25
US-10-370-959-4/c
; Sequence 4, Application US/10370959
; Publication No. US20060088907A1
; GENERAL INFORMATION:
;  APPLICANT: Millennium Pharmaceuticals, Inc
;  APPLICANT:  Meyers, Rachel E.
;  APPLICANT:  Williamson, Mark W.
;  APPLICANT:  Kapeller-Libermann, Rosana
;  APPLICANT:  MacBeth, Kyle J.
;  APPLICANT:  Hunter, John J.
;  APPLICANT:  Rudolph-Owen, Laura A.
;  APPLICANT:  Bandaru, Rajasekhar
;  APPLICANT:  Tsai, Fong-Ying
;  TITLE OF INVENTION: NOVEL 13237, 18480, 2245, 16228, 7677,
;  TITLE OF INVENTION:  26320, 46619, 33166, 16836, 46867, 21617, 55562, 39228,
;  TITLE OF INVENTION:  62088, 46745, 23155, 21657, 42755, 32229, 22325, 46863 AND
;  TITLE OF INVENTION:  32252 MOLECULES AND USES THEREFOR
;  FILE REFERENCE: MPI03-017OMNIM
;  CURRENT APPLICATION NUMBER: US/10/370,959
;  CURRENT FILING DATE:  2003-02-20
;  PRIOR APPLICATION NUMBER: US 09/910,150
;  PRIOR FILING DATE: 2001-07-18
;  PRIOR APPLICATION NUMBER: US 60/219,028
;  PRIOR FILING DATE: 2000-07-18
;  PRIOR APPLICATION NUMBER: US 10/251,507
;  PRIOR FILING DATE: 2002-09-20
;  PRIOR APPLICATION NUMBER: US 09/715,479
;  PRIOR FILING DATE: 2000-11-17
;  PRIOR APPLICATION NUMBER: US 60/218,053
;  PRIOR FILING DATE: 2000-07-13
;  PRIOR APPLICATION NUMBER: US 09/644,929
;  PRIOR FILING DATE: 2000-08-23
;  PRIOR APPLICATION NUMBER: US 60/212,439
;  PRIOR FILING DATE: 2000-06-16
;  PRIOR APPLICATION NUMBER: US 09/892,870
;  PRIOR FILING DATE: 2001-06-26
;  PRIOR APPLICATION NUMBER: US 60/214,174
;  PRIOR FILING DATE: 2000-06-26
;  PRIOR APPLICATION NUMBER: US 09/775,117
;  PRIOR FILING DATE: 2001-02-01
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 156
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 2438
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (45)...(2123)
US-10-370-959-4

  Query Match             2.4%;  Score 16;  DB 6;  Length 2438;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         51 CCACCTGGACCACCTC 66
              ||||||||||||||||
Db       1056 CCACCTGGACCACCTC 1041


RESULT 26
US-11-293-697-520/c
; Sequence 520, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 520
;   LENGTH: 2836
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-520

  Query Match             2.4%;  Score 16;  DB 7;  Length 2836;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        462 GCAGATCTTTCTGGAT 477
              ||||||||||||||||
Db       2681 GCAGATCTTTCTGGAT 2666


RESULT 27
US-11-217-529-76344
; Sequence 76344, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
```

; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76344
; LENGTH: 4293
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76344

Query Match 2.4%; Score 16; DB 7; Length 4293;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 495 TATTGATGAGCTGTTA 510
||||||||||||||||
Db 1146 TATTGATGAGCTGTTA 1161

RESULT 28
US-11-248-986-13/c
; Sequence 13, Application US/11248986
; Publication No. US20060112448A1
; GENERAL INFORMATION:
; APPLICANT: OSBOURN, ANNE E.
; APPLICANT: QI, XIAOQUAN
; TITLE OF INVENTION: ENZYMES INVOLVED IN TRITERPENE SYNTHESIS
; FILE REFERENCE: BB1550 US NA
; CURRENT APPLICATION NUMBER: US/11/248,986
; CURRENT FILING DATE: 2005-10-12
; PRIOR APPLICATION NUMBER: 60/619,203
; PRIOR FILING DATE: 2004-10-15
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 5992
; TYPE: DNA
; ORGANISM: Avena strigosa
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(5992)
; OTHER INFORMATION: Genomic sequence for AsCYP51H
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(5992)
; OTHER INFORMATION: Genomic sequence for AsCYP51H10
US-11-248-986-13

Query Match 2.4%; Score 16; DB 7; Length 5992;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 577 AAAACTAAAATCAAGC 592
||||||||||||||||
Db 2978 AAAACTAAAATCAAGC 2963

RESULT 29
US-10-511-937-2838
; Sequence 2838, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2838
; LENGTH: 6383
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-2838

Query Match 2.4%; Score 16; DB 6; Length 6383;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 349 AGAAAGACCTCTTTTA 364
||||||||||||||||
Db 438 AGAAAGACCTCTTTTA 453

RESULT 30
US-10-489-730-10
; GENERAL INFORMATION:
; APPLICANT: Melino, Gennaro
; APPLICANT: Hayes, Ian
; APPLICANT: de Laurenzi, Vincenzo
; APPLICANT: Barcaroli, Daniela
; APPLICANT: Candi, Eleonora
; APPLICANT: Bernassola, Francesca
; APPLICANT: Tobler, Andreas
; APPLICANT: Novak, Urban
; TITLE OF INVENTION: Human Delta-N p73 Molecules and Uses Thereof
; FILE REFERENCE: 19319.002
; CURRENT APPLICATION NUMBER: US/10/489,730
; CURRENT FILING DATE: 2004-03-16
; PRIOR APPLICATION NUMBER: PCT/GB02/04238
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US 60/322,436
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 39
; OTHER INFORMATION: reverse complement of exons 14 through 1 as reported in GenBank Ac
US-10-489-730-10

Query Match 2.4%; Score 16; DB 6; Length 138941;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 165 TCAGAAGGCCAGACAA 180
||||||||||||||||
Db 28208 TCAGAAGGCCAGACAA 28223

RESULT 31
US-10-489-730-10/c
; GENERAL INFORMATION:
; APPLICANT: Melino, Gennaro
; APPLICANT: Hayes, Ian
; APPLICANT: de Laurenzi, Vincenzo
; APPLICANT: Barcaroli, Daniela
; APPLICANT: Candi, Eleonora
; APPLICANT: Bernassola, Francesca
; APPLICANT: Tobler, Andreas

```
;  APPLICANT:  Novak, Urban
;  TITLE OF INVENTION: Human Delta-N p73 Molecules and Uses Thereof
;  FILE REFERENCE: 19319.002
;  CURRENT APPLICATION NUMBER: US/10/489,730
;  CURRENT FILING DATE:  2004-03-16
;  PRIOR APPLICATION NUMBER: PCT/GB02/04238
;  PRIOR FILING DATE: 2002-09-17
;  PRIOR APPLICATION NUMBER: US 60/322,436
;  PRIOR FILING DATE: 2001-09-17
;  NUMBER OF SEQ ID NOS: 39
;   OTHER INFORMATION: reverse complement of exons 14 through 1 as reported in GenBank A
US-10-489-730-10

  Query Match             2.4%;  Score 16;  DB 6;  Length 138941;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        570 TTTTTATAAAACTAAA 585
              ||||||||||||||||
Db      33604 TTTTTATAAAACTAAA 33589


RESULT 32
US-11-217-529-50447
; Sequence 50447, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 50447
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-50447

  Query Match             2.3%;  Score 15;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         33 CATCCTGGTCCTGTT 47
              |||||||||||||||
Db          8 CATCCTGGTCCTGTT 22


RESULT 33
US-11-217-529-105697/c
; Sequence 105697, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 105697
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-105697

  Query Match             2.3%;  Score 15;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        414 GGTGGAGTTCAAGGC 428
              |||||||||||||||
Db         17 GGTGGAGTTCAAGGC 3


RESULT 34
US-11-217-529-155757
; Sequence 155757, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 155757
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-155757

  Query Match             2.3%;  Score 15;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        593 TCTGCATACTTCTTC 607
              |||||||||||||||
Db          5 TCTGCATACTTCTTC 19


RESULT 35
US-11-217-529-191540/c
; Sequence 191540, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 191540
;   LENGTH: 25
;   TYPE: DNA
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```
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-191540

  Query Match             2.3%;  Score 15;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        222 TGAAGATATCACAAA 236
              |||||||||||||||
Db         19 TGAAGATATCACAAA 5


RESULT 36
US-11-217-529-191845/c
; Sequence 191845, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 191845
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-191845

  Query Match             2.3%;  Score 15;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        310 GAGATCTCTCTGATA 324
              |||||||||||||||
Db         17 GAGATCTCTCTGATA 3


RESULT 37
US-10-488-619-2364/c
; Sequence 2364, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2364
;   LENGTH: 400
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-488-619-2364

  Query Match             2.3%;  Score 15;  DB 6;  Length 400;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        519 GAATGTCAACAGTGT 533
              |||||||||||||||
Db        285 GAATGTCAACAGTGT 271


RESULT 38
US-10-488-619-857
; Sequence 857, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 857
;   LENGTH: 418
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(418)
;   OTHER INFORMATION: n is g, c, a or t
US-10-488-619-857

  Query Match             2.3%;  Score 15;  DB 6;  Length 418;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         74 CCAGGAACCTCCCCA 88
              |||||||||||||||
Db        368 CCAGGAACCTCCCCA 382


RESULT 39
US-10-473-173-354
; Sequence 354, Application US/10473173
; Publication No. US20060088823A1
; GENERAL INFORMATION:
;  APPLICANT: VAN ANDEL INSTITUTE
;  TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell
;  TITLE OF INVENTION:  Carcinoma: Prognosis and Drug Target Identification
;  FILE REFERENCE: 38345-170094
;  CURRENT APPLICATION NUMBER: US/10/473,173
;  CURRENT FILING DATE:  2003-09-29
;  PRIOR APPLICATION NUMBER: US 60/279,411
;  PRIOR FILING DATE: 2001-03-29
;  NUMBER OF SEQ ID NOS: 498
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 354
;   LENGTH: 425
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: n can be a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (23)..(24)
;   OTHER INFORMATION: n can be a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (425)..(425)
;   OTHER INFORMATION: n can be a, c, g or t
US-10-473-173-354

  Query Match             2.3%;  Score 15;  DB 6;  Length 425;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        282 CATGAATGAGAGTTG 296
              |||||||||||||||
Db         26 CATGAATGAGAGTTG 40
```

```
RESULT 40
US-10-488-619-858
; Sequence 858, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 858
;   LENGTH: 425
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(425)
;   OTHER INFORMATION: n is g, a, c or t
US-10-488-619-858

  Query Match             2.3%;  Score 15;  DB 6;  Length 425;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        282 CATGAATGAGAGTTG 296
              |||||||||||||||
Db         26 CATGAATGAGAGTTG 40


RESULT 41
US-11-217-529-190905
; Sequence 190905, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 190905
;   LENGTH: 429
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-190905

  Query Match             2.3%;  Score 15;  DB 7;  Length 429;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         85 CCCACACCCACACCA 99
              |||||||||||||||
Db        112 CCCACACCCACACCA 126


RESULT 42
US-10-488-619-2365
; Sequence 2365, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2365
;   LENGTH: 438
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(438)
;   OTHER INFORMATION: n is g, c, a or t
US-10-488-619-2365

  Query Match             2.3%;  Score 15;  DB 6;  Length 438;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        519 GAATGTCAACAGTGT 533
              |||||||||||||||
Db        105 GAATGTCAACAGTGT 119


RESULT 43
US-10-488-619-1356
; Sequence 1356, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1356
;   LENGTH: 441
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-488-619-1356

  Query Match             2.3%;  Score 15;  DB 6;  Length 441;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        233 CAAAAGATAAAACCA 247
              |||||||||||||||
Db        121 CAAAAGATAAAACCA 135


RESULT 44
US-11-217-529-166946
; Sequence 166946, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
```

```
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 166946
;   LENGTH: 459
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-166946

  Query Match             2.3%;  Score 15;  DB 7;  Length 459;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         85 CCCACACCCACACCA 99
              |||||||||||||||
Db         56 CCCACACCCACACCA 70


RESULT 45
US-11-217-529-190985
; Sequence 190985, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 190985
;   LENGTH: 462
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-190985

  Query Match             2.3%;  Score 15;  DB 7;  Length 462;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         85 CCCACACCCACACCA 99
              |||||||||||||||
Db        121 CCCACACCCACACCA 135


RESULT 46
US-11-217-529-81573
; Sequence 81573, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81573
;   LENGTH: 507
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-81573

  Query Match             2.3%;  Score 15;  DB 7;  Length 507;
  Best Local Similarity   100.0%;  Pred. No. 90;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        635 TCAATAGAATGATGA 649
              |||||||||||||||
Db         23 TCAATAGAATGATGA 37


RESULT 47
US-11-217-529-79785
; Sequence 79785, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79785
;   LENGTH: 510
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-79785

  Query Match             2.3%;  Score 15;  DB 7;  Length 510;
  Best Local Similarity   100.0%;  Pred. No. 90;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        206 CCGAAGAGATTGATC 220
              |||||||||||||||
Db         80 CCGAAGAGATTGATC 94


RESULT 48
US-11-217-529-81860
; Sequence 81860, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81860
;   LENGTH: 576
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-81860

  Query Match             2.3%;  Score 15;  DB 7;  Length 576;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy        593 TCTGCATACTTCTTC 607
              ||||||||||||||||
Db        328 TCTGCATACTTCTTC 342


RESULT 49
US-10-953-349-39845/c
; Sequence 39845, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39845
;   LENGTH: 608
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-39845

  Query Match             2.3%;  Score 15;  DB 6;  Length 608;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        312 GATCTCTCTGATAAC 326
              ||||||||||||||||
Db         67 GATCTCTCTGATAAC 53


RESULT 50
US-11-217-529-77395/c
; Sequence 77395, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77395
;   LENGTH: 612
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-77395

  Query Match             2.3%;  Score 15;  DB 7;  Length 612;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        414 GGTGGAGTTCAAGGC 428
              ||||||||||||||||
Db         24 GGTGGAGTTCAAGGC 10


RESULT 51
US-10-953-349-12334
; Sequence 12334, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12334
;   LENGTH: 630
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (591)..(591)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-12334

  Query Match             2.3%;  Score 15;  DB 6;  Length 630;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        126 CCACTCCCAAACCCT 140
              ||||||||||||||||
Db         14 CCACTCCCAAACCCT 28


RESULT 52
US-10-953-349-25972
; Sequence 25972, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25972
;   LENGTH: 630
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-10-953-349-25972

  Query Match             2.3%;  Score 15;  DB 6;  Length 630;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        126 CCACTCCCAAACCCT 140
              ||||||||||||||||
Db         14 CCACTCCCAAACCCT 28


RESULT 53
US-10-953-349-6953
; Sequence 6953, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6953
;   LENGTH: 756
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-6953
```

Query Match 2.3%; Score 15; DB 6; Length 756;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         23 TCCTTGTAACCATCC 37
              |||||||||||||||
Db        247 TCCTTGTAACCATCC 261
```

RESULT 54
US-11-217-529-190869/c
; Sequence 190869, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 190869
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-190869

Query Match 2.3%; Score 15; DB 7; Length 768;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        310 GAGATCTCTCTGATA 324
              |||||||||||||||
Db        163 GAGATCTCTCTGATA 149
```

RESULT 55
US-10-953-349-355
; Sequence 355, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 355
; LENGTH: 778
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-355

Query Match 2.3%; Score 15; DB 6; Length 778;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        203 CTTCCGAAGAGATTG 217
              |||||||||||||||
Db         41 CTTCCGAAGAGATTG 55
```

RESULT 56
US-10-488-619-1355/c
; Sequence 1355, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1355
; LENGTH: 782
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(782)
; OTHER INFORMATION: n is a, c, g, or t
US-10-488-619-1355

Query Match 2.3%; Score 15; DB 6; Length 782;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        233 CAAAAGATAAAACCA 247
              |||||||||||||||
Db        663 CAAAAGATAAAACCA 649
```

RESULT 57
US-10-953-349-33201
; Sequence 33201, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33201
; LENGTH: 814
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
US-10-953-349-33201

Query Match 2.3%; Score 15; DB 6; Length 814;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         85 CCCACACCCACACCA 99
              |||||||||||||||
Db         39 CCCACACCCACACCA 53
```

RESULT 58
US-10-953-349-9296
; Sequence 9296, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9296

```
;   LENGTH: 815
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-9296

  Query Match             2.3%;  Score 15;  DB 6;  Length 815;
  Best Local Similarity   100.0%;  Pred. No. 93;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         23 TCCTTGTAACCATCC 37
              |||||||||||||||
Db        288 TCCTTGTAACCATCC 302


RESULT 59
US-10-953-349-39705/c
; Sequence 39705, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39705
;   LENGTH: 830
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-39705

  Query Match             2.3%;  Score 15;  DB 6;  Length 830;
  Best Local Similarity   100.0%;  Pred. No. 93;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         78 GAACCTCCCCACACC 92
              |||||||||||||||
Db        472 GAACCTCCCCACACC 458


RESULT 60
US-11-217-529-5224/c
; Sequence 5224, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5224
;   LENGTH: 906
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-5224

  Query Match             2.3%;  Score 15;  DB 7;  Length 906;
  Best Local Similarity   100.0%;  Pred. No. 93;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        376 TGCCTTAGCAGTATC 390
              |||||||||||||||
Db        852 TGCCTTAGCAGTATC 838


RESULT 61
US-11-217-529-174189
; Sequence 174189, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174189
;   LENGTH: 906
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-174189

  Query Match             2.3%;  Score 15;  DB 7;  Length 906;
  Best Local Similarity   100.0%;  Pred. No. 93;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        439 AAGCTGTTAATGGAT 453
              |||||||||||||||
Db        614 AAGCTGTTAATGGAT 628


RESULT 62
US-11-217-529-4014
; Sequence 4014, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4014
;   LENGTH: 1026
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-4014

  Query Match             2.3%;  Score 15;  DB 7;  Length 1026;
  Best Local Similarity   100.0%;  Pred. No. 94;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         33 CATCCTGGTCCTGTT 47
              |||||||||||||||
Db        756 CATCCTGGTCCTGTT 770


RESULT 63
US-10-953-349-39221
```

; Sequence 39221, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39221
; LENGTH: 1046
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
US-10-953-349-39221

Query Match 2.3%; Score 15; DB 6; Length 1046;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 481 AACATGCTGACAGCT 495
||||||||||||||||
Db 383 AACATGCTGACAGCT 397

RESULT 64
US-10-953-349-17993/c
; Sequence 17993, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17993
; LENGTH: 1124
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-17993

Query Match 2.3%; Score 15; DB 6; Length 1124;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 221 ATGAAGATATCACAA 235
||||||||||||||||
Db 883 ATGAAGATATCACAA 869

RESULT 65
US-10-953-349-32852
; Sequence 32852, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32852
; LENGTH: 1151
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
US-10-953-349-32852

Query Match 2.3%; Score 15; DB 6; Length 1151;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 86 CCACACCCACACCAA 100
||||||||||||||||
Db 517 CCACACCCACACCAA 531

RESULT 66
US-10-953-349-31118/c
; Sequence 31118, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31118
; LENGTH: 1156
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-953-349-31118

Query Match 2.3%; Score 15; DB 6; Length 1156;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 321 GATAACTAATGGGAG 335
||||||||||||||||
Db 1030 GATAACTAATGGGAG 1016

RESULT 67
US-11-217-529-79991
; Sequence 79991, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79991
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79991

Query Match 2.3%; Score 15; DB 7; Length 1176;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 281 CCATGAATGAGAGTT 295
||||||||||||||||
Db 842 CCATGAATGAGAGTT 856

RESULT 68
US-10-953-349-26534

; Sequence 26534, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26534
; LENGTH: 1190
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-953-349-26534

Query Match 2.3%; Score 15; DB 6; Length 1190;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 489 GACAGCTATTGATGA 503
||||||||||||||||
Db 884 GACAGCTATTGATGA 898

RESULT 69
US-10-953-349-19889
; Sequence 19889, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19889
; LENGTH: 1206
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-19889

Query Match 2.3%; Score 15; DB 6; Length 1206;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 584 AAATCAAGCTCTGCA 598
||||||||||||||||
Db 1008 AAATCAAGCTCTGCA 1022

RESULT 70
US-11-217-529-79181
; Sequence 79181, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79181
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79181

Query Match 2.3%; Score 15; DB 7; Length 1269;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 207 CGAAGAGATTGATCA 221
||||||||||||||||
Db 348 CGAAGAGATTGATCA 362

RESULT 71
US-10-953-349-32614
; Sequence 32614, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32614
; LENGTH: 1271
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-953-349-32614

Query Match 2.3%; Score 15; DB 6; Length 1271;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 420 GTTCAAGGCCATGAA 434
||||||||||||||||
Db 1052 GTTCAAGGCCATGAA 1066

RESULT 72
US-10-953-349-9401
; Sequence 9401, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9401
; LENGTH: 1302
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-9401

Query Match 2.3%; Score 15; DB 6; Length 1302;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 470 TTCTGGATCAAAACA 484
||||||||||||||||
Db 546 TTCTGGATCAAAACA 560

RESULT 73
US-11-217-529-79465

```
; Sequence 79465, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79465
;   LENGTH: 1305
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-79465

  Query Match             2.3%;  Score 15;  DB 7;  Length 1305;
  Best Local Similarity   100.0%;  Pred. No. 95;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        228 TATCACAAAAGATAA 242
              |||||||||||||||
Db       1291 TATCACAAAAGATAA 1305


RESULT 74
US-11-217-529-190840/c
; Sequence 190840, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 190840
;   LENGTH: 1404
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-190840

  Query Match             2.3%;  Score 15;  DB 7;  Length 1404;
  Best Local Similarity   100.0%;  Pred. No. 96;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        222 TGAAGATATCACAAA 236
              |||||||||||||||
Db        838 TGAAGATATCACAAA 824


RESULT 75
US-10-953-349-3438
; Sequence 3438, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3438
;   LENGTH: 1406
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-3438

  Query Match             2.3%;  Score 15;  DB 6;  Length 1406;
  Best Local Similarity   100.0%;  Pred. No. 96;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        441 GCTGTTAATGGATCC 455
              |||||||||||||||
Db        976 GCTGTTAATGGATCC 990


RESULT 76
US-10-953-349-31490/c
; Sequence 31490, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31490
;   LENGTH: 1450
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-10-953-349-31490

  Query Match             2.3%;  Score 15;  DB 6;  Length 1450;
  Best Local Similarity   100.0%;  Pred. No. 96;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         25 CTTGTAACCATCCTG 39
              |||||||||||||||
Db       1204 CTTGTAACCATCCTG 1190


RESULT 77
US-10-953-349-31780
; Sequence 31780, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31780
;   LENGTH: 1451
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-10-953-349-31780

  Query Match             2.3%;  Score 15;  DB 6;  Length 1451;
  Best Local Similarity   100.0%;  Pred. No. 96;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         92 CCACACCAAGCCCAG 106
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                ||||||||||||||||
Db        480 CCACACCAAGCCCAG 494


RESULT 78
US-10-953-349-20272/c
; Sequence 20272, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20272
;   LENGTH: 1493
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-20272

  Query Match             2.3%;  Score 15;  DB 6;  Length 1493;
  Best Local Similarity   100.0%;  Pred. No. 96;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        241 AAAACCAGCACAGTG 255
                ||||||||||||||||
Db        184 AAAACCAGCACAGTG 170


RESULT 79
US-10-953-349-10170
; Sequence 10170, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10170
;   LENGTH: 1504
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-10170

  Query Match             2.3%;  Score 15;  DB 6;  Length 1504;
  Best Local Similarity   100.0%;  Pred. No. 96;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        470 TTCTGGATCAAAACA 484
                ||||||||||||||||
Db        583 TTCTGGATCAAAACA 597


RESULT 80
US-10-953-349-34123
; Sequence 34123, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34123
;   LENGTH: 1511
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-34123

  Query Match             2.3%;  Score 15;  DB 6;  Length 1511;
  Best Local Similarity   100.0%;  Pred. No. 96;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         84 CCCCACACCCACACC 98
                ||||||||||||||||
Db       1045 CCCCACACCCACACC 1059


RESULT 81
US-10-953-349-13708
; Sequence 13708, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13708
;   LENGTH: 1539
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-13708

  Query Match             2.3%;  Score 15;  DB 6;  Length 1539;
  Best Local Similarity   100.0%;  Pred. No. 96;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        550 TCCTCCCTGGAAGAA 564
                ||||||||||||||||
Db         42 TCCTCCCTGGAAGAA 56


RESULT 82
US-11-217-529-1240/c
; Sequence 1240, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1240
;   LENGTH: 1551
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-1240

  Query Match             2.3%;  Score 15;  DB 7;  Length 1551;
  Best Local Similarity   100.0%;  Pred. No. 96;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        225 AGATATCACAAAAGA 239
```

```
                ||||||||||||||||
Db        673 AGATATCACAAAAGA 659


RESULT 83
US-10-953-349-21319
; Sequence 21319, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21319
;   LENGTH: 1719
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-21319

  Query Match             2.3%;  Score 15;  DB 6;  Length 1719;
  Best Local Similarity   100.0%;  Pred. No. 97;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 TGGCCTCCTCCTTGT 29
                ||||||||||||||
Db        125 TGGCCTCCTCCTTGT 139


RESULT 84
US-10-953-349-1943
; Sequence 1943, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1943
;   LENGTH: 1821
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-1943

  Query Match             2.3%;  Score 15;  DB 6;  Length 1821;
  Best Local Similarity   100.0%;  Pred. No. 97;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        492 AGCTATTGATGAGCT 506
                ||||||||||||||
Db        600 AGCTATTGATGAGCT 614


RESULT 85
US-10-953-349-12445
; Sequence 12445, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12445
;   LENGTH: 1869
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (532)..(532)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-12445

  Query Match             2.3%;  Score 15;  DB 6;  Length 1869;
  Best Local Similarity   100.0%;  Pred. No. 97;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        297 CCTGGCTTCCAGAGA 311
                ||||||||||||||
Db        144 CCTGGCTTCCAGAGA 158


RESULT 86
US-11-293-697-2269
; Sequence 2269, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2269
;   LENGTH: 1902
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-2269

  Query Match             2.3%;  Score 15;  DB 7;  Length 1902;
  Best Local Similarity   100.0%;  Pred. No. 97;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        526 AACAGTGTGACTGTG 540
                ||||||||||||||
Db        235 AACAGTGTGACTGTG 249


RESULT 87
US-11-293-697-773/c
; Sequence 773, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 773
;   LENGTH: 2043
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-773

  Query Match             2.3%;  Score 15;  DB 7;  Length 2043;
  Best Local Similarity   100.0%;  Pred. No. 98;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        320 TGATAACTAATGGGA 334
```

```
              ||||||||||||||||
Db        802 TGATAACTAATGGGA 788


RESULT 88
US-10-953-349-11750/c
; Sequence 11750, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11750
;   LENGTH: 2105
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-11750

  Query Match             2.3%;  Score 15;  DB 6;  Length 2105;
  Best Local Similarity   100.0%;  Pred. No. 98;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         94 ACACCAAGCCCAGGA 108
              ||||||||||||||||
Db       2085 ACACCAAGCCCAGGA 2071


RESULT 89
US-11-293-697-153
; Sequence 153, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 153
;   LENGTH: 2151
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-153

  Query Match             2.3%;  Score 15;  DB 7;  Length 2151;
  Best Local Similarity   100.0%;  Pred. No. 98;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        136 ACCCTGCTGCGAGCC 150
              ||||||||||||||||
Db       1116 ACCCTGCTGCGAGCC 1130


RESULT 90
US-11-293-697-56
; Sequence 56, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
;   LENGTH: 2205
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-56

  Query Match             2.3%;  Score 15;  DB 7;  Length 2205;
  Best Local Similarity   100.0%;  Pred. No. 98;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        641 GAATGATGAGCTATC 655
              ||||||||||||||||
Db       1538 GAATGATGAGCTATC 1552


RESULT 91
US-11-217-529-2489
; Sequence 2489, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2489
;   LENGTH: 2241
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-2489

  Query Match             2.3%;  Score 15;  DB 7;  Length 2241;
  Best Local Similarity   100.0%;  Pred. No. 98;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        397 GACTTGAAGATGTAC 411
              ||||||||||||||||
Db       1711 GACTTGAAGATGTAC 1725


RESULT 92
US-11-293-697-2380
; Sequence 2380, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2380
;   LENGTH: 2308
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-2380

  Query Match             2.3%;  Score 15;  DB 7;  Length 2308;
  Best Local Similarity   100.0%;  Pred. No. 99;
```

```
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         22 CTCCTTGTAACCATC 36
              |||||||||||||||
Db       1934 CTCCTTGTAACCATC 1948


RESULT 93
US-11-217-529-80988/c
; Sequence 80988, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80988
;   LENGTH: 2400
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-80988

  Query Match             2.3%;  Score 15;  DB 7;  Length 2400;
  Best Local Similarity   100.0%;  Pred. No. 99;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        469 TTTCTGGATCAAAAC 483
              |||||||||||||||
Db        472 TTTCTGGATCAAAAC 458


RESULT 94
US-11-293-697-2092/c
; Sequence 2092, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2092
;   LENGTH: 2537
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-2092

  Query Match             2.3%;  Score 15;  DB 7;  Length 2537;
  Best Local Similarity   100.0%;  Pred. No. 99;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        119 GCCTCAACCACTCCC 133
              |||||||||||||||
Db       1344 GCCTCAACCACTCCC 1330


RESULT 95
US-11-293-697-749/c
; Sequence 749, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 749
;   LENGTH: 2650
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-749

  Query Match             2.3%;  Score 15;  DB 7;  Length 2650;
  Best Local Similarity   100.0%;  Pred. No. 99;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        467 TCTTTCTGGATCAAA 481
              |||||||||||||||
Db       1786 TCTTTCTGGATCAAA 1772


RESULT 96
US-10-511-937-363
; Sequence 363, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
;  APPLICANT: EXPRESSION DIAGNOSTICS, INC.
;  APPLICANT:  Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  APPLICANT:  Prentice, James
;  APPLICANT:  Morris, MacDonald
;  APPLICANT:  Rosenberg, Steven
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
;  TITLE OF INVENTION:  AND MONITORING TRANSPLANT REJECTION
;  FILE REFERENCE: 506612000104
;  CURRENT APPLICATION NUMBER: US/10/511,937
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: PCT/US2003/012946
;  PRIOR FILING DATE: 2003-04-24
;  PRIOR APPLICATION NUMBER: US 10/131,831
;  PRIOR FILING DATE: 2002-04-24
;  PRIOR APPLICATION NUMBER: US 10/325,899
;  PRIOR FILING DATE: 2002-12-20
;  NUMBER OF SEQ ID NOS: 3117
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 363
;   LENGTH: 3334
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-511-937-363

  Query Match             2.3%;  Score 15;  DB 6;  Length 3334;
  Best Local Similarity   100.0%;  Pred. No. 1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         31 ACCATCCTGGTCCTG 45
              |||||||||||||||
Db       3066 ACCATCCTGGTCCTG 3080


RESULT 97
US-10-505-928-637/c
; Sequence 637, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
;  APPLICANT: Ludwig Institute for Cancer Research et al.
```

```
;  TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
;  FILE REFERENCE: 28967/39178
;  CURRENT APPLICATION NUMBER: US/10/505,928
;  CURRENT FILING DATE:  2004-08-27
;  PRIOR APPLICATION NUMBER: US 60/363,019
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: PatentIn 3.2
; SEQ ID NO 637
;   LENGTH: 3350
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-505-928-637

  Query Match             2.3%;  Score 15;  DB 6;  Length 3350;
  Best Local Similarity   100.0%;  Pred. No. 1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         81 CCTCCCCACACCCAC 95
              |||||||||||||||
Db        973 CCTCCCCACACCCAC 959


RESULT 98
US-10-505-928-641/c
; Sequence 641, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
;  APPLICANT: Ludwig Institute for Cancer Research et al.
;  TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
;  FILE REFERENCE: 28967/39178
;  CURRENT APPLICATION NUMBER: US/10/505,928
;  CURRENT FILING DATE:  2004-08-27
;  PRIOR APPLICATION NUMBER: US 60/363,019
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: PatentIn 3.2
; SEQ ID NO 641
;   LENGTH: 3350
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-505-928-641

  Query Match             2.3%;  Score 15;  DB 6;  Length 3350;
  Best Local Similarity   100.0%;  Pred. No. 1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         81 CCTCCCCACACCCAC 95
              |||||||||||||||
Db        973 CCTCCCCACACCCAC 959


RESULT 99
US-11-217-529-1172
; Sequence 1172, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1172
;   LENGTH: 4533
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-1172

  Query Match             2.3%;  Score 15;  DB 7;  Length 4533;
  Best Local Similarity   100.0%;  Pred. No. 1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        213 GATTGATCATGAAGA 227
              |||||||||||||||
Db       2550 GATTGATCATGAAGA 2564


RESULT 100
US-10-501-834-216
; Sequence 216, Application US/10501834
; Publication No. US20060088828A1
; GENERAL INFORMATION:
;  APPLICANT: Harris, Peter C., Ward, Christopher J., Rossetti, Sandro, and Torres,
;  APPLICANT:  Vicente E.
;  TITLE OF INVENTION: Polycystic Kidney Disease Nucleic Acids
;  TITLE OF INVENTION:  and Proteins
;  FILE REFERENCE: 07039/386US1
;  CURRENT APPLICATION NUMBER: US/10/501,834
;  CURRENT FILING DATE:  2004-07-19
;  PRIOR APPLICATION NUMBER: PCT/US03/02038
;  PRIOR FILING DATE: 2003-01-23
;  PRIOR APPLICATION NUMBER: 60/351,110
;  PRIOR FILING DATE: 2002-01-23
;  NUMBER OF SEQ ID NOS: 221
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 216
;   LENGTH: 5171
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-501-834-216

  Query Match             2.3%;  Score 15;  DB 6;  Length 5171;
  Best Local Similarity   100.0%;  Pred. No. 1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        536 CTGTGCCACAGAACT 550
              |||||||||||||||
Db       2813 CTGTGCCACAGAACT 2827


Search completed: June  9, 2006, 23:43:14
Job time : 17.4095 secs
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 12, 2006, 15:14:42 ; Search time 3010.25 Seconds
(without alignments)
7073.997 Million cell updates/sec

Title: US-10-821-670A-33
Perfect score: 1129
Sequence: 1 MCPPRGLLLVTILVLLNHLD.....HAFRIRAVTINRMMSYLNAS 222

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss06h
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-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
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2: gb_pat:*
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6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		1129	100.0	666	2	AR595952	AR595952 Sequence
2	c	1129	100.0	666	2	AR595953	AR595953 Sequence
3		1129	100.0	669	14	FCIL12P35	Y07761 Felis catus
4		1126	99.7	689	2	AR242451	AR242451 Sequence
5		1126	99.7	689	2	AR280219	AR280219 Sequence
6		1126	99.7	689	2	AR322434	AR322434 Sequence
7		1126	99.7	1441	2	AR242438	AR242438 Sequence
8		1126	99.7	1441	2	AR280206	AR280206 Sequence
9		1126	99.7	1441	2	AR322421	AR322421 Sequence
10		1121	99.3	669	14	FCU83185	U83185 Felis catus
11		1108	98.1	669	2	AX076201	AX076201 Sequence
12		1108	98.1	669	2	AX076483	AX076483 Sequence
13		1108	98.1	4201	2	AX076477	AX076477 Sequence
14		1043	92.4	666	2	AR595961	AR595961 Sequence
15	c	1043	92.4	666	2	AR595962	AR595962 Sequence
16		1043	92.4	669	2	AR151072	AR151072 Sequence
17		1043	92.4	669	2	BD014664	BD014664 Process f
18		1043	92.4	669	2	E15018	E15018 Canine mRNA
19		1043	92.4	669	2	AR316471	AR316471 Sequence
20		1043	92.4	1282	2	BD171283	BD171283 Novel can
21		1043	92.4	1455	2	AR596009	AR596009 Sequence
22	c	1043	92.4	1455	2	AR596010	AR596010 Sequence
23		1030	91.2	669	14	CFU49085	U49085 Canis famil
24		1014	89.8	669	2	AR151062	AR151062 Sequence
25		1014	89.8	669	2	BD014654	BD014654 Process f
26		1014	89.8	669	2	AR316461	AR316461 Sequence
27		1002	88.8	1533	2	AR595959	AR595959 Sequence
28	c	1002	88.8	1533	2	AR595960	AR595960 Sequence
29		1002	88.8	1599	2	AR595956	AR595956 Sequence
30	c	1002	88.8	1599	2	AR595957	AR595957 Sequence
31		1001	88.7	591	2	AR595954	AR595954 Sequence
32	c	1001	88.7	591	2	AR595955	AR595955 Sequence
33		998	88.4	591	2	AR242439	AR242439 Sequence
34		998	88.4	591	2	AR280207	AR280207 Sequence
35		998	88.4	591	2	AR322422	AR322422 Sequence
36		995.5	88.2	660	2	AX154619	AX154619 Sequence
37		993.5	88.0	660	2	AX154614	AX154614 Sequence
38		993.5	88.0	660	2	AX154621	AX154621 Sequence
39		988.5	87.6	660	2	AX154618	AX154618 Sequence
40		984.5	87.2	657	8	AY191828	AY191828 Synthetic
41		984.5	87.2	660	2	AX154617	AX154617 Sequence
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43		976.5	86.5	660	2	AX154620	AX154620 Sequence
44		974.5	86.3	660	2	AX154616	AX154616 Sequence
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ALIGNMENTS

RESULT 1
AR595952
LOCUS AR595952 666 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 32 from patent US 6818444.
ACCESSION AR595952
VERSION AR595952.1 GI:56646933
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 666)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 32 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .666
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.: 1.59e-109 Length: 666
Score: 1129.00 Matches: 222
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0

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DB:                    2             Gaps:          0

US-10-821-670A-33 (1-222) x AR595952 (1-666)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
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Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
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Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
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Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
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Db        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
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Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
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Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
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Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
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Db        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
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Db        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        221 AlaSer 222
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Db        661 GCTTCC 666

RESULT 2
AR595953/c
LOCUS       AR595953                666 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 34 from patent US 6818444.
ACCESSION   AR595953
VERSION     AR595953.1  GI:56646934
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 34 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                1.59e-109      Length:          666
Score:                    1129.00        Matches:         222
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-33 (1-222) x AR595953 (1-666)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
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Db        666 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 607

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
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Db        606 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 547

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
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Db        546 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
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Db        486 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 427

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
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Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
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Db        366 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 307

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
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Db        306 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 247

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
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Db        246 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 187

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
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Db        186 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 127

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
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Db        126 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
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Db         66 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 7

Qy        221 AlaSer 222
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Db          6 GCTTCC 1

RESULT 3
FCIL12P35
LOCUS       FCIL12P35               669 bp    mRNA    linear   MAM 18-APR-2005
DEFINITION  Felis catus mRNA for interleukin-12 p35 chain.
ACCESSION   Y07761
VERSION     Y07761.1  GI:2102662
KEYWORDS    interleukin-12 subunit p35.
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1
  AUTHORS   Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
  TITLE     Molecular cloning of cat interleukin-12
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  JOURNAL   Immunogenetics 45 (6), 462-463 (1997)
   PUBMED   9089110
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Schijns,V.E.C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
            Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
            Utrecht, NETHERLANDS
FEATURES             Location/Qualifiers
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                     /cell_type="lymphocyte"
                     /tissue_type="peripheral blood"
     gene            1. .669
                     /gene="IL-12.p35"
     CDS             1. .669
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                     /codon_start=1
                     /product="interleukin-12 p35 chain"
                     /protein_id="CAA69067.1"
                     /db_xref="GI:2102663"
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                     /db_xref="UniProtKB/Swiss-Prot:O02743"
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                     LNAS"
ORIGIN

Alignment Scores:
Pred. No.:              1.6e-109        Length:         669
Score:                  1129.00         Matches:        222
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-33 (1-222) x FCIL12P35 (1-669)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
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Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
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Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
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Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
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Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuGlnAlaLeuAsnValAsnSerValThrVal 180
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Db        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        221 AlaSer 222
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Db        661 GCTTCC 666

RESULT 4
AR242451
LOCUS       AR242451                689 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 26 from patent US 6472509.
ACCESSION   AR242451
VERSION     AR242451.1  GI:27288868
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 26 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .689
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                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.43e-109       Length:         689
Score:                  1126.00         Matches:        221
Percent Similarity:     100.0%          Conservative:   1
Best Local Similarity:  99.5%           Mismatches:     0
Query Match:            99.7%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-33 (1-222) x AR242451 (1-689)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
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Db          7 ATGTGCCCCCCCCCGTGGCCTCCTCCTGGTGACCATCCTGGTCCTGCTGAACCACCTGGAC 66

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
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Db         67 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 126

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
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Db        127 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 186

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
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Db        187 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 246

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
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Db        247 AAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTG 306
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Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
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Db        307 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 366

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
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Db        427 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 486

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 546

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
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Db        547 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 606

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666

Qy        221 AlaSer 222
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Db        667 TCTTCC 672

RESULT 5
AR280219
LOCUS       AR280219                689 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 26 from patent US 6518045.
ACCESSION   AR280219
VERSION     AR280219.1  GI:29715609
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 26 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .689
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.43e-109      Length:         689
Score:                  1126.00        Matches:        221
Percent Similarity:     100.0%         Conservative:   1
Best Local Similarity:  99.5%          Mismatches:     0
Query Match:            99.7%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-33 (1-222) x AR280219 (1-689)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7 ATGTGCCCCCCCCGTGGCCTCCTCCTGGTGACCATCCTGGTCCTGCTGAACCACCTGGAC 66

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 126

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 186

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 246

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 AAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTG 306

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 366

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 426

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 486

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 546

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 606

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666

Qy        221 AlaSer 222
              :::|||
Db        667 TCTTCC 672

RESULT 6
AR322434
LOCUS       AR322434                689 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 26 from patent US 6566097.
ACCESSION   AR322434
VERSION     AR322434.1  GI:33708187
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 26 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .689
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.43e-109      Length:         689
Score:                  1126.00        Matches:        221
Percent Similarity:     100.0%         Conservative:   1
Best Local Similarity:  99.5%          Mismatches:     0
Query Match:            99.7%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-33 (1-222) x AR322434 (1-689)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
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Db          7 ATGTGCCCCCCCCGTGGCCTCCTCCTGGTGACCATCCTGGTCCTGCTGAACCACCTGGAC 66
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Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 126

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 186

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 246

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 AAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTG 306

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 366

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 426

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 486

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 546

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 606

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666

Qy        221 AlaSer 222
              :::|||
Db        667 TCTTCC 672

RESULT 7
AR242438
LOCUS       AR242438               1441 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 8 from patent US 6472509.
ACCESSION   AR242438
VERSION     AR242438.1  GI:27288855
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1441)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 8 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .1441
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                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              8.14e-109      Length:         1441
Score:                  1126.00        Matches:        221
Percent Similarity:     100.0%         Conservative:   1
Best Local Similarity:  99.5%          Mismatches:     0
Query Match:            99.7%          Indels:         0
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DB:                     2              Gaps:           0

US-10-821-670A-33 (1-222) x AR242438 (1-1441)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
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Db        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
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Db        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
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Db        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
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Db        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
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Db        683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
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Db        743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

Qy        221 AlaSer 222
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Db        803 TCTTCC 808

RESULT 8
AR280206
LOCUS       AR280206               1441 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 8 from patent US 6518045.
ACCESSION   AR280206
VERSION     AR280206.1  GI:29715596
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1441)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 8 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .1441
                     /organism="unknown"
                     /mol_type="mRNA"
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ORIGIN

Alignment Scores:
Pred. No.:                8.14e-109      Length:          1441
Score:                    1126.00        Matches:         221
Percent Similarity:       100.0%         Conservative:    1
Best Local Similarity:    99.5%          Mismatches:      0
Query Match:              99.7%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-33 (1-222) x AR280206 (1-1441)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
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Db        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
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Db        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
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Db        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

Qy        221 AlaSer 222
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Db        803 TCTTCC 808

RESULT 9
AR322421
LOCUS       AR322421               1441 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 8 from patent US 6566097.
ACCESSION   AR322421
VERSION     AR322421.1  GI:33708174
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1441)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 8 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .1441
                     /organism="unknown"
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ORIGIN

Alignment Scores:
Pred. No.:                8.14e-109      Length:          1441
Score:                    1126.00        Matches:         221
Percent Similarity:       100.0%         Conservative:    1
Best Local Similarity:    99.5%          Mismatches:      0
Query Match:              99.7%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-33 (1-222) x AR322421 (1-1441)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
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Db        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
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Db        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
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Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
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Db        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

Qy        221 AlaSer 222
              :::|||
Db        803 TCTTCC 808

RESULT 10
FCU83185
LOCUS       FCU83185               669 bp    mRNA    linear   MAM 16-JUL-1999
DEFINITION  Felis catus interleukin-12 p35 subunit (IL-12) mRNA, complete cds.
ACCESSION   U83185
```

```
VERSION     U83185.1  GI:2735052
KEYWORDS    .
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Nucleotide and predicted peptide sequence of feline interleukin-12
            (IL-12)
  JOURNAL   DNA Seq. 8 (1-2), 77-82 (1997)
   PUBMED   9522125
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal
            Veterinary Medicine, University of Zurich, Winterthurerstrasse 260,
            Zurich, ZH 8057, Switzerland
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Felis catus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
     CDS             1. .669
                     /note="cytokine"
                     /codon_start=1
                     /product="interleukin-12 p35 subunit"
                     /protein_id="AAB93836.1"
                     /db_xref="GI:2735053"
                     /translation="MCPPRGLLLVTILVLLNHLDHLSLARNLPTPTPSPGMFQCLNHS
                     QTLLRAISNTLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
                     REISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAMNAKLLMDPKRQIFLDQ
                     NMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSY
                     LNSS"
ORIGIN

Alignment Scores:
Pred. No.:              1.11e-108       Length:         669
Score:                  1121.00         Matches:        220
Percent Similarity:     99.5%           Conservative:   1
Best Local Similarity:  99.1%           Mismatches:     1
Query Match:            99.3%           Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-33 (1-222) x FCU83185 (1-669)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuMetGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGATGCAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        221 AlaSer 222
              :::|||
Db        661 TCTTCC 666

RESULT 11
AX076201
LOCUS       AX076201                669 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 2 from Patent WO0104155.
ACCESSION   AX076201
VERSION     AX076201.1  GI:12710826
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 2 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="feline IL-12 p35"
ORIGIN

Alignment Scores:
Pred. No.:              2.62e-107       Length:         669
Score:                  1108.00         Matches:        217
Percent Similarity:     98.2%           Conservative:   1
Best Local Similarity:  97.7%           Mismatches:     4
Query Match:            98.1%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-33 (1-222) x AX076201 (1-669)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
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Db        181 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCT 360

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||:::|||||||||||   ||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        221 AlaSer 222
              ||||||
Db        661 GCTTCC 666

RESULT 12
AX076483
LOCUS       AX076483                669 bp    DNA     linear   PAT 07-FEB-2001
DEFINITION  Sequence 9 from Patent WO0104280.
ACCESSION   AX076483
VERSION     AX076483.1  GI:12711035
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 9 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Sequence coding for SEQ ID NO 3, IL-12 p35"
ORIGIN

Alignment Scores:
Pred. No.:              2.62e-107      Length:        669
Score:                  1108.00        Matches:       217
Percent Similarity:     98.2%          Conservative:  1
Best Local Similarity:  97.7%          Mismatches:    4
Query Match:            98.1%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-33 (1-222) x AX076483 (1-669)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCT 360

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||:::|||||||||||   ||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        221 AlaSer 222
              ||||||
Db        661 GCTTCC 666

RESULT 13
AX076477
LOCUS       AX076477                4201 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 3 from Patent WO0104280.
ACCESSION   AX076477
VERSION     AX076477.1  GI:12711029
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 3 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .4201
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="IL-12p35 (pMOLfIL-12p35 (e-,_e31-)clone61)"
ORIGIN

Alignment Scores:
Pred. No.:              2.26e-106      Length:        4201
Score:                  1108.00        Matches:       217
Percent Similarity:     98.2%          Conservative:  1
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Best Local Similarity:  97.7%          Mismatches:    4
Query Match:            98.1%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-33 (1-222) x AX076477 (1-4201)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3047 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 3106

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3107 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 3166

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3167 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 3226

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db       3227 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 3286

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db       3287 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTG 3346

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db       3347 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCT 3406

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3407 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 3466

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3467 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 3526

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||:::||||||||||||   ||||||||||||||||
Db       3527 AACATGCTGACAGCTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTG 3586

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3587 CCACAGAACTCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 3646

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3647 CTTCTTCATGCTTTCAGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 3706

Qy        221 AlaSer 222
              ||||||
Db       3707 GCTTCC 3712

RESULT 14
AR595961
LOCUS       AR595961                 666 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 46 from patent US 6818444.
ACCESSION   AR595961
VERSION     AR595961.1  GI:56646942
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 46 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="unknown"
                     /mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.:              1.86e-100      Length:        666
Score:                  1043.00        Matches:       204
Percent Similarity:     95.9%          Conservative:  9
Best Local Similarity:  91.9%          Mismatches:    9
Query Match:            92.4%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-33 (1-222) x AR595961 (1-666)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||:::   |||||:::|||||||||   :::|||||||||||||:::|||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||   ||||||||||:::|||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||   |||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||:::|||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
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Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        221 AlaSer 222
              :::|||
Db        661 TCTTCC 666

RESULT 15
AR595962/c
LOCUS       AR595962                 666 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 48 from patent US 6818444.
ACCESSION   AR595962
VERSION     AR595962.1  GI:56646943
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
```

```
  JOURNAL   Patent: US 6818444-A 48 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.86e-100       Length:         666
Score:                  1043.00         Matches:        204
Percent Similarity:     95.9%           Conservative:   9
Best Local Similarity:  91.9%           Mismatches:     9
Query Match:            92.4%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-33 (1-222) x AR595962 (1-666)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db        666 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 607

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||:::   ||||||:::|||||||||   :::|||||||||||:::|||||||||
Db        606 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 547

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||   ||||||||||||:::||||||||||||||||||||||||||||
Db        546 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 427

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||   |||   |||
Db        366 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 307

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              |||||||||   ||||||||||||||||||||||||||||||||||||:::|||
Db        306 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 247

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 187

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        186 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 127

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||||
Db         66 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 7

Qy        221 AlaSer 222
              :::|||
Db          6 TCTTCC 1


Search completed: June 13, 2006, 03:25:53
Job time : 3016.25 secs
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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 9, 2006, 23:43:41 ; Search time 473.894 Seconds
(without alignments)
4899.317 Million cell updates/sec

Title: US-10-821-670A-33
Perfect score: 1129
Sequence: 1 MCPPRGLLLVTILVLLNHLD.....HAFRIRAVTINRMMSYLNAS 222

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/abss/ABSSWEB_spool/US10821670/runat_07062006_110100_26141/app_query.fasta_1
-DB=N_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05h
-USER=US10821670_@CGN_1_1_2027_@runat_07062006_110100_26141 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_8:*
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11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	1129	100.0	666	6	ABK98947	Abk98947 Feline in
	2	1129	100.0	666	6	ABK98946	Abk98946 Feline in
	3	1129	100.0	666	14	ADV34685	Adv34685 Feline si
c	4	1129	100.0	666	14	ADV34687	Adv34687 Feline si
	5	1126	99.7	689	2	AAV56641	Aav56641 Feline FL
	6	1126	99.7	1441	2	AAV56628	Aav56628 Feline FL
	7	1108	98.1	669	4	AAF26083	Aaf26083 Feline IL
	8	1108	98.1	669	4	AAF26086	Aaf26086 Feline IL
	9	1108	98.1	4201	4	AAF26077	Aaf26077 Feline IL
	10	1092	96.7	679	4	AAF26097	Aaf26097 Feline fi
	11	1043	92.4	666	6	ABK98955	Abk98955 Canine in
c	12	1043	92.4	666	6	ABK98956	Abk98956 Canine in
c	13	1043	92.4	666	14	ADV34700	Adv34700 Canine si
	14	1043	92.4	666	14	ADV34698	Adv34698 Canine si
	15	1043	92.4	669	2	AAV13819	Aav13819 Canine IL
	16	1043	92.4	669	2	AAX03163	Aax03163 Nucleic a
	17	1043	92.4	669	2	AAX35626	Aax35626 Nucleic a
	18	1043	92.4	669	4	AAI64389	Aai64389 Canine co
	19	1043	92.4	1282	2	AAX18178	Aax18178 Canine fu
	20	1043	92.4	1455	6	ABK99003	Abk99003 Canine in
c	21	1043	92.4	1455	6	ABK99004	Abk99004 Canine in
c	22	1043	92.4	1455	14	ADV34756	Adv34756 Canine si
	23	1043	92.4	1455	14	ADV34754	Adv34754 Canine si
	24	1030	91.2	669	13	ADT04852	Adt04852 Canine in
	25	1014	89.8	669	2	AAV13818	Aav13818 Canine IL
	26	1014	89.8	669	2	AAX03153	Aax03153 Nucleic a
	27	1014	89.8	669	2	AAX35616	Aax35616 Nucleic a
	28	1014	89.8	669	4	AAI64379	Aai64379 Canine co
	29	1014	89.8	669	11	ADZ25701	Adz25701 Canine in
	30	1003	88.8	639	4	AAF26098	Aaf26098 Plasmid p
c	31	1002	88.8	1533	6	ABK98954	Abk98954 Feline in
	32	1002	88.8	1533	6	ABK98953	Abk98953 Feline in
c	33	1002	88.8	1533	14	ADV34697	Adv34697 Feline si
	34	1002	88.8	1533	14	ADV34695	Adv34695 Feline si
	35	1002	88.8	1599	6	ABK98950	Abk98950 Feline in
c	36	1002	88.8	1599	6	ABK98951	Abk98951 Feline in
	37	1002	88.8	1599	14	ADV34691	Adv34691 Feline si
c	38	1002	88.8	1599	14	ADV34693	Adv34693 Feline si
	39	1001	88.7	591	6	ABK98948	Abk98948 Feline in
c	40	1001	88.7	591	6	ABK98949	Abk98949 Feline in
	41	1001	88.7	591	14	ADV34688	Adv34688 Feline si
c	42	1001	88.7	591	14	ADV34690	Adv34690 Feline si
	43	998	88.4	591	2	AAV56629	Aav56629 Feline FL
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ALIGNMENTS

RESULT 1
ABK98947/c
ID ABK98947 standard; cDNA; 666 BP.
XX
AC ABK98947;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p35-666 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX

```
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 3; Page 56; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 666 BP; 160 A; 138 C; 179 G; 189 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              8.53e-111      Length:        666
Score:                  1129.00        Matches:       222
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            100.0%         Indels:        0
DB:                     6              Gaps:          0

US-10-821-670A-33 (1-222) x ABK98947 (1-666)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
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Db        666 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 607

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 547

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 427

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 307

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 247

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 187

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 127

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 7

Qy        221 AlaSer 222
              ||||||
Db          6 GCTTCC 1

RESULT 2
ABK98946
ID   ABK98946 standard; cDNA; 666 BP.
XX
AC   ABK98946;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p35-666 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69304.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 54-55; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 666 BP; 189 A; 179 C; 138 G; 160 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              8.53e-111      Length:        666
Score:                  1129.00        Matches:       222
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            100.0%         Indels:        0
DB:                     6              Gaps:          0
```

```
US-10-821-670A-33 (1-222) x ABK98946 (1-666)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        221 AlaSer 222
              ||||||
Db        661 GCTTCC 666

RESULT 3
ADV34685
ID   ADV34685 standard; cDNA; 666 BP.
XX
AC   ADV34685;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12p35 full-length cDNA, nFeIL-12p35 666.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .666
FT                   /*tag=  a
FT                   /product= "PFeIL-12p35 222 protein "
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34686.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 23; SEQ ID NO 32; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12p35 subunit protein
CC   encoding full-length cDNA.
XX
SQ   Sequence 666 BP; 189 A; 179 C; 138 G; 160 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                8.53e-111       Length:          666
Score:                    1129.00         Matches:         222
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              100.0%          Indels:          0
DB:                       14              Gaps:            0

US-10-821-670A-33 (1-222) x ADV34685 (1-666)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        221 AlaSer 222
              ||||||
Db        661 GCTTCC 666

RESULT 4
ADV34687/c
ID   ADV34687 standard; DNA; 666 BP.
XX
AC   ADV34687;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12p35 complementary DNA, nFeIL-12p35 666.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 34; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12p35 subunit full-length
CC   complementary DNA.
XX
SQ   Sequence 666 BP; 160 A; 138 C; 179 G; 189 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              8.53e-111       Length:         666
Score:                  1129.00         Matches:        222
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-33 (1-222) x ADV34687 (1-666)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 607

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 547

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 427

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 307

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 247

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 187

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 127

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 7

Qy        221 AlaSer 222
              ||||||
Db          6 GCTTCC 1

RESULT 5
AAV56641
ID   AAV56641 standard; DNA; 689 BP.
XX
AC   AAV56641;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp35 DNA fragment.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ss.
XX
OS   Felis catus.
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP001824.
XX
PR   04-JUN-1996;   96JP-00165249.
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XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
XX
PT   Novel feline cytokine protein - useful for treating feline auto:immune
PT   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS   Claim 24; Page 67; 94pp; Japanese.
XX
CC   This sequence encodes a fragment of a novel feline cytokine protein,
CC   FLAFp35. This protein can be used in the production of a FLAFp35/FLAFp40
CC   heterodimer which can potentiate the cytotoxic activity of feline
CC   cytotoxic T lymphocyte cells. Such proteins are used for treatment of
CC   feline autoimmune diseases e.g. as caused by feline herpes virus or
CC   feline calcivirus
XX
SQ   Sequence 689 BP; 192 A; 193 C; 145 G; 159 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.87e-110      Length:        689
Score:                  1126.00        Matches:       221
Percent Similarity:     100.0%         Conservative:  1
Best Local Similarity:  99.5%          Mismatches:    0
Query Match:            99.7%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-33 (1-222) x AAV56641 (1-689)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7 ATGTGCCCCCCCCCGTGGCCTCCTCCTGGTGACCATCCTGGTCCTGCTGAACCACCTGGAC 66

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 126

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 186

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 246

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 AAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTG 306

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 366

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 426

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 486

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 546

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 606

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666

Qy        221 AlaSer 222
              ::::||
Db        667 TCTTCC 672

RESULT 6
AAV56628
ID   AAV56628 standard; cDNA; 1441 BP.
XX
AC   AAV56628;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp35 cDNA.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             133. .811
FT                   /*tag=  a
FT   sig_peptide     133. .217
FT                   /*tag=  b
FT   mat_peptide     218. .808
FT                   /*tag=  c
FT                   /product= "FLAFp35"
FT                   /note= "feline cytokine"
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP001824.
XX
PR   04-JUN-1996;   96JP-00165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76175.
XX
PT   Novel feline cytokine protein - useful for treating feline auto:immune
PT   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS   Claim 22; Page 57-58; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine protein, FLAFp35. This
CC   protein can be used in the production of a FLAFp35/FLAFp40 heterodimer
CC   which can potentiate the cytotoxic activity of feline cytotoxic T
CC   lymphocyte cells. Such proteins are used for treatment of feline
CC   autoimmune diseases e.g. as caused by feline herpes virus or feline
CC   calcivirus
XX
SQ   Sequence 1441 BP; 451 A; 325 C; 258 G; 407 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              5.13e-110      Length:        1441
Score:                  1126.00        Matches:       221
Percent Similarity:     100.0%         Conservative:  1
Best Local Similarity:  99.5%          Mismatches:    0
Query Match:            99.7%          Indels:        0
DB:                     2              Gaps:          0

US-10-821-670A-33 (1-222) x AAV56628 (1-1441)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202
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```
Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

Qy        221 AlaSer 222
              :::|||
Db        803 TCTTCC 808
```

RESULT 7
AAF26083
ID AAF26083 standard; DNA; 669 BP.
XX
AC AAF26083;
XX
DT 24-APR-2001 (first entry)
XX
DE Feline IL-12p35 encoding DNA SEQ ID 4.
XX
KW Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS Felis sp.
XX
PN WO200104280-A2.
XX
PD 18-JAN-2001.
XX
PF 08-JUL-2000; 2000WO-DE002262.
XX
PR 08-JUL-1999; 99CH-00001258.
XX
PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA (UYZU-) UNIV ZUERICH.
XX
PI Leutenegger C, Schroff M, Wittig B, Lutz H;
XX
DR WPI; 2001-147190/15.
XX
PT Vaccine for treating or preventing lentivirus infection in cats, contains
PT nucleic acid sequence encoding viral protein under control of eukaryotic
PT promoter.
XX
PS Claim 14; Page 37; 37pp; German.
XX
CC This invention describes a novel vaccine (A) for prevention or treatment
CC of lentivirus infection in felines which comprises an immunizing nucleic
CC acid sequence (I) that contains, or comprises, at least part of a gene
CC encoding a protein (II) of the virus, under control of a eukaryotic
CC promoter functional in the relevant animal. (II) is especially the
CC envelope (env) protein. The invention also describes (1) vaccine (A)
CC containing an immunizing protein, or fragment, from a lentivirus plus at
CC least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC lentivirus protein, or fragment, especially derived from feline immune
CC deficiency virus (FIV), by expressing the corresponding nucleic acid
CC sequence in a host cell. The products of the invention have antiviral
CC activity. The vaccine (A) and related protein-based vaccines, are
CC particularly used to treat or prevent lentivirus infections in domestic
CC cats, especially feline immune deficiency virus (FIV). Vaccination with
CC (A) allows differentiation between vaccinated and infected animals, from
CC the antibody status. The vaccines may be formulated with an adjuvant
CC (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC immune response, particularly a Th1 response
XX
SQ Sequence 669 BP; 189 A; 179 C; 140 G; 161 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.5e-108	Length:	669
Score:	1108.00	Matches:	217
Percent Similarity:	98.2%	Conservative:	1
Best Local Similarity:	97.7%	Mismatches:	4
Query Match:	98.1%	Indels:	0
DB:	4	Gaps:	0

US-10-821-670A-33 (1-222) x AAF26083 (1-669)

```
Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCT 360

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||:::|||||||||||  ||||||||||||||||
```

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Db        481 AACATGCTGACAGCTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        221 AlaSer 222
              ||||||
Db        661 GCTTCC 666

RESULT 8
AAF26086
ID   AAF26086 standard; DNA; 669 BP.
XX
AC   AAF26086;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p35 encoding DNA.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS   Felis sp.
XX
PN   WO200104155-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002263.
XX
PR   08-JUL-1999;   99CH-00001259.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Lutz H,  Leutenegger C,  Pedersen N,  Schroff M,  Wittig B;
XX
DR   WPI; 2001-147178/15.
XX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs.
XX
PS   Claim 3; Page 31; 35pp; German.
XX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
CC   following: (i) as immunostimulant, for preventative or therapeutic use;
CC   and (ii) treating tumors and autoimmune diseases, or diseases associated
CC   with a Th1 defect, especially pre-existing infections by feline immune
CC   deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ   Sequence 669 BP; 189 A; 179 C; 140 G; 161 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.5e-108        Length:         669
Score:                  1108.00         Matches:        217
Percent Similarity:     98.2%           Conservative:   1
Best Local Similarity:  97.7%           Mismatches:     4
Query Match:            98.1%           Indels:         0
DB:                     4               Gaps:           0

US-10-821-670A-33 (1-222) x AAF26086 (1-669)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCT 360

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||:::||||||||||||   ||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        221 AlaSer 222
              ||||||
Db        661 GCTTCC 666

RESULT 9
AAF26077
ID   AAF26077 standard; DNA; 4201 BP.
XX
AC   AAF26077;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p35 encoding DNA SEQ ID 3.
XX
KW   Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW   interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
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XX
OS   Felis sp.
XX
PN   WO200104280-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002262.
XX
PR   08-JUL-1999;   99CH-00001258.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
XX
PI   Leutenegger C,  Schroff M,  Wittig B,  Lutz H;
XX
DR   WPI; 2001-147190/15.
XX
PT   Vaccine for treating or preventing lentivirus infection in cats, contains
PT   nucleic acid sequence encoding viral protein under control of eukaryotic
PT   promoter.
XX
PS   Disclosure; Page 31-33; 37pp; German.
XX
CC   This invention describes a novel vaccine (A) for prevention or treatment
CC   of lentivirus infection in felines which comprises an immunizing nucleic
CC   acid sequence (I) that contains, or comprises, at least part of a gene
CC   encoding a protein (II) of the virus, under control of a eukaryotic
CC   promoter functional in the relevant animal. (II) is especially the
CC   envelope (env) protein. The invention also describes (1) vaccine (A)
CC   containing an immunizing protein, or fragment, from a lentivirus plus at
CC   least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC   lentivirus protein, or fragment, especially derived from feline immune
CC   deficiency virus (FIV), by expressing the corresponding nucleic acid
CC   sequence in a host cell. The products of the invention have antiviral
CC   activity. The vaccine (A) and related protein-based vaccines, are
CC   particularly used to treat or prevent lentivirus infections in domestic
CC   cats, especially feline immune deficiency virus (FIV). Vaccination with
CC   (A) allows differentiation between vaccinated and infected animals, from
CC   the antibody status. The vaccines may be formulated with an adjuvant
CC   (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC   immune response, particularly a Th1 response
XX
SQ   Sequence 4201 BP; 1086 A; 1055 C; 999 G; 1061 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.85e-107      Length:          4201
Score:                  1108.00        Matches:         217
Percent Similarity:     98.2%          Conservative:    1
Best Local Similarity:  97.7%          Mismatches:      4
Query Match:            98.1%          Indels:          0
DB:                     4              Gaps:            0

US-10-821-670A-33 (1-222) x AAF26077 (1-4201)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3047 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 3106

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3107 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 3166

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3167 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 3226

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db       3227 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 3286

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db       3287 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTG 3346

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db       3347 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCT 3406

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3407 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 3466

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3467 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 3526

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||:::||||||||||||   ||||||||||||||||
Db       3527 AACATGCTGACAGCTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTG 3586

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3587 CCACAGAACTCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 3646

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3647 CTTCTTCATGCTTTCAGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 3706

Qy        221 AlaSer 222
              ||||||
Db       3707 GCTTCC 3712

RESULT 10
AAF26097
ID   AAF26097 standard; DNA; 679 BP.
XX
AC   AAF26097;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline fil12p35a DNA.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS   Felis sp.
XX
PN   WO200104155-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002263.
XX
PR   08-JUL-1999;   99CH-00001259.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Lutz H,  Leutenegger C,  Pedersen N,  Schroff M,  Wittig B;
XX
DR   WPI; 2001-147178/15.
XX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs.
XX
PS   Disclosure; Fig 2; 35pp; German.
XX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
```

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CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
CC   following: (i) as immunostimulant, for preventative or therapeutic use;
CC   and (ii) treating tumors and autoimmune diseases, or diseases associated
CC   with a Th1 defect, especially pre-existing infections by feline immune
CC   deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ   Sequence 679 BP; 196 A; 180 C; 140 G; 163 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              7.79e-107      Length:         679
Score:                  1092.00        Matches:        215
Percent Similarity:     98.2%          Conservative:   3
Best Local Similarity:  96.8%          Mismatches:     4
Query Match:            96.7%          Indels:         0
DB:                     4              Gaps:           0

US-10-821-670A-33 (1-222) x AAF26097 (1-679)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              |||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGGCTGGCCTCCAGAAAGACCTCT 360

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAACCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAAAGTGATGAGCTATCTGAAT 660

Qy        221 AlaSer 222
              :::|||
Db        661 TCTTCC 666

RESULT 11
ABK98955
ID   ABK98955 standard; cDNA; 666 BP.
XX
AC   ABK98955;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p35-666 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69308.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 67-68; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 666 BP; 182 A; 177 C; 145 G; 162 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.29e-101      Length:         666
Score:                  1043.00        Matches:        204
Percent Similarity:     95.9%          Conservative:   9
Best Local Similarity:  91.9%          Mismatches:     9
Query Match:            92.4%          Indels:         0
DB:                     6              Gaps:           0

US-10-821-670A-33 (1-222) x ABK98955 (1-666)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
```

```
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60

Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80

Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100

Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120

Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140

Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160

Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180

Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200

Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220

Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        221 AlaSer 222

Db        661 TCTTCC 666
```

RESULT 12
ABK98956/c
ID ABK98956 standard; cDNA; 666 BP.
XX
AC ABK98956;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12p35-66 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Disclosure; Page 68-69; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 666 BP; 162 A; 145 C; 177 G; 182 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.29e-101	Length:	666
Score:	1043.00	Matches:	204
Percent Similarity:	95.9%	Conservative:	9
Best Local Similarity:	91.9%	Mismatches:	9
Query Match:	92.4%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-33 (1-222) x ABK98956 (1-666)

```
Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20

Db        666 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 607

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40

Db        606 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 547

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60

Db        546 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80

Db        486 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 427

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100

Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120

Db        366 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 307

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140

Db        306 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 247

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160

Db        246 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 187

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180

Db        186 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 127

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200

Db        126 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67
```

```
Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db         66 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 7

Qy        221 AlaSer 222
              :::|||
Db          6 TCTTCC 1

RESULT 13
ADV34700/c
ID   ADV34700 standard; DNA; 666 BP.
XX
AC   ADV34700;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p35 complementary DNA, nCaIL-12p35 666.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 48; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p35 subunit full-length
CC   complementary DNA.
XX
SQ   Sequence 666 BP; 162 A; 145 C; 177 G; 182 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.29e-101      Length:         666
Score:                  1043.00        Matches:        204
Percent Similarity:     95.9%          Conservative:   9
Best Local Similarity:  91.9%          Mismatches:     9
Query Match:            92.4%          Indels:         0
DB:                     14             Gaps:           0

US-10-821-670A-33 (1-222) x ADV34700 (1-666)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db        666 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 607

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||:::   ||||||:::|||||||||   :::|||||||||||:::|||||||||
Db        606 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 547

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||   ||||||||||||:::|||||||||||||||||||||||||||
Db        546 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 427

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||   |||   |||
Db        366 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 307

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              |||||||||   ||||||||||||||||||||||||||||||||||||||:::|||
Db        306 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 247

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 187

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        186 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 127

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||||
Db         66 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 7

Qy        221 AlaSer 222
              :::|||
Db          6 TCTTCC 1

RESULT 14
ADV34698
ID   ADV34698 standard; cDNA; 666 BP.
XX
AC   ADV34698;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p35 full-length cDNA, nCaIL-12p35 666.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .666
FT                   /*tag=  a
FT                   /product= "PCaIL-12p222 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
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PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34699.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 46; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p35 subunit protein
CC   encoding full-length cDNA.
XX
SQ   Sequence 666 BP; 182 A; 177 C; 145 G; 162 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.29e-101      Length:          666
Score:                    1043.00        Matches:         204
Percent Similarity:       95.9%          Conservative:    9
Best Local Similarity:    91.9%          Mismatches:      9
Query Match:              92.4%          Indels:          0
DB:                       14             Gaps:            0

US-10-821-670A-33 (1-222) x ADV34698 (1-666)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              |||||||:::   |||||||:::|||||||||   :::|||||||||||||:::|||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||   ||||||||||||:::|||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||   |||   |||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              |||||||||   ||||||||||||||||||||||||||||||||||||||||:::|||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||   |||||||||||||||||
Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        221 AlaSer 222
              :::|||
Db        661 TCTTCC 666

RESULT 15
AAV13819
ID   AAV13819 standard; cDNA to mRNA; 669 BP.
XX
AC   AAV13819;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P35 subunit cDNA.
XX
KW   Canine; interleukin-12 P35 subunit; IL-12 P35 subunit; antitumour;
KW   antiviral; vaccine adjuvant; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag=  a
FT                   /product= "interleukin-12_P35_subunit"
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-00296789.
XX
PR   08-NOV-1995;   95JP-00289729.
PR   23-MAY-1996;   96JP-00128104.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   P-PSDB; AAW41793.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected.
XX
PS   Claim 11; Page 11-12; 12pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin-12 (IL-12) P35 subunit.
CC   A canine IL-12 comprising a P40 and P35 subunit is capable of inducing an
CC   antiviral activating factor and the expression of class II MHC molecules
CC   in canine tumour cells, stimulating proliferation of canine blastogenic
CC   lymphocytes and activating canine leukocytes to inhibit canine tumour
CC   cells. The canine IL-12 can be used in veterinary medicines, e.g.
CC   antitumour, antivirus and vaccine adjuvant activities are expected
XX
SQ   Sequence 669 BP; 185 A; 177 C; 144 G; 163 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.3e-101       Length:          669
Score:                    1043.00        Matches:         204
Percent Similarity:       95.9%          Conservative:    9
Best Local Similarity:    91.9%          Mismatches:      9
Query Match:              92.4%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-33 (1-222) x AAV13819 (1-669)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
```

```
Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||:::   ||||||:::|||||||||   :::||||||||||||:::|||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||   ||||||||||||:::||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||   |||   |||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              |||||||||   ||||||||||||||||||||||||||||||||||||||:::|||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||:::|||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        221 AlaSer 222
              :::|||
Db        661 TCTTCC 666


Search completed: June 10, 2006, 01:16:54
Job time : 479.894 secs
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 10, 2006, 00:20:47 ; Search time 2720.99 Seconds
(without alignments)
6843.525 Million cell updates/sec

Title: US-10-821-670A-33
Perfect score: 1129
Sequence: 1 MCPPRGLLLVTILVLLNHLD.....HAFRIRAVTINRMMSYLNAS 222

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/abss/ABSSWEB_spool/US10821670/runat_07062006_110104_26172/app_query.fasta_1
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-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	957.5	84.8	762	14	DQ033872	DQ033872 Homo sapi
2	947.5	83.9	762	14	DQ033873	DQ033873 Pan trogl
3	930	82.4	1136	4	CD013915	CD013915 90138132
4	883.5	78.3	935	4	CD013914	CD013914 90138124
5	823	72.9	1938	6	BC035571	BC035571 Homo sapi
6	737.5	65.3	863	4	CD013916	CD013916 90138296
7	487	43.1	812	2	BG702253	BG702253 602683459
8	460	40.7	1299	6	AK153729	AK153729 Mus muscu
9	418.5	37.1	563	3	BU698113	BU698113 LL2in1206
10	404	35.8	589	1	AI050362	AI050362 ub30a07.r
c 11	374.5	33.2	1099	2	BI523344	BI523344 603175938
12	373.5	33.1	581	3	BP260963	BP260963 BP260963
13	372.5	33.0	832	2	BI523569	BI523569 603175938
c 14	355	31.4	778	1	AJ820622	AJ820622 AJ820622
15	349.5	31.0	561	3	BU699383	BU699383 LL2in1157
16	345	30.6	373	7	BF552757	BF552757 UI-R-C0-i
17	344	30.5	692	5	CJ137697	CJ137697 CJ137697
18	321	28.4	456	10	DT913216	DT913216 S13.1426
19	320	28.3	427	10	DT930939	DT930939 S13.1784
20	305.5	27.1	571	3	BP261459	BP261459 BP261459
21	300	26.6	371	3	BU699957	BU699957 B4-79 Hem
22	295	26.1	412	4	CB801533	CB801533 AMGNNUC:S
c 23	295	26.1	777	4	CB168830	CB168830 CWI602769
24	287	25.4	354	4	BY230958	BY230958 BY230958
25	265	23.5	777	14	CT080894	CT080894 Sus scrof
26	263.5	23.3	342	2	BM257856	BM257856 521721 MA
27	221	19.6	551	10	DT919655	DT919655 PCRS30821
28	215.5	19.1	373	3	BU695376	BU695376 B1-30 Hem
29	204.5	18.1	508	9	DA505380	DA505380 DA505380
30	204.5	18.1	571	9	DN829917	DN829917 pat.pk005
31	199.5	17.7	463	9	DR007201	DR007201 TC124111
32	171.5	15.2	382	4	CB809298	CB809298 AMGNNUC:T
c 33	156.5	13.9	940	14	BX963061	BX963061 Forward s
34	150	13.3	840	11	BZ261813	BZ261813 CH230-420
35	140.5	12.4	817	3	BU474924	BU474924 603761859
36	137	12.1	592	12	CE159257	CE159257 tigr-gss-
37	129	11.4	447	2	BI824638	BI824638 603033580
38	126	11.2	558	9	CX570753	CX570753 RVL1941 W
39	115	10.2	451	4	BX258840	BX258840 BX258840
40	114.5	10.1	361	3	BU694675	BU694675 B2-56 Hem
41	114	10.1	344	14	BX537236	BX537236 INRA porc
c 42	102	9.0	528	1	AI332701	AI332701 qq19a07.x
43	101	8.9	477	4	BX258839	BX258839 BX258839
44	100	8.9	905	3	BU540821	BU540821 AGENCOURT
45	97.5	8.6	994	3	BQ222548	BQ222548 AGENCOURT

ALIGNMENTS

RESULT 1
DQ033872
LOCUS DQ033872 762 bp DNA linear GSS 02-JUN-2005
DEFINITION Homo sapiens IL12A gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION DQ033872
VERSION DQ033872.1 GI:66885081
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 762)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 762)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

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COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.  Translation starts at the beginning of
            alignment.
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     source          1. .762
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
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                     /gene="IL12A"
                     /locus_tag="HC3464"
ORIGIN

Alignment Scores:
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Score:                  957.50          Matches:        191
Percent Similarity:     88.3%           Conservative:   5
Best Local Similarity:  86.0%           Mismatches:     23
Query Match:            84.8%           Indels:         3
DB:                     14              Gaps:           1

US-10-821-670A-33 (1-222) x DQ033872 (1-762)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              |||||||||   |||   ||||||||||||      |||||||||          ||||||
Db        103 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCTC---------CTGGAC 153

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              |||||||||||||||||||||||||||||       ||||||   ||||||||||||   |||
Db        154 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 213

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              |||:::|||||||||   ||||||||||||:::||||||   ||||||||||||||||||
Db        214 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 273

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        274 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 333

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        334 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTA 393

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
                 |||||||||   |||   ||||||||||||||||||||||||||||||||||||||||
Db        394 AATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 453

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||      ||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 TTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAG 513

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 TTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAA 573

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              |||||||||       ||||||||||||:::||||||||||||   ||||||   ||||||
Db        574 AACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTG 633

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
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Db        634 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 693

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
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Db        694 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAAT 753

Qy        221 AlaSer 222
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Db        754 GCTTCC 759

RESULT 2
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LOCUS       DQ033873                762 bp    DNA     linear   GSS 02-JUN-2005
DEFINITION  Pan troglodytes IL12A gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   DQ033873
VERSION     DQ033873.1  GI:66885082
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     A Scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
  JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
   PUBMED   15869325
REFERENCE   2  (bases 1 to 762)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.  Translation starts at the beginning of
            alignment.
FEATURES             Location/Qualifiers
     source          1. .762
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     gene            <1. .>762
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ORIGIN

Alignment Scores:
Pred. No.:              1.1e-96         Length:         762
Score:                  947.50          Matches:        190
Percent Similarity:     87.8%           Conservative:   5
Best Local Similarity:  85.6%           Mismatches:     24
Query Match:            83.9%           Indels:         3
DB:                     14              Gaps:           1

US-10-821-670A-33 (1-222) x DQ033873 (1-762)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              |||||||||   |||   ||||||||||||      |||||||||          ||||||
Db        103 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCTC---------CTGGAC 153

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              |||||||||||||||||||||||||||||       ||||||   ||||||||||||   |||
Db        154 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACCCCAGACCCAGGAATGTTCCCATGC 213

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              |||:::|||||||||   ||||||||||||:::||||||   ||||||||||||||||||
Db        214 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 273

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        274 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 333

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
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Db        334 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTA 393

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
                 |||||||||   |||   ||||||||||||||||||||||||||||||||||||||||
Db        394 AATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 453
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Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||      ||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 TTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAG 513

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
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Db        634 CCACAAAAATCCTCCCTTGAAGAACTGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 693

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||:::|||:::||||||||||||||||||
Db        694 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAAT 753

Qy        221 AlaSer 222
              ||||||
Db        754 GCTTCC 759
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RESULT 3
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LOCUS       CD013915               1136 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION  90138132 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD013915
VERSION     CD013915.1  GI:37777445
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1136)
  AUTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
            Au-Young,J. and Stuve,L.L.
  TITLE     PCR isolation and cloning of novel splice variant mRNAs from known
            drug target genes
  JOURNAL   Genomics 83 (4), 566-571 (2004)
   PUBMED   15028279
COMMENT     Contact: Jin, P.
            Incyte Corporation
            3160 Porter Drive, Palo Alto, CA 94304, USA
            Tel: 650 621 8639
            Fax: 650 621 8965
            Email: pjin@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .1136
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Single gene library"
                     /note="Vector: pDrive Cloning Vector; RT-PCR was performed
                     using gene-specific primers flanking the open-reading
                     frame. PCR products were subcloned into pDrive Cloning
                     Vector and sequenced completely using M13 forward and
                     reverse primers. Sequencing gaps were closed by
                     re-sequencig using primers flanking the gapped areas."
ORIGIN

Alignment Scores:
Pred. No.:              1.9e-94        Length:         1136
Score:                  930.00         Matches:        190
Percent Similarity:     79.4%          Conservative:   6
Best Local Similarity:  76.9%          Mismatches:     23
Query Match:            82.4%          Indels:         28
DB:                     4              Gaps:           2

US-10-821-670A-33 (1-222) x CD013915 (1-1136)
```

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Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||   |||   ||||||||||||      |||||||||          ||||||
Db        290 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCTC---------CTGGAC 340

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||:::||||||      ||||||   ||||||||||||   |||
Db        341 CACCTCAGTTTGGCCAGAGACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 400

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              |||:::|||||||||   ||||||||||:::||||||   ||||||||||||||||||
Db        401 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 460

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        461 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 520

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        521 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTA 580

Qy        101 AlaSerArgGluIleSerLeuIleThr---------------------------------- 109
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Qy        110 ----------------------------------------AsnGlySerCysLeuAla 115
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Qy        116 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 135
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Db        761 ATGTACCAGGTGGAGTTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAG 820

Qy        156 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 175
              ||||||||||||||||||||||||      ||||||||||:::||||||||||||
Db        821 ATCTTTCTAGATCAAAACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTC 880

Qy        176 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 195
              ||||||   ||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        881 AACAGTGAGACTGTGCCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAA 940

Qy        196 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::|||:::
Db        941 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTG 1000

Qy        216 MetSerTyrLeuAsnAlaSer 222
              ||||||||||||||||||||
Db       1001 ATGAGCTATCTGAATGCTTCC 1021
```

```
RESULT 4
CD013914
LOCUS       CD013914               935 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION  90138124 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD013914
VERSION     CD013914.1  GI:37777444
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 935)
  AUTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
            Au-Young,J. and Stuve,L.L.
  TITLE     PCR isolation and cloning of novel splice variant mRNAs from known
            drug target genes
  JOURNAL   Genomics 83 (4), 566-571 (2004)
   PUBMED   15028279
COMMENT     Contact: Jin, P.
```

Incyte Corporation
3160 Porter Drive, Palo Alto, CA 94304, USA
Tel: 650 621 8639
Fax: 650 621 8965
Email: pjin@incyte.com.

```
FEATURES             Location/Qualifiers
     source          1. .935
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Single gene library"
                     /note="Vector: pDrive Cloning Vector; RT-PCR was performed
                     using gene-specific primers flanking the open-reading
                     frame. PCR products were subcloned into pDrive Cloning
                     Vector and sequenced completely using M13 forward and
                     reverse primers. Sequencing gaps were closed by
                     re-sequencig using primers flanking the gapped areas."
ORIGIN

Alignment Scores:
Pred. No.:              2.75e-89        Length:         935
Score:                  883.50          Matches:        179
Percent Similarity:     83.3%           Conservative:   6
Best Local Similarity:  80.6%           Mismatches:     20
Query Match:            78.3%           Indels:         17
DB:                     4               Gaps:           2

US-10-821-670A-33 (1-222) x CD013914 (1-935)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              |||||||||   |||   ||||||||||||      |||||||||         ||||||
Db        206 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCTC---------CTGGAC 256

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||:::||||||      ||||||   ||||||||||||   |||
Db        257 CACCTCAGTTTGGCCAGAGACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 316

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              |||:::|||||||||   ||||||||||||:::|||||||   ||||||||||||||||||
Db        317 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 376

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        377 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 436

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||
Db        437 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACC------------------ 478

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
                                       ||||||||||||||||||||||||||||||||
Db        479 ----------------------AAGAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 514

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||      ||||||||||||||||||||||||||||||||||||||||||||||||
Db        515 TTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAG 574

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        575 TTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAA 634

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              |||||||||      ||||||||||||:::||||||||||||   ||||||   ||||||
Db        635 AACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTG 694

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        695 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 754

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||:::|||:::|||||||||||||||||
Db        755 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAAT 814

Qy        221 AlaSer 222
              ||||||
Db        815 GCTTCC 820

RESULT 5
BC035571
LOCUS       BC035571                1938 bp    mRNA    linear   HTC 04-MAR-2003
DEFINITION  Homo sapiens, clone IMAGE:5240216, mRNA.
ACCESSION   BC035571
VERSION     BC035571.1  GI:23958681
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1938)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 69 Row: b Column: 15
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 4504638
            This clone has the following problem: retained intron.
FEATURES             Location/Qualifiers
     source          1. .1938
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240216"
                     /tissue_type="Brain, fetal, whole pooled"
                     /clone_lib="NIH_MGC_121"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
ORIGIN

Alignment Scores:
Pred. No.:              5.79e-82        Length:         1938
Score:                  823.00          Matches:        191
Percent Similarity:     50.9%           Conservative:   6
Best Local Similarity:  49.4%           Mismatches:     22
Query Match:            72.9%           Indels:         168
DB:                     6               Gaps:           4

US-10-821-670A-33 (1-222) x BC035571 (1-1938)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              |||||||||   |||   ||||||||||||      |||||||||         ||||||
```

```
Db        295 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCTC---------CTGGAC 345

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40

Db        346 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 405

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60

Db        406 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 465

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80

Db        466 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 525

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThr---------------- 94

Db        526 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGGTATAAAGGATTTTC 585

Qy         94 ------------------------------------------------------------ 94

Db        586 CTCCCAGAGCATGCAGTGTGGTTAAAAACTGTGCATCAAATCTCACCTGCTTCTAAAAAT 645

Qy         94 ------------------------------------------------------------ 94

Db        646 TCACGTTTCTGGTATCCATCATTATGGGATTTTAACTGGTCCTACTTCAGAAGTTAGATT 705

Qy         94 ------------------------------------------------------------ 94

Db        706 TGGGAGAAAAATTATTTTTAAAAAATGGTTTTTTTTGCAACAATGTGAATACACTTAACA 765

Qy         94 ------------------------------------------------------------ 94

Db        766 CTTAAAAATAGTTCAGATGCTAAATATTATGATATGTGTTTTTACCATAATAAAAAAAAT 825

Qy         94 ------------------------------------------------------------ 94

Db        826 TTGAGACCTGAAGAGTCAGAAAGATTTATACTAAGAATTAATACTTTGATATATGATTTT 885

Qy         95 ------Met-AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThr-------- 109

Db        886 TTCCCTCTAGAATGAGAGTTGCCTAAATTCCAGAGAGACCTCTTTCATAACTGTAAGTCA 945

Qy        109 ------------------------------------------------------------ 109

Db        946 AAAAATGAAAAGTTTCAGCCTGTATGATGAATTCATATCACTGATGTCTGATTATTTTTT 1005

Qy        110 -------AsnGlySerCysLeuAlaSerArgLysThrSerPheMet-------------- 122

Db       1006 CCTCTAGAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATGGTAAGACACAC 1065

Qy        122 ------------------------------------------------------------ 122

Db       1066 AGCTCTTTCCTCAAATGCAATGGGGGAAATGTTTTTAGCCCATCTCAATGGATACTTCCC 1125

Qy        123 ----------------ThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetT 137

Db       1126 CATCTTGTCATGTCACCCAGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGT 1185

Qy        137 yrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIleP 157

Db       1186 ACCAGGTGGAGTTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCT 1245

Qy        157 heLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnS 177

Db       1246 TTCTAGATCAAAACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACA 1305

Qy        177 erValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleL 197

Db       1306 GTGAGACTGTGCCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCA 1365

Qy        197 ysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetS 217

Db       1366 AGCTCTGCATACTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGA 1425

Qy        217 erTyrLeuAsnAlaSer 222

Db       1426 GCTATCTGAATGCTTCC 1442
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RESULT 6
CD013916

```
LOCUS       CD013916                863 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION  90138296 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD013916
VERSION     CD013916.1  GI:37777446
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 863)
  AUTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
            Au-Young,J. and Stuve,L.L.
  TITLE     PCR isolation and cloning of novel splice variant mRNAs from known
            drug target genes
  JOURNAL   Genomics 83 (4), 566-571 (2004)
   PUBMED   15028279
COMMENT     Contact: Jin, P.
            Incyte Corporation
            3160 Porter Drive, Palo Alto, CA 94304, USA
            Tel: 650 621 8639
            Fax: 650 621 8965
            Email: pjin@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .863
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Single gene library"
                     /note="Vector: pDrive Cloning Vector; RT-PCR was performed
                     using gene-specific primers flanking the open-reading
                     frame. PCR products were subcloned into pDrive Cloning
                     Vector and sequenced completely using M13 forward and
                     reverse primers. Sequencing gaps were closed by
                     re-sequencig using primers flanking the gapped areas."
ORIGIN
```

Alignment Scores:

Pred. No.:	9.35e-73	Length:	863
Score:	737.50	Matches:	154
Percent Similarity:	72.1%	Conservative:	6
Best Local Similarity:	69.4%	Mismatches:	21
Query Match:	65.3%	Indels:	41
DB:	4	Gaps:	2

US-10-821-670A-33 (1-222) x CD013916 (1-863)

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Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20

Db        206 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCTC---------CTGGAC 256

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40

Db        257 CACCTCAGTTTGGCCAGAGACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 316

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60

Db        317 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAG--------- 367

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80

Db        367 ------------------------------------------------------------ 367

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100

Db        368 ---------------------------------------------AATGAGAGTTGCCTA 382
```

```
Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              |||||||||   |||   ||||||||||||||||||||||||||||||||||||||||||
Db        383 AATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 442

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||      ||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 TTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAG 502

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAA 562

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              |||||||||      |||||||||||:::||||||||||||   ||||||   ||||||
Db        563 AACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTG 622

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 682

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||:::|||:::|||||||||||||||||
Db        683 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAAT 742

Qy        221 AlaSer 222
              ||||||
Db        743 GCTTCC 748
```

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RESULT 7
BG702253
LOCUS       BG702253                812 bp    mRNA    linear   EST 07-MAY-2001
DEFINITION  602683459F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4816118 5',
            mRNA sequence.
ACCESSION   BG702253
VERSION     BG702253.1  GI:13973409
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 812)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10714  row: e  column: 15
            High quality sequence stop: 804.
FEATURES             Location/Qualifiers
     source          1. .812
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4816118"
                     /tissue_type="hippocampus"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_95"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
                     (gtcgag); Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTTTVN-3', size-selected for  average
                     insert size 2.5 kb and normalized to ROT 5. This is a
                     primary library enriched for  full-length clones and
                     constructed using the Cap-trapper method (Carninci, in
                     preparation).  Library constructed by M. Brownstein
                     (NIMH/NHGRI, National Institutes of Health).  Note: this
                     is a NIH_MGC Library."
ORIGIN
```

```
Alignment Scores:
Pred. No.:              2.41e-44        Length:         812
Score:                  487.00          Matches:        110
Percent Similarity:     83.0%           Conservative:   2
Best Local Similarity:  81.5%           Mismatches:     20
Query Match:            43.1%           Indels:         6
DB:                     2               Gaps:           1

US-10-821-670A-33 (1-222) x BG702253 (1-812)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              |||||||||   |||   ||||||||||||      |||||||||           ||||||
Db        417 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCTC---------CTGGAC 467

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||      ||||||   ||||||||||||   |||
Db        468 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 527

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              |||:::|||||||||   ||||||||||:::||||||   ||||||||||||||||||||
Db        528 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 587

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        588 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATCGATCATGAAGATATCACAAAAGAT 647

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db        648 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCT-- 705

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              |||||||||   |||   ||||||||||||||||||||   ||||||||||||||||||
Db        706 AAATCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGC-TCCAGAAAGACCTCT 764

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 135
              ||||||      ||||||||||||||||   ||||||||||||||
Db        765 TTTATGATGTGCCTGTGCCTTAGTAGTAT-TATGAAGACTTGAAA 808
```

```
RESULT 8
AK153729
LOCUS       AK153729                1299 bp    mRNA    linear   HTC 21-SEP-2005
DEFINITION  Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
            library, clone:A630064E02 product:interleukin 12a, full insert
            sequence.
ACCESSION   AK153729
VERSION     AK153729.1  GI:74148962
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
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Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
CONSRTM RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
PUBMED 11217851
REFERENCE 5
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
CONSRTM FANTOM Consortium
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420 (6915), 563-573 (2002)
PUBMED 12466851
REFERENCE 6
AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.
CONSRTM FANTOM Consortium
TITLE The transcriptional landscape of the mammalian genome
JOURNAL Science 309 (5740), 1559-1563 (2005)
PUBMED 16141072
REFERENCE 7
AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.
CONSRTM RIKEN Genome Exploration Research Group
TITLE Antisense transcription in the mammalian transcriptome
JOURNAL Science 309 (5740), 1564-1566 (2005)
PUBMED 16141073
REFERENCE 8 (bases 1 to 1299)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
FEATURES Location/Qualifiers
source 1. .1299

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                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM_DB:A630064E02"
                     /db_xref="taxon:10090"
                     /clone="A630064E02"
                     /tissue_type="thymus"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="3 days neonate"
     misc_feature    1. .1299
                     /note="interleukin 12a (MGD|MGI:96539 GB|NM_008351,
                     evidence: BLASTN, 100%, match=776)
                     putative"
ORIGIN

Alignment Scores:
Pred. No.:              5.51e-41        Length:         1299
Score:                  460.00          Matches:        103
Percent Similarity:     57.0%           Conservative:   27
Best Local Similarity:  45.2%           Mismatches:     43
Query Match:            40.7%           Indels:         55
DB:                     6               Gaps:           2

US-10-821-670A-33 (1-222) x AK153729 (1-1299)

Qy          50 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 69
               :::   |||           :::||||||:::   |||:::   ||||||||||||:::
Db         118 AGCTTCTCCTTATGTTTTTCCCAGGCCAGAGAAAAACTGAAACATTATTCCTGCACTGCT 177

Qy          70 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeu 89
               |||:::|||||||||||||||||||:::|||:::|||||||||::::::   ||||||
Db         178 GAAGACATCGATCATGAAGACATCACACGGGACCAAACCAGCACATTGAAGACCTGTTTA 237

Qy          90 ProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSer--------- 106
               ||||||||||||      ||||||||||||||||||:::||||||   |||
Db         238 CCACTGGAACTACACAAGAACGAGAGTTGCCTGGCTACTAGAGAGACTTCTTCCACAACA 297

Qy         106 ------------------------------------------------------------ 106

Db         298 GTAAGTAAGCACTCTAAGGGTTCCTTCCCCATGACGGATTCATAACACTGATGCCTGGTC 357

Qy         107 ---Leu-IleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThr----- 123
                  ||| :::      ||||||||||||      :::|||||||||   |||
Db         358 ATTCTTTCTCTAGAGAGGGAGCTGCCTGCCCCCACAGAAGACGTCTTTGATGATGGTAAG 417

Qy         123 ------------------------------------------------------------ 123

Db         418 CCACATCACTTTTCTGAAATGCAGCAGGGTCCTGTAGTTCCAGCCCATCTCAATGATTCC 477

Qy         124 ------------------------ThrLeuCysLeuSerSerIleTyrGluAspLeuLy 135
                                        ||||||||||||   ||||||||||||||||||
Db         478 TTGCCCATTGTGTCCTGCGCTCTAGACCCTGTGCCTTGGTAGCATCTATGAGGACTTGAA 537

Qy         135 sMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGl 155
               ||||||||||   ||||||:::|||:::||||||   |||                :::||
Db         538 GATGTACCAGACAGAGTTCCAGGCCATCAACGCAGCACTTCAGAATCACAACCATCAGCA 597

Qy         155 nIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVa 175
               ||||   ||||||:::   ||||||   ||||||||||||||||:::|||:::||||||
Db         598 GATCATTCTAGACAAGGGCATGCTGGTGGCCATCGATGAGCTGATGCAGTCTCTGAATCA 657

Qy         175 lAsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLy 195
               |||      |||:::   |||         :::   |||   |||   |||:::   ||
Db         658 TAATGGCGAGACTCTGCGCCAGAAACCTCCTGTGGGAGAAGCAGACCCTTACAGAGTGAA 717

Qy         195 sIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMe 215
               |:::||||||||||||||||||||||||||      |||   ||||||||||||||::
Db         718 AATGAAGCTCTGCATCCTGCTTCACGCCTTCAGCACCCGCGTCGTGACCATCAACAGGGT 777

Qy         215 tMetSerTyrLeuAsnAlaSer 222
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Db         778 GATGGGCTATCTGAGCTCCGCC 799
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RESULT 9
BU698113
LOCUS       BU698113                563 bp    mRNA    linear   EST 09-OCT-2002
DEFINITION  LL2in12067T7 Hematopoietic Stem Cell Subtracted Library Mus
            musculus cDNA 5' similar to interleukin 12 p35 subunit, mRNA
            sequence.
ACCESSION   BU698113
VERSION     BU698113.1  GI:23610620
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 563)
  AUTHORS   Phillips,R.L., Ernst,R.E., Brunk,B.P., Ivanova,N., Mahan,M.A.,
            Deanehan,J.K., Moore,K.A., Overton,G.C. and Lemischka,I.R.
  TITLE     The genetic program of hematopoietic stem cells
  JOURNAL   Science 288 (5471), 1635-1640 (2000)
   PUBMED   10834841
COMMENT     Contact: Lemischka, Ihor R.
            Department of Molecular Biology
            Princeton University
            Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544, USA
            Tel: 609 258 2838
            Fax: 609 258 2759
            Email: ilemischka@molbio.princeton.edu
            These ESTs are derived from a subtracted cDNA library enriched for
            gene products expressed in day 14-14.5 fetal liver hematopoietic
            stem cells defined as Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E
            (Sca-1)pos
            Seq primer: M13Reverse or T7.
FEATURES             Location/Qualifiers
     source          1. .563
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /tissue_type="Hematopoietic"
                     /cell_type="Stem Cells; Lineageneg/lo, AA4.1pos, cKitpos,
                     Ly6A/E (Sca-1)pos"
                     /dev_stage="Embryonic day 14-14.5"
                     /lab_host="DH10B"
                     /clone_lib="Hematopoietic Stem Cell Subtracted Library"
                     /note="Organ: Fetal Liver; Vector: Sport 1; Site_1: Sal I;
                     Site_2: Not I; Two directionally cloned cDNA libraries
                     were made from fetal liver  hematopoietic stem cells
                     enriched to be Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E
                     (Sca-1)pos called Scapos and from AA4.1neg fetal liver
                     cells. Subtractive hybridization was  performed by
                     hybridization of the target, Scapos, single stranded cDNA
                     library in pSport1 to  biotinylated RNA transcribed from
                     the driver, AA4.1neg cDNA library in pSport2 with  inserts
                     cloned in the complementary orientation. For detailed
                     protocols and additional  information please see our
                     website at http://stemcell.princeton.edu."
ORIGIN

Alignment Scores:
Pred. No.:              8.61e-37        Length:         563
Score:                  418.50          Matches:        88
Percent Similarity:     72.5%           Conservative:   23
Best Local Similarity:  57.5%           Mismatches:     40
Query Match:            37.1%           Indels:         2
DB:                     3               Gaps:           1

US-10-821-670A-33 (1-222) x BU698113 (1-563)

Qy          50 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 69
               :::   |||           :::||||||:::   |||:::   ||||||||||||:::
Db          78 AGCTTCTCCTTATGTTTTTCCCAGGCCAGAGAAAAACTGAAACATTATTCCTGCACTGCT 137

Qy          70 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeu 89
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                ||||:::|||||||||||||||||||||:::|||:::|||||||||:::::::   ||||||
Db        138 GAAGACATCGATCATGAAGACATCACACGGGACCAAACCAGCACATTGAAGACCTGTTTA 197

Qy         90 ProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThr 109
                ||||||||||||      ||||||||||||||||||:::||||||   |||       |||
Db        198 CCACTGGAACTACACAAGAACGAGAGTTGCCTGGCTACTAGAGAGACTTCTTCCACAACA 257

Qy        110 AsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSer 129
                  ||||||||||||       :::|||||||||   |||   ||||||||||||   |||
Db        258 AGAGGGAGCTGCCTGCCCCCACAGAAGACGTCTTTGATGATGACCCTGTGCCTTGGTAGC 317

Qy        130 IleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeu 149
                ||||||||||||||||||||||||||   ||||||:::|||:::||||||   |||
Db        318 ATCTATGAGGACTTGAAGATGTACCAGACAGAGTTCCAGGCCATCAACGCAGCACTTCAG 377

Qy        150 MetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 169
                      :::||||||   ||||||:::   ||||||   ||||||||||||||||
Db        378 AATCACAACCATCAGCAGATCATTCTAGACAAGGGCATGCTGGTGGCCATCGATGAGCTG 437

Qy        170 LeuGlnAlaLeuAsnValAsnSerVal-ThrVal---ProGlnAsnSerSerLeuGluGl 188
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Db        438 ATGCAGTCTCTGAATCATAATGGGNGAGACTCTTGCGCCAGAAACCTTCCTGTGGGAGAA 497

Qy        188 uProAspPheTyrLysThrLysIleLysLeuCysIle 200
                :   |||   |||:::   |||:::||||||   |||
Db        498 GCAGGACCCTTACAGAGTGAAAATGAAGCTCTTGATT 534

RESULT 10
AI050362
LOCUS       AI050362                589 bp    mRNA    linear   EST 09-JUL-1998
DEFINITION  ub30a07.r1 Soares_thymus_2NbMT Mus musculus cDNA clone
            IMAGE:1379220 5' similar to gb:M65291 INTERLEUKIN-12 ALPHA CHAIN
            PRECURSOR (HUMAN); gb:M86672 Mus musculus interleukin 12 p35
            subunit, complete cds (MOUSE);, mRNA sequence.
ACCESSION   AI050362
VERSION     AI050362.1  GI:3299479
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 589)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:901688
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 60.
FEATURES             Location/Qualifiers
     source          1. .589
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                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1379220"
                     /sex="male"
                     /tissue_type="Thymus"
                     /dev_stage="4 weeks"
                     /lab_host="DH10B"
                     /clone_lib="Soares_thymus_2NbMT"
                     /note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI;
                     1st strand cDNA was primed with a Not I - oligo(dT) primer
                     [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGTTTTTTTTTTTTTTTTTTTTTTT
                     3']; double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. RNA
                     provided by Dr. Bertrand Jordan. Library went through two
                     rounds of normalization, and was constructed by Bento
                     Soares and M.Fatima Bonaldo."
ORIGIN

Alignment Scores:
Pred. No.:                4.07e-35      Length:          589
Score:                    404.00        Matches:         94
Percent Similarity:       68.8%         Conservative:    23
Best Local Similarity:    55.3%         Mismatches:      46
Query Match:              35.8%         Indels:          8
DB:                       1             Gaps:            3

US-10-821-670A-33 (1-222) x AI050362 (1-589)

Qy         50 AlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSer 69
                :::   |||          :::||||||:::   |||:::   ||||||||||||:::
Db         87 AGCTTCTCCTTATGTTTTTCCCAGGCCAGAGAAAAACTGAAACATTATTCCTGCACTGCT 146

Qy         70 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeu 89
                |||:::|||||||||||||||||||||:::|||:::||||||||:::::   ||||||
Db        147 GAAGACATCGATCATGAAGACATCACACGGGACCAAACCAGCACATTGAAGACCTGTTTA 206

Qy         90 ProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThr 109
                ||||||||||||      ||||||||||||||||||:::||||||   |||       |||
Db        207 CCACTGGAACTACACAAGAACGAGAGTTGCCTGGCTACTAGAGAGACTTCTTCCACAACA 266

Qy        110 AsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSer 129
                  ||||||||||||       :::|||||||||   |||   ||||||||||||   |||
Db        267 AGAGGGAGCTGCCTGCCCCCACAGAAGACGTCTTTGATGATGACCCTGTGCCTTGGTAGC 326

Qy        130 IleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeu 149
                ||||||||||||||||||||||||||   ||||||:::|||:::||||||   |||
Db        327 ATCTATGAGGACTTGAAGATGTACCAGACAGAGTTCCAGGCCATCAACGCAGCACTTCAG 386

Qy        150 MetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeu 169
                      :::||||||   ||||||:::   ||||||       ||||||||||||
Db        387 AATCACAACCATCAGCAGATCATTCTAGACAAGGGCATGCTGGGTGGCATCGATGAGCTG 446

Qy        170 LeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLeu------Glu 187
                ::::|||:::||||||   |||       |||:::   |||   :::||||||      |||
Db        447 ATGCAGTCTCTGAATCATAATGGCGAGACTCTGCGCCAGAA-ACCTCCCTGTGGGGAGAA 505

Qy        188 GluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIle 207
                          :::   |||       :::   |||||||||         |||:::
Db        506 GCAGACCCCTTACAGGAGTGAAAATGAAGCGTCTGAATCCTGCTTTCA------CGCCTT 559

Qy        208 ArgAla---------ValThrIleAsnArg 214
                |||         ||||||||||||||
Db        560 TCAGCACCCGGCGTCGTGACCATCAACAGG 589

RESULT 11
BI523344/c
LOCUS       BI523344                1099 bp    mRNA    linear   EST 29-AUG-2001
DEFINITION  603175938T1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 3',
            mRNA sequence.
ACCESSION   BI523344
VERSION     BI523344.1  GI:15348136
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1099)
```

```
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11605  row: l  column: 09
            High quality sequence start: 40
            High quality sequence stop: 727.
FEATURES             Location/Qualifiers
     source          1. .1099
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240216"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_121"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 017. Note:
                     this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:                2.23e-31        Length:         1099
Score:                    374.50          Matches:        90
Percent Similarity:       80.7%           Conservative:   6
Best Local Similarity:    75.6%           Mismatches:     15
Query Match:              33.2%           Indels:         9
DB:                       2               Gaps:           1

US-10-821-670A-33 (1-222) x BI523344 (1-1099)

Qy        107 LeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCys 126
              |||   |||      :::  |||  ||||||:::                    ||||||
Db        776 TTGGATACTTTCCGCAATCTGCTCATGTCACGTCAG--------------GCCCTGTGC 732

Qy        127 LeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAla 146
              ||||||||||||||||||  ||||||||||||||||||||||  |||||||||
Db        731 TTTAGTAGTATTTATGAAGACTG-AAGATGTACCAGGTGGAGTTCAAGACCATGAATGCA 673

Qy        147 LysLeu-LeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIl 166
              |||||| ||||||||||||||||||||||||||||||||||||||||||||      ||
Db        672 AAGCTTCCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCAGTTAT 613

Qy        166 eAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSerLe 186
              ||||||||||:::||||||||||||   ||||||   ||||||||||||   ||||||||
Db        612 TGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCCCT 553

Qy        186 uGluGluProAsp--PheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
              ||||||||||||  |||   ||||||:::|||||||||||||||||||||||||||||||
Db        552 TGAAGAACCGGATTGTTTATCAAAACTGAAATCAAGCTCTGCATACTTCTTCATGCTTTC 493

Qy        206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
              ||||||||||||||||||||:::|||:::||||||||||||||||||||
Db        492 AGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTCC 442

RESULT 12
BP260963
LOCUS       BP260963                 581 bp    mRNA    linear   EST 16-SEP-2004
DEFINITION  BP260963 Sugano cDNA library, small intestine Homo sapiens cDNA
            clone HSI02082, mRNA sequence.
ACCESSION   BP260963
VERSION     BP260963.1  GI:52176194
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 581)
  AUTHORS   Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
            Mizushima-Sugano,J., Nakai,K. and Sugano,S.
  TITLE     Sequence comparison of human and mouse genes reveals a homologous
            block structure in the promoter regions
  JOURNAL   Genome Res. 14 (9), 1711-1718 (2004)
   PUBMED   15342556
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Tel: 81-3-5449-5343
            Fax: 81-3-5449-5416
            Email: ysuzuki@hgc.jp.
FEATURES             Location/Qualifiers
     source          1. .581
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HSI02082"
                     /tissue_type="small intestine"
                     /clone_lib="Sugano cDNA library, small intestine"
ORIGIN

Alignment Scores:
Pred. No.:                1.16e-31        Length:         581
Score:                    373.50          Matches:        74
Percent Similarity:       84.4%           Conservative:   2
Best Local Similarity:    82.2%           Mismatches:     11
Query Match:              33.1%           Indels:         3
DB:                       3               Gaps:           1

US-10-821-670A-33 (1-222) x BP260963 (1-581)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              |||||||||   |||  ||||||||||||       |||||||||          ||||||
Db        319 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCTC---------CTGGAC 369

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||      ||||||   ||||||||||||   |||
Db        370 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 429

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              |||:::|||||||||   ||||||||||||:::||||||   ||||||||||||||||||
Db        430 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 489

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        490 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 549

Qy         81 LysThrSerThrValGluAlaCysLeuPro 90
              |||||||||||||||||||||||||||||
Db        550 AAAACCAGCACAGTGGAGGCCTGTTTACCA 579

RESULT 13
BI523569
LOCUS       BI523569                 832 bp    mRNA    linear   EST 29-AUG-2001
DEFINITION  603175938F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 5',
            mRNA sequence.
ACCESSION   BI523569
VERSION     BI523569.1  GI:15348361
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominidae; Homo.
REFERENCE  1  (bases 1 to 832)
  AUTHORS  NIH-MGC http://mgc.nci.nih.gov/.
  TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL  Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM11605  row: l  column: 09
           High quality sequence start: 23
           High quality sequence stop: 821.
FEATURES             Location/Qualifiers
     source          1. .832
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240216"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_121"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 017. Note:
                     this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              2.52e-31      Length:         832
Score:                  372.50        Matches:        77
Percent Similarity:     83.2%         Conservative:   2
Best Local Similarity:  81.1%         Mismatches:     12
Query Match:            33.0%         Indels:         4
DB:                     2             Gaps:           1

US-10-821-670A-33 (1-222) x BI523569 (1-832)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              |||||||||   |||   ||||||||||||      |||||||||         ||||||
Db        321 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCTC---------CTGGAC 371

Qy         21 HisLeuSerLeuAlaArg-AsnLeuProThrProThrProSerProGlyMetPheGlnCy 40
              ||||||||||||||||    |||||||||       ||||||   ||||||||||||    ||
Db        372 CACCTCAGTTTGGCCATGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATG 431

Qy         40 sLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGl 60
              ||||:::|||||||||   ||||||||||||:::||||||   ||||||||||||||||||
Db        432 CCTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACA 491

Qy         60 nThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAs 80
              ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        492 AACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGA 551

Qy         80 pLysThrSerThrValGluAlaCysLeuProLeuGluLeuThr 94
              |||||||||||||||||||||||||||||||||||||||||||
Db        552 TAAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACC 594

RESULT 14
AJ820622/c
LOCUS       AJ820622                 778 bp    mRNA    linear   EST 12-MAY-2005
DEFINITION  AJ820622 KN206 Bos sp. cDNA clone C0006020h12, mRNA sequence.
ACCESSION   AJ820622
VERSION     AJ820622.1  GI:51888098
KEYWORDS    EST.
SOURCE      Bos sp.
  ORGANISM  Bos sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 778)
  AUTHORS   McGuire,K. and Glass,E.J.
  TITLE     The expanding role of microarrays in the investigation of
            macrophage responses to pathogens
  JOURNAL   Vet. Immunol. Immunopathol. 105 (3-4), 259-275 (2005)
COMMENT     Contact: McGuire K
            Genomics and Genetics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
            Single pass sequencing. Bases called and trimmed with phred
            v0.020425.c. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options. Vector:pBluescriptII(SK+) R. Site
            1:EcoRV(lost) R. Site 2:NotI Seq Primer: T7 Normalised library
            constructed from pooled monocytes from Bos taurus (Holstein) and
            Bos indicus (Sahiwals) cattle subjected to various stimuli,
            including infection with the protozoan parasite Theileria annulata.
FEATURES             Location/Qualifiers
     source          1. .778
                     /organism="Bos sp."
                     /mol_type="mRNA"
                     /db_xref="taxon:29061"
                     /clone="C0006020h12"
                     /tissue_type="blood"
                     /cell_type="bovine monocyte"
                     /clone_lib="KN206"
                     /note="Vector: pBluescriptII(SK+); Site_1: EcoRV(lost);
                     Site_2: NotI; Normalised library constructed from pooled
                     monocytes from Bos taurus (Holstein) and Bos indicus
                     (Sahiwals) cattle subjected to various stimuli, including
                     infection with the protozoan parasite Theileria annulata"
ORIGIN

Alignment Scores:
Pred. No.:              2.23e-29      Length:         778
Score:                  355.00        Matches:        71
Percent Similarity:     90.8%         Conservative:   8
Best Local Similarity:  81.6%         Mismatches:     8
Query Match:            31.4%         Indels:         0
DB:                     1             Gaps:           0

US-10-821-670A-33 (1-222) x AJ820622 (1-778)

Qy        136 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 155
              ||||||   |||||||||:::||||||||||||||||||||||||||||||||||||||||
Db        777 ATGTACCACGTGGAGTTCCAGGCCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAA 718

Qy        156 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 175
              ||||||||||||||||||||||||   ||||||   ||||||:::||||||||||||||
Db        717 ATCTTTCTAGACCAGAACATGCTGGCAGCTATTGCTGAGCTGATGCAGGCCCTGAATTTC 658

Qy        176 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 195
              :::|||   ||||||||||||       ||||||:::|||   ||||||||||||||||||
Db        657 GACAGTGAGACTGTGCCACAGAAACCCTCCCTGAAAGAACTGGATTTTTACAAGACAAAA 598

Qy        196 IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMet 215
              :::||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        597 GTCAAGCTCTGCATCCTTCTTCACGCCTTCAGAATTCGTGCGGTGACCATCGACAGAATG 538

Qy        216 MetSerTyrLeuAsnAlaSer 222
              ||||||||||||::::::|||
Db        537 ATGAGCTATCTGAGTTCTTCC 517

RESULT 15
BU699383
LOCUS       BU699383                 561 bp    mRNA    linear   EST 09-OCT-2002
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DEFINITION  LL2in11573T7 Hematopoietic Stem Cell Subtracted Library Mus
            musculus cDNA 5' similar to interleukin 12 p35 subunit, mRNA
            sequence.
ACCESSION   BU699383
VERSION     BU699383.1  GI:23615967
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 561)
  AUTHORS   Phillips,R.L., Ernst,R.E., Brunk,B.P., Ivanova,N., Mahan,M.A.,
            Deanehan,J.K., Moore,K.A., Overton,G.C. and Lemischka,I.R.
  TITLE     The genetic program of hematopoietic stem cells
  JOURNAL   Science 288 (5471), 1635-1640 (2000)
   PUBMED   10834841
COMMENT     Contact: Lemischka, Ihor R.
            Department of Molecular Biology
            Princeton University
            Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544, USA
            Tel: 609 258 2838
            Fax: 609 258 2759
            Email: ilemischka@molbio.princeton.edu
            These ESTs are derived from a subtracted cDNA library enriched for
            gene products expressed in day 14-14.5 fetal liver hematopoietic
            stem cells defined as Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E
            (Sca-1)pos
            Seq primer: M13Reverse or T7.
FEATURES             Location/Qualifiers
     source          1. .561
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /tissue_type="Hematopoietic"
                     /cell_type="Stem Cells; Lineageneg/lo, AA4.1pos, cKitpos,
                     Ly6A/E (Sca-1)pos"
                     /dev_stage="Embryonic day 14-14.5"
                     /lab_host="DH10B"
                     /clone_lib="Hematopoietic Stem Cell Subtracted Library"
                     /note="Organ: Fetal Liver; Vector: Sport 1; Site_1: Sal I;
                     Site_2: Not I; Two directionally cloned cDNA libraries
                     were made from fetal liver  hematopoietic stem cells
                     enriched to be Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E
                     (Sca-1)pos called Scapos and from AA4.1neg fetal liver
                     cells. Subtractive hybridization was  performed by
                     hybridization of the target, Scapos, single stranded cDNA
                     library in pSport1 to  biotinylated RNA transcribed from
                     the driver, AA4.1neg cDNA library in pSport2 with  inserts
                     cloned in the complementary orientation. For detailed
                     protocols and additional  information please see our
                     website at http://stemcell.princeton.edu."
ORIGIN

Alignment Scores:
Pred. No.:              5.88e-29        Length:         561
Score:                  349.50          Matches:        76
Percent Similarity:     68.1%           Conservative:   22
Best Local Similarity:  52.8%           Mismatches:     45
Query Match:            31.0%           Indels:         2
DB:                     3               Gaps:           1

US-10-821-670A-33 (1-222) x BU699383 (1-561)

Qy          72 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 91
               :::|||||||||||||||||||:::|||:::|||||||||:::::   ||||||||||||
Db         128 CTCGATCATGAAGACATCACACGGGACCAAACCAGCACATTGAAGACCTGTTTACCACTG 187

Qy          92 GluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGly 111
               ||||||      ||||||||||||||||||:::|||||   |||       |||   |||
Db         188 GAACTACACAAGAACGAGAGTTGCCTGGCTACTAGAGAGACTTCTTCCACAACAAGAGGG 247

Qy         112 SerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyr 131
               |||||||||       :::|||||||||   |||   ||||||||||||   |||||||||
Db         248 AGCTGCCTGCCCCCACAGAAGACGTCTTTGATGATGACCCTGTGCCTTGGTAGCATCTAT 307

Qy         132 GluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAsp 151
               ||||||||||||||||||||||   ||||||:::|||:::|||||   |||
Db         308 GAGGACTTGAAGATGTACCAGACAGAGTTCCAGGCCATCAACGCAGCACTTCAGAATCAC 367

Qy         152 ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGln 171
                     :::|||||||   ||||||:::   ||||||       ||||||||||||:::|||
Db         368 AACCATCAGCAGATCATTCTAGACAAGGGCATGCTGGTGGGCATCGATGAGCTGATGCAG 427

Qy         172 AlaLeuAsnValAsnSer---ValThrValProGlnAsnSerSerLeuGluGluProAsp 190
               :::|||:::   |||         :::      :::   |||         :::
Db         428 TCTCTGGATCATAATGGGCGAGACTCTGCGGCAAAAANCTCCTGTNGGGNGAAGCAGANC 487

Qy         191 PheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaVal 210
               |||:::   ::::::||||||      ||||||:::   |||      |||
Db         488 CTTTACAGAGTGGAAATGAAGCTCTG-NATCTGCTTTACGGCTTTAGCANCCGGTTGTGA 546

Qy         211 ThrIleAsnArg 214
                  :::   |||
Db         547 NCATTAAANAGG 558


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Job time : 2728.99 secs
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 10, 2006, 01:16:39 ; Search time 114.652 Seconds
(without alignments)
5434.532 Million cell updates/sec

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Perfect score: 1129
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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c 2	1129	100.0	666	3	US-09-917-265A-34	Sequence 34, Appl
3	1126	99.7	689	3	US-09-011-143-26	Sequence 26, Appl
4	1126	99.7	689	3	US-09-302-495-26	Sequence 26, Appl
5	1126	99.7	689	3	US-10-079-616-26	Sequence 26, Appl
6	1126	99.7	1441	3	US-09-011-143-8	Sequence 8, Appli
7	1126	99.7	1441	3	US-09-302-495-8	Sequence 8, Appli
8	1126	99.7	1441	3	US-10-079-616-8	Sequence 8, Appli
9	1043	92.4	666	3	US-09-917-265A-46	Sequence 46, Appl
c 10	1043	92.4	666	3	US-09-917-265A-48	Sequence 48, Appl
11	1043	92.4	669	3	US-09-079-984A-12	Sequence 12, Appl
12	1043	92.4	669	3	US-09-390-729-12	Sequence 12, Appl
13	1043	92.4	1455	3	US-09-917-265A-104	Sequence 104, App
c 14	1043	92.4	1455	3	US-09-917-265A-106	Sequence 106, App
15	1014	89.8	669	3	US-09-079-984A-2	Sequence 2, Appli
16	1014	89.8	669	3	US-09-390-729-2	Sequence 2, Appli
17	1002	88.8	1533	3	US-09-917-265A-43	Sequence 43, Appl
c 18	1002	88.8	1533	3	US-09-917-265A-45	Sequence 45, Appl
19	1002	88.8	1599	3	US-09-917-265A-38	Sequence 38, Appl
c 20	1002	88.8	1599	3	US-09-917-265A-40	Sequence 40, Appl
21	1001	88.7	591	3	US-09-917-265A-35	Sequence 35, Appl
c 22	1001	88.7	591	3	US-09-917-265A-37	Sequence 37, Appl
23	998	88.4	591	3	US-09-011-143-9	Sequence 9, Appli
24	998	88.4	591	3	US-09-302-495-9	Sequence 9, Appli
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26	961	85.1	1533	3	US-09-917-265A-66	Sequence 66, Appl
c 27	961	85.1	1533	3	US-09-917-265A-68	Sequence 68, Appl
28	961	85.1	1599	3	US-09-917-265A-61	Sequence 61, Appl
c 29	961	85.1	1599	3	US-09-917-265A-63	Sequence 63, Appl
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44	957.5	84.8	4521	5	US-09-543-679A-2893	Sequence 2893, Ap
45	951.5	84.3	721	2	US-08-184-009-199	Sequence 199, App

ALIGNMENTS

RESULT 1
US-09-917-265A-32
; Sequence 32, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(666)
US-09-917-265A-32

Alignment Scores:

Pred. No.:	3.55e-137	Length:	666
Score:	1129.00	Matches:	222
Percent Similarity:	100.0%	Conservative:	0
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Query Match:	100.0%	Indels:	0
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Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
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RESULT 2
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; Sequence 34, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-34

Alignment Scores:
Pred. No.:              3.55e-137     Length:          666
Score:                  1129.00       Matches:         222
Percent Similarity:     100.0%        Conservative:    0
Best Local Similarity:  100.0%        Mismatches:      0
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Qy        221 AlaSer 222
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RESULT 3
US-09-011-143-26
; Sequence 26, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
```

```
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  26:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  689 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-26

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Pred. No.:              9.22e-137      Length:         689
Score:                  1126.00        Matches:        221
Percent Similarity:     100.0%         Conservative:   1
Best Local Similarity:  99.5%          Mismatches:     0
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Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
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Db        367 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 426

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
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Db        427 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 486

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
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Db        487 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 546

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
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Db        547 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 606

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
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Db        607 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666

Qy        221 AlaSer 222
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Db        667 TCTTCC 672

RESULT 4
US-09-302-495-26
; Sequence 26, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 26:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 689 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-302-495-26

Alignment Scores:
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Pred. No.:              9.22e-137       Length:         689
Score:                  1126.00         Matches:        221
Percent Similarity:     100.0%          Conservative:   1
Best Local Similarity:  99.5%           Mismatches:     0
Query Match:            99.7%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-33 (1-222) x US-09-302-495-26 (1-689)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7 ATGTGCCCCCCCCCGTGGCCTCCTCCTGGTGACCATCCTGGTCCTGCTGAACCACCTGGAC 66

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 126

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 186

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 246

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 AAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTG 306

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 366

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 426

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 486

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 546

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 606

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666

Qy        221 AlaSer 222
              :::|||
Db        667 TCTTCC 672

RESULT 5
US-10-079-616-26
; Sequence 26, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 26:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 689 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-079-616-26

Alignment Scores:
Pred. No.:              9.22e-137       Length:         689
Score:                  1126.00         Matches:        221
Percent Similarity:     100.0%          Conservative:   1
Best Local Similarity:  99.5%           Mismatches:     0
Query Match:            99.7%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-33 (1-222) x US-10-079-616-26 (1-689)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7 ATGTGCCCCCCCCCGTGGCCTCCTCCTGGTGACCATCCTGGTCCTGCTGAACCACCTGGAC 66

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 126

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 186

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 246

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 AAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTG 306

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 366

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 426
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Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 486

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 546

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 606

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666

Qy        221 AlaSer 222
              :::|||
Db        667 TCTTCC 672

RESULT 6
US-09-011-143-8
; Sequence 8, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1441 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-8

Alignment Scores:
Pred. No.:              3.05e-136      Length:        1441
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Score:                  1126.00        Matches:       221
Percent Similarity:     100.0%         Conservative:  1
Best Local Similarity:  99.5%          Mismatches:    0
Query Match:            99.7%          Indels:        0
DB:                     3              Gaps:          0

US-10-821-670A-33 (1-222) x US-09-011-143-8 (1-1441)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
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Db        743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

Qy        221 AlaSer 222
              :::|||
Db        803 TCTTCC 808

RESULT 7
US-09-302-495-8
; Sequence 8, Application US/09302495
; Patent No. 6518045
;  GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
```

```
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;    INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1441 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-302-495-8

Alignment Scores:
Pred. No.:                3.05e-136      Length:          1441
Score:                    1126.00        Matches:         221
Percent Similarity:       100.0%         Conservative:    1
Best Local Similarity:    99.5%          Mismatches:      0
Query Match:              99.7%          Indels:          0
DB:                       3              Gaps:            0

US-10-821-670A-33 (1-222) x US-09-302-495-8 (1-1441)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

Qy        221 AlaSer 222
              :::|||
Db        803 TCTTCC 808

RESULT 8
US-10-079-616-8
; Sequence 8, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;    INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1441 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-079-616-8

Alignment Scores:
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Pred. No.:              3.05e-136       Length:         1441
Score:                  1126.00         Matches:        221
Percent Similarity:     100.0%          Conservative:   1
Best Local Similarity:  99.5%           Mismatches:     0
Query Match:            99.7%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-33 (1-222) x US-10-079-616-8 (1-1441)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

Qy        221 AlaSer 222
              :::|||
Db        803 TCTTCC 808

RESULT 9
US-09-917-265A-46
; Sequence 46, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
;
; SEQ ID NO 46
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
US-09-917-265A-46

Alignment Scores:
Pred. No.:              5.63e-126       Length:         666
Score:                  1043.00         Matches:        204
Percent Similarity:     95.9%           Conservative:   9
Best Local Similarity:  91.9%           Mismatches:     9
Query Match:            92.4%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-33 (1-222) x US-09-917-265A-46 (1-666)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||:::  ||||||:::|||||||||  :::||||||||||||:::|||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||  |||  |||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              |||||||||  ||||||||||||||||||||||||||||||||||||||:::|||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||
Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||:::|||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        221 AlaSer 222
              :::|||
Db        661 TCTTCC 666

RESULT 10
US-09-917-265A-48/c
; Sequence 48, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
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;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-48

Alignment Scores:
Pred. No.:              5.63e-126       Length:         666
Score:                  1043.00         Matches:        204
Percent Similarity:     95.9%           Conservative:   9
Best Local Similarity:  91.9%           Mismatches:     9
Query Match:            92.4%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-33 (1-222) x US-09-917-265A-48 (1-666)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db        666 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 607

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||:::   ||||||:::|||||||||   :::|||||||||||:::|||||||||
Db        606 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 547

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||   ||||||||||:::||||||||||||||||||||||||||||||
Db        546 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 427

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||   |||   |||
Db        366 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 307

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              |||||||||   ||||||||||||||||||||||||||||||||||||||||:::|||
Db        306 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 247

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 187

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              |||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        186 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 127

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||:::|||||||||||||||||||||||
Db         66 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 7

Qy        221 AlaSer 222
              :::|||
Db          6 TCTTCC 1
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RESULT 11
US-09-079-984A-12
; Sequence 12, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,984A
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  669 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 666
;      IDENTIFICATION METHOD:  Similarity
US-09-079-984A-12

Alignment Scores:
Pred. No.:              5.67e-126       Length:         669
Score:                  1043.00         Matches:        204
Percent Similarity:     95.9%           Conservative:   9
Best Local Similarity:  91.9%           Mismatches:     9
Query Match:            92.4%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-33 (1-222) x US-09-079-984A-12 (1-669)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||:::   ||||||:::|||||||||   :::|||||||||||:::|||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||   ||||||||||:::||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
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                ||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||   |||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
               |||||||||  ||||||||||||||||||||||||||||||||||||||||||:::|||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
               ||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
               ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
               ||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        221 AlaSer 222
               :::|||
Db        661 TCTTCC 666
```

RESULT 12
US-09-390-729-12
; Sequence 12, Application US/09390729
; Patent No. 6562334
; GENERAL INFORMATION:
; APPLICANT: Okano, Fumiyoshi, Satoh, Massahiro,
; APPLICANT: Yamada, Katsushige
; TITLE OF INVENTION: Canine interleukin 12, a production method
; TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
; TITLE OF INVENTION: method using it
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Miller & Christenbury Intellectual Property
; ADDRESSEE: Department of Schnader, Harrison, Segal and Lewis, LLP
; STREET: 1600 Market Street, 39th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/390,729
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/079,984
; FILING DATE: 15-MAY-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Austin R. Miller
; REGISTRATION NUMBER: 16,602
; REFERENCE/DOCKET NUMBER: 1051-98
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-1810
; TELEFAX: (215) 568-6946
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 669 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: Canine IL12
; LOCATION: 1 to 666
; IDENTIFICATION METHOD: Similarity
US-09-390-729-12

Alignment Scores:

Pred. No.:	5.67e-126	Length:	669
Score:	1043.00	Matches:	204
Percent Similarity:	95.9%	Conservative:	9
Best Local Similarity:	91.9%	Mismatches:	9
Query Match:	92.4%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-33 (1-222) x US-09-390-729-12 (1-669)

```
Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||:::  ||||||:::|||||||||  :::|||||||||||:::|||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||  ||||||||||:::||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||   |||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              |||||||||  ||||||||||||||||||||||||||||||||||||||||||:::|||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        221 AlaSer 222
              :::|||
Db        661 TCTTCC 666
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RESULT 13

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US-09-917-265A-104
; Sequence 104, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 104
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (232)..(897)
US-09-917-265A-104

Alignment Scores:
Pred. No.:              2e-125          Length:         1455
Score:                  1043.00         Matches:        204
Percent Similarity:     95.9%           Conservative:   9
Best Local Similarity:  91.9%           Mismatches:     9
Query Match:            92.4%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-33 (1-222) x US-09-917-265A-104 (1-1455)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
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Db        232 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 291

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
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Db        292 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 351

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||   ||||||||||:::|||||||||||||||||||||||||||||||
Db        352 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 411

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 471

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 531

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||   |||   |||
Db        532 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 591

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||:::|||
Db        592 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 651

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 711

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
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Db        712 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 771

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        772 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 831

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||||
Db        832 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 891

Qy        221 AlaSer 222
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Db        892 TCTTCC 897

RESULT 14
US-09-917-265A-106/c
; Sequence 106, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 106
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-106

Alignment Scores:
Pred. No.:              2e-125          Length:         1455
Score:                  1043.00         Matches:        204
Percent Similarity:     95.9%           Conservative:   9
Best Local Similarity:  91.9%           Mismatches:     9
Query Match:            92.4%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-33 (1-222) x US-09-917-265A-106 (1-1455)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
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Db       1224 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 1165

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||:::   ||||||:::|||||||||   :::|||||||||||||:::|||||||||
Db       1164 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 1105

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||   ||||||||||:::|||||||||||||||||||||||||||||||
Db       1104 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 1045

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1044 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 985

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        984 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 925

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||   |||   |||
Db        924 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 865

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||:::|||
Db        864 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 805

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        804 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 745
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Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        744 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 685

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 625

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
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Db        624 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 565

Qy        221 AlaSer 222
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Db        564 TCTTCC 559

RESULT 15
US-09-079-984A-2
; Sequence 2, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,984A
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  669 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 666
;      IDENTIFICATION METHOD:  Similarity
US-09-079-984A-2

Alignment Scores:
Pred. No.:              3.39e-122      Length:          669
Score:                  1014.00        Matches:         199
Percent Similarity:     94.1%          Conservative:    10
Best Local Similarity:  89.6%          Mismatches:      13
Query Match:            89.8%          Indels:          0
DB:                     3              Gaps:            0
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Db          1 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTCGCTACCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||:::   ||||||:::|||||||||   :::|||||||||||||:::|||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||   ||||||||||||:::||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
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Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||   |||   |||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              |||||||||   ||||||||||||||||||||||||||||||||||||||:::|||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        481 AACATGCTGACGGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||:::|||||||||||||||||||:::
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGACAGAATGATGAGCTATCTGAGT 660

Qy        221 AlaSer 222
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Db        661 TCTTCC 666


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Job time : 119.652 secs
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

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Run on: June 10, 2006, 01:18:38 ; Search time 868.637 Seconds
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	3	1129	100.0	666	9	US-10-821-670-32	Sequence 32, Appl
c	4	1129	100.0	666	9	US-10-821-670-34	Sequence 34, Appl
	5	1126	99.7	689	6	US-10-079-616-26	Sequence 26, Appl
	6	1126	99.7	1441	6	US-10-079-616-8	Sequence 8, Appli
	7	1108	98.1	669	7	US-10-041-672C-2	Sequence 2, Appli
	8	1043	92.4	666	3	US-09-917-265-46	Sequence 46, Appl
c	9	1043	92.4	666	3	US-09-917-265-48	Sequence 48, Appl
	10	1043	92.4	666	9	US-10-821-670-46	Sequence 46, Appl
c	11	1043	92.4	666	9	US-10-821-670-48	Sequence 48, Appl
	12	1043	92.4	1455	3	US-09-917-265-104	Sequence 104, App
c	13	1043	92.4	1455	3	US-09-917-265-106	Sequence 106, App
	14	1043	92.4	1455	9	US-10-821-670-104	Sequence 104, App
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	16	1002	88.8	1533	3	US-09-917-265-43	Sequence 43, Appl
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	18	1002	88.8	1533	9	US-10-821-670-43	Sequence 43, Appl
c	19	1002	88.8	1533	9	US-10-821-670-45	Sequence 45, Appl
	20	1002	88.8	1599	3	US-09-917-265-38	Sequence 38, Appl
c	21	1002	88.8	1599	3	US-09-917-265-40	Sequence 40, Appl
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c	25	1001	88.7	591	3	US-09-917-265-37	Sequence 37, Appl
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	28	998	88.4	591	6	US-10-079-616-9	Sequence 9, Appli
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	31	961	85.1	1533	9	US-10-821-670-66	Sequence 66, Appl
c	32	961	85.1	1533	9	US-10-821-670-68	Sequence 68, Appl
	33	961	85.1	1599	3	US-09-917-265-61	Sequence 61, Appl
c	34	961	85.1	1599	3	US-09-917-265-63	Sequence 63, Appl
	35	961	85.1	1599	9	US-10-821-670-61	Sequence 61, Appl
c	36	961	85.1	1599	9	US-10-821-670-63	Sequence 63, Appl
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	38	957.5	84.8	762	9	US-10-785-577-21	Sequence 21, Appl
	39	957.5	84.8	762	9	US-10-688-845-57	Sequence 57, Appl
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ALIGNMENTS

RESULT 1
US-09-917-265-32
; Sequence 32, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(666)
; OTHER INFORMATION:
US-09-917-265-32

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Alignment Scores:
Pred. No.:              1.11e-135       Length:         666
Score:                  1129.00         Matches:        222
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-33 (1-222) x US-09-917-265-32 (1-666)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        221 AlaSer 222
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Db        661 GCTTCC 666

RESULT 2
US-09-917-265-34/c
; Sequence 34, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-34

Alignment Scores:
Pred. No.:              1.11e-135       Length:         666
Score:                  1129.00         Matches:        222
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-33 (1-222) x US-09-917-265-34 (1-666)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 607

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 547

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 427

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 307

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 247

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 187

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 127

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 7

Qy        221 AlaSer 222
              ||||||
Db          6 GCTTCC 1

RESULT 3
US-10-821-670-32
; Sequence 32, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
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;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
US-10-821-670-32

Alignment Scores:
Pred. No.:              1.11e-135      Length:         666
Score:                  1129.00        Matches:        222
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     9              Gaps:           0

US-10-821-670A-33 (1-222) x US-10-821-670-32 (1-666)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        221 AlaSer 222
              ||||||
Db        661 GCTTCC 666
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RESULT 4
US-10-821-670-34/c
; Sequence 34, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-34

Alignment Scores:
Pred. No.:              1.11e-135      Length:         666
Score:                  1129.00        Matches:        222
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     9              Gaps:           0

US-10-821-670A-33 (1-222) x US-10-821-670-34 (1-666)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
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Db        666 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 607

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 547

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 427

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 307

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 247

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 187

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 127

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67
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Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 7

Qy        221 AlaSer 222
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Db          6 GCTTCC 1

RESULT 5
US-10-079-616-26
; Sequence 26, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 26:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 689 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-079-616-26

Alignment Scores:
Pred. No.:              2.89e-135      Length:         689
Score:                  1126.00        Matches:        221
Percent Similarity:     100.0%         Conservative:   1
Best Local Similarity:  99.5%          Mismatches:     0
Query Match:            99.7%          Indels:         0
DB:                     6              Gaps:           0

US-10-821-670A-33 (1-222) x US-10-079-616-26 (1-689)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
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Db          7 ATGTGCCCCCCCCCGTGGCCTCCTCCTGGTGACCATCCTGGTCCTGCTGAACCACCTGGAC 66

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 126

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 186

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 246

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 AAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTG 306

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 366

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 426

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 486

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 546

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 606

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666

Qy        221 AlaSer 222
              ::::|||
Db        667 TCTTCC 672

RESULT 6
US-10-079-616-8
; Sequence 8, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
```

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;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;    INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1441 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-079-616-8

Alignment Scores:
Pred. No.:              9.72e-135       Length:         1441
Score:                  1126.00         Matches:        221
Percent Similarity:     100.0%          Conservative:   1
Best Local Similarity:  99.5%           Mismatches:     0
Query Match:            99.7%           Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-33 (1-222) x US-10-079-616-8 (1-1441)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

Qy        221 AlaSer 222
              :::|||
Db        803 TCTTCC 808

RESULT 7
US-10-041-672C-2
; Sequence 2, Application US/10041672C
; Publication No. US20030157059A1
; GENERAL INFORMATION:
;  APPLICANT: Mologen Forschungs-, Entwicklungs- und Vetriebs GmbH
;  APPLICANT:  Universitat Zurich
;  TITLE OF INVENTION: FELINE INTERLEUKIN-12 AS IMMUNOSTIMULANT
;  FILE REFERENCE: NHL-NP-36
;  CURRENT APPLICATION NUMBER: US/10/041,672C
;  CURRENT FILING DATE:  2002-01-08
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 669
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: feline IL-12 p35
US-10-041-672C-2

Alignment Scores:
Pred. No.:              6e-133          Length:         669
Score:                  1108.00         Matches:        217
Percent Similarity:     98.2%           Conservative:   1
Best Local Similarity:  97.7%           Mismatches:     4
Query Match:            98.1%           Indels:         0
DB:                     7               Gaps:           0

US-10-821-670A-33 (1-222) x US-10-041-672C-2 (1-669)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||    ||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCT 360

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
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Db        481 AACATGCTGACAGCTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200

Db        541 CCACAGAACTCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220

Db        601 CTTCTTCATGCTTTCAGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        221 AlaSer 222

Db        661 GCTTCC 666

RESULT 8
US-09-917-265-46
; Sequence 46, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
;   OTHER INFORMATION:
US-09-917-265-46

Alignment Scores:
Pred. No.:              1.66e-124       Length:         666
Score:                  1043.00         Matches:        204
Percent Similarity:     95.9%           Conservative:   9
Best Local Similarity:  91.9%           Mismatches:     9
Query Match:            92.4%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-33 (1-222) x US-09-917-265-46 (1-666)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20

Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40

Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60

Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80

Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100

Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120

Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140

Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160

Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180

Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200

Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220

Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        221 AlaSer 222

Db        661 TCTTCC 666

RESULT 9
US-09-917-265-48/c
; Sequence 48, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-48

Alignment Scores:
Pred. No.:              1.66e-124       Length:         666
Score:                  1043.00         Matches:        204
Percent Similarity:     95.9%           Conservative:   9
Best Local Similarity:  91.9%           Mismatches:     9
Query Match:            92.4%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-33 (1-222) x US-09-917-265-48 (1-666)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20

Db        666 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 607

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40

Db        606 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 547

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60

Db        546 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80

Db        486 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 427

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
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Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db        666 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 607

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              |||||||:::   ||||||:::|||||||||   :::|||||||||||:::|||||||||
Db        606 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 547

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||   ||||||||||||:::||||||||||||||||||||||||||||
Db        546 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 427

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||   |||   |||
Db        366 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 307

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              |||||||||   ||||||||||||||||||||||||||||||||||||||:::|||
Db        306 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 247

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 187

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        186 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 127

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||||
Db         66 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 7

Qy        221 AlaSer 222
              :::|||
Db          6 TCTTCC 1
```

RESULT 12
US-09-917-265-104
; Sequence 104, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(897)
; OTHER INFORMATION:
US-09-917-265-104

Alignment Scores:

Pred. No.:	5.99e-124	Length:	1455
Score:	1043.00	Matches:	204
Percent Similarity:	95.9%	Conservative:	9
Best Local Similarity:	91.9%	Mismatches:	9
Query Match:	92.4%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-33 (1-222) x US-09-917-265-104 (1-1455)

```
Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db        232 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 291

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              |||||||:::   ||||||:::|||||||||   :::|||||||||||:::|||||||||
Db        292 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 351

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||   ||||||||||||:::||||||||||||||||||||||||||||
Db        352 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 411

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 471

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 531

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||   |||   |||
Db        532 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 591

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              |||||||||   ||||||||||||||||||||||||||||||||||||||:::|||
Db        592 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 651

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 711

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        712 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 771

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        772 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 831

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||||
Db        832 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 891

Qy        221 AlaSer 222
              :::|||
Db        892 TCTTCC 897
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RESULT 13
US-09-917-265-106/c
; Sequence 106, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 106
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-106

Alignment Scores:
Pred. No.:              5.99e-124       Length:         1455
Score:                  1043.00         Matches:        204
Percent Similarity:     95.9%           Conservative:   9
Best Local Similarity:  91.9%           Mismatches:     9
Query Match:            92.4%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-33 (1-222) x US-09-917-265-106 (1-1455)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              |||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db       1224 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 1165

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||:::   ||||||:::|||||||||   :::|||||||||||:::|||||||||
Db       1164 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 1105

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||   ||||||||||:::|||||||||||||||||||||||||||||
Db       1104 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 1045

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   |||||||||||||||||||||||||||||||||||||||||||||||
Db       1044 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 985

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        984 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 925

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||   |||   |||
Db        924 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 865

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              |||||||||   |||||||||||||||||||||||||||||||||||||||:::|||
Db        864 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 805

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        804 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 745

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        744 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 685

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 625

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||:::|||||||||||||||||||||||
Db        624 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 565

Qy        221 AlaSer 222
              :::|||
Db        564 TCTTCC 559

RESULT 14
US-10-821-670-104
; Sequence 104, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 104
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (232)..(897)
US-10-821-670-104

Alignment Scores:
Pred. No.:              5.99e-124       Length:         1455
Score:                  1043.00         Matches:        204
Percent Similarity:     95.9%           Conservative:   9
Best Local Similarity:  91.9%           Mismatches:     9
Query Match:            92.4%           Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-33 (1-222) x US-10-821-670-104 (1-1455)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
              |||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db        232 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 291

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||:::   ||||||:::|||||||||   :::|||||||||||:::|||||||||
Db        292 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 351

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||   ||||||||||:::|||||||||||||||||||||||||||||
Db        352 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 411

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   |||||||||||||||||||||||||||||||||||||||||||||||
Db        412 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 471

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 531

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||   |||   |||
Db        532 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 591

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              |||||||||   |||||||||||||||||||||||||||||||||||||||:::|||
Db        592 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 651

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 711

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        712 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 771

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        772 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 831

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||:::|||||||||||||||||||||||
Db        832 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 891

Qy        221 AlaSer 222
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Db        892 TCTTCC 897
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RESULT 15
US-10-821-670-106/c
; Sequence 106, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 106
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-106

Alignment Scores:
Pred. No.:              5.99e-124       Length:         1455
Score:                  1043.00         Matches:        204
Percent Similarity:     95.9%           Conservative:   9
Best Local Similarity:  91.9%           Mismatches:     9
Query Match:            92.4%           Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-33 (1-222) x US-10-821-670-106 (1-1455)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAsp 20
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Db       1224 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 1165

Qy         21 HisLeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCys 40
              ||||||:::  ||||||:::|||||||||  :::|||||||||||:::|||||||||
Db       1164 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 1105

Qy         41 LeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||  ||||||||||||:::||||||||||||||||||||||||||||
Db       1104 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 1045

Qy         61 ThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1044 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 985

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        984 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 925

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||   |||   |||
Db        924 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 865

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
              |||||||||  ||||||||||||||||||||||||||||||||||||||||||:::|||
Db        864 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 805

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        804 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 745

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        744 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 685

Qy        181 ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 625

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||:::|||||||||||||||||||||
Db        624 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 565

Qy        221 AlaSer 222
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Db        564 TCTTCC 559


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(without alignments)
3659.318 Million cell updates/sec

Title: US-10-821-670A-33
Perfect score: 1129
Sequence: 1 MCPPRGLLLVTILVLLNHLD.....HAFRIRAVTINRMMSYLNAS 222

Scoring table: BLOSUM62
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Searched: 253354 seqs, 63461778 residues

Total number of hits satisfying chosen parameters: 506708

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	2	92.5	8.2	2366	7	US-11-293-697-1960	Sequence 1960, Ap
	3	90	8.0	2480	6	US-10-953-349-35629	Sequence 35629, A
	4	86	7.6	1836	7	US-11-217-529-2301	Sequence 2301, Ap
	5	86	7.6	2310	7	US-11-217-529-4722	Sequence 4722, Ap
	6	85	7.5	1875	7	US-11-217-529-174200	Sequence 174200,
	7	84	7.4	990	7	US-11-217-529-79916	Sequence 79916, A
	8	84	7.4	2406	7	US-11-217-529-76395	Sequence 76395, A
c	9	83	7.4	1647	6	US-10-953-349-3750	Sequence 3750, Ap
	10	83	7.4	5198	6	US-10-505-928-342	Sequence 342, App
	11	82.5	7.3	2289	7	US-11-122-986-339	Sequence 339, App
	12	82.5	7.3	2292	7	US-11-122-986-337	Sequence 337, App
	13	82	7.3	9588	6	US-10-505-928-101	Sequence 101, App
c	14	80	7.1	1798	6	US-10-953-349-5587	Sequence 5587, Ap
	15	80	7.1	1956	7	US-11-217-529-76747	Sequence 76747, A
	16	79	7.0	762	7	US-11-217-529-166587	Sequence 166587,
	17	79	7.0	2244	7	US-11-217-529-78602	Sequence 78602, A
	18	79	7.0	3405	7	US-11-217-529-77844	Sequence 77844, A
	19	79	7.0	6429	7	US-11-217-529-4027	Sequence 4027, Ap
	20	78.5	7.0	1448	6	US-10-953-349-28874	Sequence 28874, A
	21	78	6.9	3228	7	US-11-217-529-190982	Sequence 190982,
	22	78	6.9	3741	7	US-11-217-529-78696	Sequence 78696, A
	23	78	6.9	4080	7	US-11-217-529-1846	Sequence 1846, Ap
	24	78	6.9	4573	6	US-10-505-928-409	Sequence 409, App
	25	78	6.9	4585	6	US-10-505-928-47	Sequence 47, Appl
	26	77.5	6.9	1374	6	US-10-953-349-13043	Sequence 13043, A
	27	77.5	6.9	2463	7	US-11-217-529-79273	Sequence 79273, A
	28	77.5	6.9	2583	7	US-11-217-529-5733	Sequence 5733, Ap
c	29	77.5	6.9	3403	7	US-11-145-307A-74	Sequence 74, Appl
	30	77.5	6.9	28605	6	US-10-471-571A-4495	Sequence 4495, Ap
	31	77	6.8	1371	7	US-11-264-784-37	Sequence 37, Appl
	32	77	6.8	1371	7	US-11-264-737-42	Sequence 42, Appl
	33	77	6.8	1371	7	US-11-265-761-37	Sequence 37, Appl
	34	77	6.8	1473	7	US-11-217-529-81075	Sequence 81075, A
c	35	77	6.8	1542	7	US-11-217-529-4965	Sequence 4965, Ap
	36	77	6.8	2490	7	US-11-217-529-3503	Sequence 3503, Ap
c	37	76	6.7	1488	6	US-10-953-349-7853	Sequence 7853, Ap
	38	75.5	6.7	951	7	US-11-217-529-3315	Sequence 3315, Ap
	39	75.5	6.7	1567	6	US-10-953-349-2350	Sequence 2350, Ap
	40	75.5	6.7	1613	6	US-10-953-349-23055	Sequence 23055, A
	41	75.5	6.7	1902	7	US-11-217-529-78885	Sequence 78885, A
	42	75.5	6.7	2733	7	US-11-217-529-76578	Sequence 76578, A
c	43	75	6.6	1509	7	US-11-217-529-174422	Sequence 174422,
	44	75	6.6	1953	7	US-11-217-529-984	Sequence 984, App
	45	75	6.6	2025	7	US-11-217-529-507	Sequence 507, App

ALIGNMENTS

RESULT 1
US-11-293-697-1794
; Sequence 1794, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1794
; LENGTH: 1751
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-1794

Alignment Scores:

Pred. No.:	0.0974	Length:	1751
Score:	95.00	Matches:	51
Percent Similarity:	36.9%	Conservative:	36
Best Local Similarity:	21.6%	Mismatches:	87
Query Match:	8.4%	Indels:	62
DB:	7	Gaps:	10

US-10-821-670A-33 (1-222) x US-11-293-697-1794 (1-1751)

```
Qy          4 ProArgGlyLeuLeuLeuValThrIle------LeuValLeuLeuAsnHisLeuAspHis 21
              |||:::   |||||||||:::            :::|||||||:::   :::|||
Db        198 CCCAAGATTCTGCTACTGCTCCTATTTTTTGGAGTTGTCCTGGTCATCTACTTGGCCCCC 257
```

```
Qy          22 LeuSerLeuAla--------------------ArgAsnLeuProThrProThrProSer 34
               |||   ::::::                    |||:::||||||         |||
Db         258 CTATGCATCTCCTCACCCTGCATCATGGAACCCAGAGACTTACCA---------CCCAAG 308

Qy          35 ProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThr 54
               ||||||:::         :::   |||             :::   |||      ||||||
Db         309 CCTGGGCTG---------GTGGGACACCGAGGGGCCCCCATGCTGGCTCCCGAGAACACC 359

Qy          55 LeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAsp--- 73
               |||         |||:::|||   |||           |||       |||   |||
Db         360 CTGATGTCCTTGCGGAAGACAGCTGAA---TGCGGAGCTACTGTGTTTGAGACTGATGTG 416

Qy          74 ------------------------------HisGluAspIleThrLysAspLysThrSer 83
                                            |||                 :::|||:::
Db         417 ATGGTCAGCTCCGATGGGGTCCCCTTCCTCATGCATGATGAGCACCTCAGCAGGACCACG 476

Qy          84 ThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArg 103
               |||   :::      |||       :::|||   :::   |||       :::
Db         477 AATGTAGCCTCTGTATTCCCAACCCGAATCACAGCCCACAGCAGTGACTTCTCCTGGACT 536

Qy         104 GluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLys--------------- 118
               |||:::      :::      ||||||              ||:::
Db         537 GAACTGAAGAGACTCAATGCTGGATCCTGGTTCCTAGAGAGGCGACCCTTCTGGGGGGCC 596

Qy         119 ------------------------------ThrSerPheMetThrThrLeuCysLeuSer 128
                                                  |||         |||
Db         597 AAACCGCTGGCAGGCCCTGATCAGAAAGAGGCTGAGAGTCAGACGGTACCAGCATTAGAA 656

Qy         129 SerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeu 148
               :::   |||                  |||      |||:::|||      :::
Db         657 GAGCTATTGGAG--------------------GAAGCTGCAGCCCTCAACCTTTCCATC 695

Qy         149 LeuMetAsp------------ProLysArgGlnIlePheLeuAspGlnAsnMetLeuThr 164
               :::   |||            |||:::       :::   |||       ::::::
Db         696 ATGTTCGACTTGCGCCGACCCCCACAGAACCACACATACTATGACACTTTTGTGATCCAG 755

Qy         165 AlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerVal------------------ 178
               ::::::   :::|||   |||             ::::::
Db         756 ACATTGGAGACTGTGCTGAATGCAAGGGTGCCCCAAGCCATGGTGATGTTGCCAGGACCC 815

Qy         179 ---------ThrValProGlnAsnSerSerLeuGluGluProAspPhe 191
                        |||:::|||               :::|||   ||||||
Db         816 CCTCTCCCCACCCTGCCTTCCCTAGGCCATGATGATGAGGATGATTTT 863
```

RESULT 2
US-11-293-697-1960
; Sequence 1960, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1960
; LENGTH: 2366
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-1960

Alignment Scores:

Pred. No.:	0.298	Length:	2366
Score:	92.50	Matches:	47
Percent Similarity:	38.7%	Conservative:	30
Best Local Similarity:	23.6%	Mismatches:	85
Query Match:	8.2%	Indels:	37
DB:	7	Gaps:	9

US-10-821-670A-33 (1-222) x US-11-293-697-1960 (1-2366)

```
Qy          29 ProThrProThrProSerProGlyMetPheGlnCysLeuAsn------HisSerGlnThr 46
               |||       |||             :::|||:::   ::::::            :::
Db         883 CCAGAAAGCACCCAGGAGGAAAGATTGTTTGAATTAGTAAGTGATTTTGATCGTAAAGAA 942

Qy          47 LeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSer 66
               |||:::      :::|||::::::|||                    |||      :::|||
Db         943 TTGATGAACCCATTGAGTGACTCTCTTAGTTCCATATCAATACCTTTGAATTCCTGGTCG 1002

Qy          67 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 86
                                    |||   |||:::   :::|||                :::
Db        1003 GCATGT--------------CATAGAGATTTACTAGAAGAT---------GCAAAAGAT 1038

Qy          87 AlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSer 106
                  ||||||   ||||||            :::   |||:::      ::::::
Db        1039 GATGCATTGCCAGCTGAGTTATTGGAAGCCCTGAACACATTGTCAGAAGCCAAGGTGGAA 1098

Qy         107 LeuIleThrAsn-----------GlySerCysLeuAlaSerArgLysThrSerPheMet 122
                  |||   :::            ||||||   |||   :::|||
Db        1099 ACCATCTGTCACAGAAAAGAGGGAGGTAGCAGTCTCATTGCCAGAAATGAATGTTTAGAA 1158

Qy         123 ThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLys 142
                           |||   ||||||
Db        1159 GTGGAGTTCAATACGTCTCAGACCAATGAAGATTGTACACAAATA--------------- 1203

Qy         143 AlaMetAsnAlaLysLeuLeuMetAspProLys---------ArgGlnIlePheLeuAsp 159
                  |||:::   |||   ||||||                  |||
Db        1204 ---------GCAGAGACTCTGCAAGACCCAAATCCATCTGGATTGCAAACTTTGGCTCAT 1254

Qy         160 GlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThr 179
               ||||||   :::|||:::   :::   |||             |||   ||||||||||||
Db        1255 CAAAAT---ATCACTTCTTGTGAGCCACTAAGTAATAAGAGAAATTCAAATTCAGTGACA 1311

Qy         180 ValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCys 199
                     |||||||||   :::|||                                |||
Db        1312 ---------AATAGCTCTGATCAGGAA-----------------------ACTGCGTGT 1338

Qy         200 IleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArgMetMetSerTyr 218
               :::|||      :::   |||:::      :::   ::::::|||         |||
Db        1339 GTGTTGAGGAGATCATCCAGACTAGAAAAACTGAAAGTAAGCAGAGATGCAAAGTAC 1395
```

RESULT 3
US-10-953-349-35629
; Sequence 35629, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35629
; LENGTH: 2480
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (601)..(601)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (603)..(603)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (621)..(621)
; OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-35629

```
Alignment Scores:
Pred. No.:                0.624          Length:          2480
Score:                    90.00          Matches:           38
Percent Similarity:       43.3%          Conservative:      33
Best Local Similarity:    23.2%          Mismatches:        60
Query Match:              8.0%           Indels:            34
DB:                       6              Gaps:               6

US-10-821-670A-33 (1-222) x US-10-953-349-35629 (1-2480)

Qy         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
              |||   |||   ::::::|||      |||   ::::::            :::
Db       1328 TATCTTTGCTTGACCAAGGAAGCAACGCACAACAATCTATTGTTGCACTTGAGCAGGAAA 1387

Qy         85 ValGluAlaCysLeuProLeu--------------------------GluLeuThrMet 95
              :::   :::   :::   |||                        |||||||||
Db       1388 TTGCACTCCTCAGTCAGTTTGAACATGAAAATATAGTCCAGTATTATGGAACTGACAAG- 1446

Qy         96 AsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAla 115
              ||||||   |||         |||   |||:::|||   ||||||
Db       1447 GAAGAATCCAAACTCTATATT---TTTATTGAGCTTGTCACGCAAGGATCT--------- 1494

Qy        116 SerArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLys 135
                                        |||||||||:::|||:::      |||
Db       1495 --------------------------------CTTTCATCCCTCTACCAAAAGTATAAA 1521

Qy        136 MetTyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGln 155
              :::   :::   :::      |||         ::::::|||
Db       1522 CTACGAGAATCACAAGTCTCTGCATACACAAGGCAGATTCTT---------AACGGATTG 1572

Qy        156 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 175
              ::::::|||   :::      :::         |||               :::
Db       1573 GTTTACCTGCATGAGAGAAATGTGGTCCACAGAGAT--------------ATCAAGTGT 1617

Qy        176 AsnSerValThrValProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLys 195
                 ::::::   |||       |||   |||::::::      ||||||          |||
Db       1618 GCCAATATATTGGTGCATGCAAATGGATCTGTAAAGCTTGCAGATTTTGGATTGGCAAAG 1677

Qy        196 ---IleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAsnArg 214
                 :::   ||||||:::   :::|||   |||   :::|||:::|||   ::::::
Db       1678 GAGGTTACCCTTTGTCTTTCTGTTCATTATTTCCATGTTCGCAGTGTCAAATTGTCTTAT 1737

Qy        215 MetMetSerTyr 218
                    |||:::
Db       1738 GGTTGTAGTTTT 1749

RESULT 4
US-11-217-529-2301
; Sequence 2301, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2301
;   LENGTH: 1836
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-2301

Alignment Scores:
Pred. No.:                1.16           Length:          1836
Score:                    86.00          Matches:           41
Percent Similarity:       36.4%          Conservative:      31
Best Local Similarity:    20.7%          Mismatches:        95
Query Match:              7.6%           Indels:            31
DB:                       7              Gaps:               3

US-10-821-670A-33 (1-222) x US-11-217-529-2301 (1-1836)

Qy         22 LeuSerLeuAlaArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeu 41
              ||||||   :::   |||:::      |||        |||        |||
Db       340 TTGAGTCGTTCCAATAATATCAAGGAACCGCAGAGAGACCCAGCGGGAAGCCAA------ 393

Qy         42 AsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThr 61
                                     |||:::   :::|||   |||            ||||||
Db       394 --------------------AGATCAAAAAACAATGCCCTTTCCTTACCAACACAGACA 432

Qy         62 LeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLys 81
                        :::   :::|||                              :::   |||
Db       433 ACTTCTTCGTCCACCTCCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTATGATTCT 492

Qy         82 ThrSerThrValGluAlaCysLeuProLeuGluLeuThr------------MetAsnGlu 97
                        :::      :::   ::::::                        |||:::
Db       493 GTAAGAAGGACTGATAATAGCGTTAGAATGCAAAAGAATAAACACTCCAGATTCAACAAG 552

Qy         98 SerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArg 117
                        |||||||||   |||   :::   :::|||||   ::::::
Db       553 GAATTACCCCGCAGCAGGGAAAGCTCAAATATGAATTCTGGATCTATCATCAGTCAATAC 612

Qy        118 LysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyr 137
                           |||      :::|||   :::   :::      :::
Db       613 AATGTCGATACTCAGGCAACCGCTATAATGAGCGATATGCAAAAACAATATGAGTCGCAG 672

Qy        138 GlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIle--- 156
              |||:::            :::|||      ||||||:::||||||      ::::::
Db       673 CAACTGCCTTCGTTGTTTATAAACGAGACTTTACTGATTGATCCAAATGGTAAAGTTTCA 732

Qy        157 ----------------------------------------------PheLeuAspGln 160
                                                           |||   |||
Db       733 GAGGTTATAAAGTTGATATTTGAAGAAGTCGGCTACAAATTTGATGATTTTAGTGATATT 792

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSer-ValThrVa 180
              ::::::          :::   |||:::   |||   :::      :::||| |||
Db       793 TCCGTTTTCCAACTGATGCAAGAAATGTATCAATTAATTAAGAAGGATTCTAGTAATAAA 852

Qy        180 lProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLys 197
              ||||||      |||      |||      |||   |||   |||
Db       853 AAGTCAAAATTAACTACTTTTGCCTCCAAAGTAAAAGAAAAAGAAATGCAAG 904

RESULT 5
US-11-217-529-4722
; Sequence 4722, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4722
;   LENGTH: 2310
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-4722
```

```
Alignment Scores:
Pred. No.:              1.64          Length:        2310
Score:                  86.00         Matches:       51
Percent Similarity:     39.7%         Conservative:  43
Best Local Similarity:  21.5%         Mismatches:    87
Query Match:            7.6%          Indels:        56
DB:                     7             Gaps:          11

US-10-821-670A-33 (1-222) x US-11-217-529-4722 (1-2310)

Qy          6 GlyLeuLeuLeuValThr----------IleLeuValLeuLeuAsnHisLeuAspHis 21
              ||||||   :::   |||                  :::   |||:::
Db        946 GGGTTAAAAATAGCTACCAGTGAAAATGGCACTGCGGCGATTACTAACAATAGCACCCCG 1005

Qy         22 LeuSerLeuAlaArgAsn----------------------LeuProThrPro---Thr 32
                |||||||||:::|||                        |||:::|||   :::
Db       1006 TCATCTCTGGCACAAAATAATGACCCGATATCGCCCCTATCATCACCCTCCCCATCTTCA 1065

Qy         33 ProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSer 52
              |||||||||   :::         |||:::   |||   :::      :::::::::|||
Db       1066 CCTTCACCAACATTAACTGCAGTCTTATCCCCATCTCCATCGAATACTAAATCTGTTTCT 1125

Qy         53 AsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIle 72
              :::|||            :::||||||            |||            |||:::
Db       1126 CATACCGCTTCGCCAGTTAAGCAGACTAATAACGACATCAGT---AATGAACCAGAACTG 1182

Qy         73 AspHisGluAsp------IleThrLysAspLysThrSerThrValGluAlaCysLeuPro 90
                |||   |||      ||||||  ::::::|||:::      :::
Db       1183 CAACACAATGATCAACCTATAACGAATGAACAAACAACAAGAACAAAG------------ 1230

Qy         91 LeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsn 110
                        |||      :::   ::::::|||   |||:::|||          :::
Db       1231 ---------ATGATGGCGGCGGCAACAGTATCATCTGAAGAATTGAGTTTCGCTGATGAT 1281

Qy        111 --------------GlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
                           ||||||                  :::   |||   :::
Db       1282 CTCGTTGAAAAAGTTTTCAGCTGCAATGATAAGCTATCAGATAAGTACAATACTCAAATA 1341

Qy        126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
                :::                |||      |||::::::||||||      :::
Db       1342 TCGGCCAATATAGAACCTCCATTGCTGACATCATACAAGTTAGAATTCCCCAATATTCCG 1401

Qy        146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
                      |||      |||                |||   ::::::::::::::
Db       1402 AGAAGTGCACTC------CCGGCAGAA---------ACGGATGCGGACGTTATATCATCT 1446

Qy        166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
              ::::::   |||                              :::      ||||||
Db       1447 TTAGAGTCGTTGTACCAC----------------------ATCCATTGCAACTCCGTT 1482

Qy        186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
                |||          |||   ||||||
Db       1483 TATGAAAGCATCAAATTTTTGAAAACCGAT---------------------------- 1512

Qy        206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
                           ||||||:::      :::|||:::   |||::::::
Db       1513 --------------ACTATATCAAATGCTTTATCTTTCTCCAACTCCAAT 1548

RESULT 6
US-11-217-529-174200
; Sequence 174200, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174200
;   LENGTH: 1875
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-174200

Alignment Scores:
Pred. No.:              1.57          Length:        1875
Score:                  85.00         Matches:       43
Percent Similarity:     40.0%         Conservative:  33
Best Local Similarity:  22.6%         Mismatches:    65
Query Match:            7.5%          Indels:        49
DB:                     7             Gaps:          9

US-10-821-670A-33 (1-222) x US-11-217-529-174200 (1-1875)

Qy         26 ArgAsnLeuProThrProThrProSerProGlyMetPheGlnCysLeuAsnHisSerGln 45
              |||   :::   ||||||      |||   |||      :::         ||||||
Db        178 AGATTTATCATGACACCTTTATATTCCAGTGGCTCACAGGAACTT------CACTCAGAT 231

Qy         46 ThrLeuLeuArgAlaIle---------SerAsnThrLeuGlnLysAlaArgGlnThrLeu 62
                 |||::::::::::|||         :::|||::::::   :::             |||
Db        232 TTTTTGGTTAAAAGCATCCAAGATCTTACGAATTCGATGTTACAATTTAGTGATCCATTG 291

Qy         63 GluPheTyrSerCysThrSerGlu---GluIleAspHisGluAspIleThrLysAspLys 81
                 |||:::          |||   :::|||         |||   :::   |||
Db        292 ACCACATATAATAGGTACAAAGAAGATGACATTAGCTCTTCAGACAGTAGTAGTGATCTC 351

Qy         82 ThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAla 101
              |||   :::||||||      |||
Db        352 AACTCTAATATAGAAGCTTCAAAACCA-------------------------------- 378

Qy        102 SerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPhe 121
                                      |||||||||                       :::
Db        379 -----------------GCCGCAAATGGTTCTTATACTCTTCAAAATATGCGGAACAAG 420

Qy        122 MetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPhe 141
                        :::   |||:::   :::                      ::::::
Db        421 GCCCTTAATGTAGCCTTAGCGAAATTG--------------------AAAATAGCATTA 459

Qy        142 LysAlaMetAsnAlaLysLeuLeuMet---------AspProLysArg---------Gln 155
              |||   :::      :::|||::::::         ||||||                :::
Db        460 AAGGACGTTACCATACGTTTAATAGTAAATGATAGAGATCCTTCCGATAACATCGTGGAG 519

Qy        156 IlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnVal 175
              :::   |||:::          |||          |||      |||:::   :::|||:::
Db        520 GTTCATCTAGAAAGCATACAACTTATTACTACAGACGCAAATTTACGACATATAAACATT 579

Qy        176 AsnSerValThrVal-ProGlnAsnSerSerLeuGluGluProAspPheTyrLysThrLy 195
                  ::::::|||::: ||||||                        ||||||    ||
Db        580 GAAAATATCACCATTTCCTCAA-------------------------TACAAAAACAA 612

Qy        195 sIle---------LysLeuCysIleLeu 201
              |:::           ||||||||||||
Db        613 GCTGTACCCGACTCTCCTGTGCATCCTT 640

RESULT 7
US-11-217-529-79916
; Sequence 79916, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
```

```
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79916
;   LENGTH: 990
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-79916

Alignment Scores:
Pred. No.:              0.793          Length:         990
Score:                  84.00          Matches:        46
Percent Similarity:     41.1%          Conservative:   32
Best Local Similarity:  24.2%          Mismatches:     68
Query Match:            7.4%           Indels:         44
DB:                     7              Gaps:           8

US-10-821-670A-33 (1-222) x US-11-217-529-79916 (1-990)

Qy         42 AsnHisSerGlnThrLeuLeuArgAlaIleSer------AsnThrLeuGlnLysAlaArg 59
              |||   |||::::::||||||       |||         |||   :::||||||
Db         40 AATACCTCTGAATCGTTATTAGTTGATATTCAAGAATACAATCAAATTCAAAAACAAATT 99

Qy         60 GlnThrLeuGluPhe---TyrSerCysThrSerGluGluIleAspHisGluAspIleThr 78
              :::|||::::::   :::     :::||||||:::   :::          |||
Db        100 GAGACCATTCAGGCTGATCTCAACCATGTAACGGAAGAGCTACAGACGCAATATGCTACA 159

Qy         79 LysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeu--------------- 93
              ||||||   |||:::::::::   |||   |||   |||
Db        160 TCGCAAAAAACAAAGACCATTCAAAGTGATTTAAATCTCTCGTTGCATAAATTGGATTTG 219

Qy         94 --------------------ThrMetAsnGluSerCysLeuAlaSerArgGluIleSer 106
                                  :::         :::|||      |||
Db        220 GCTAAGCGTAATCTCGACGCGAATCCATCTTCCCAAATAATTGCGAGGAATGAAGAAATT 279

Qy        107 LeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThr---ThrLeu 125
              |||         |||  |||                |||||      |||:::
Db        280 TTGAGGGACATTGGAGAATGTGAGAATGAAATCAAAACCAAGCAAATGAGCTTAAAGAAA 339

Qy        126 Cys---------LeuSerSerIleTyrGluAspLeuLysMetTyr--------------- 137
              |||         :::|||:::|||   :::|||:::|||   |||
Db        340 TGTCAAGAAGAAGTTTCGACCATTGAAAAAGACATGAAGGAGTACGATAGCGATAAAGGA 399

Qy        138 -----------------GlnValGluPheLysAlaMetAsnAlaLysLeu---------- 148
                              :::   |||   |||   :::      :::|||
Db        400 TCCAAGTTAAATGAATTAAAGAAGGAATTGAAACTATTGGCGAAAGAGCTGGAGGAGCAG 459

Qy        149 LeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGlu 168
                 :::   :::|||:::      |||   ||||||:::                :::::
Db        460 GAATCGGAGTCAGAACGTAAATATGACTTGTTTCAAAACTTGGAATTAGAAACAGAGCAA 519

Qy        169 LeuLeuGlnAlaLeuAsnValAsnSerValThrValPro-------------------- 181
              |||         |||:::   |||         :::
Db        520 TTGAGCTCAGAACTAGATTCTAATAAGACGCTATTGCAAAACCATTTGAAATCTATTGAA 579

Qy        182 ------------GlnAsnSerSerLeuGlu 187
                          :::||||||   ||||||
Db        580 AGTTTGAAATTGGAAAATTCTGATTTGGAG 609

RESULT 8
US-11-217-529-76395
; Sequence 76395, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76395
;   LENGTH: 2406
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-76395

Alignment Scores:
Pred. No.:              2.98           Length:         2406
Score:                  84.00          Matches:        52
Percent Similarity:     38.8%          Conservative:   33
Best Local Similarity:  23.7%          Mismatches:     90
Query Match:            7.4%           Indels:         44
DB:                     7              Gaps:           9

US-10-821-670A-33 (1-222) x US-11-217-529-76395 (1-2406)

Qy          4 ProArgGlyLeuLeuLeuValThrIleLeu---------ValLeuLeuAsnHisLeuAsp 20
              |||               :::|||   :::|||            |||   :::   |||
Db         58 CCAGAAGCTCAGACCATAGTGGGTTTACTGGACGATTCGTACCTTTTTGATAAGCTAAAA 117

Qy         21 HisLeuSerLeuAla------------ArgAsnLeuProThrProThrProSerProGly 36
                 ||||||||||||                 |||                 |||   |||
Db        118 AAGCTGTCTTTGGCTGTGGAAAATTCTGACGGTCTGCAAAGAACTGATGTCTCAGAAGGT 177

Qy         37 MetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGln 56
                 :::   :::|||   |||:::          |||
Db        178 TGTTCAGAG---GTTAATGGTTCTGAAGCTACGACTTCTGCGGATGTAAAAAAGACAAAC 234

Qy         57 LysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAsp 76
              |||                  :::         :::   :::||||||
Db        235 AAGTATTTGTATTATACTACCTATTTGGACCGGTTAAACATTAAGATAGACGAGTATAAA 294

Qy         77 IleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsn 96
              :::      |||:::|||      |||                          ::::::
Db        295 GTTGTTCTGGATCAAACACGCCAGGTTAATGAT-----------------CAATTGGAT 336

Qy         97 GluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
                 |||         |||:::||||||      |||   |||:::   :::
Db        337 AGTTCCATCAAGAAATTTCGGAAAATCTCTCAGGATACT---GGAGCTTTCATTGAGGAA 393

Qy        117 ArgLysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMet 136
                 ||||||   :::              ||||||:::::   |||   :::
Db        394 ACGAAGACGATCTATGAAAAGCAGTCTAAATTAAGCAATCTAACTGAGTCAATCCCT--- 450

Qy        137 TyrGlnValGluPheLysAlaMetAsnAlaLysLeuLeuMetAspPro------------ 152
                           ||||||::::::          ::::::||||||
Db        451 --------------AAAGCTCTCCATTATTTTGAAGTTTTGGACCCTATAATGCGTCGC 495

Qy        153 ------------------------------LysArgGlnIlePheLeuAspGlnAsnMet 162
                                           |||:::   |||         |||
Db        496 TTGAACCATGCCACTTCTCCCGCTATTGTCAAGAAGAGCTCCTTT------ACGACGATG 549

Qy        163 LeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGln 182
              |||      |||||||||   |||:::   |||:::                     :::
Db        550 TTGGCGACTATCGACGAGTCTTTACGTTTTTTGGAT--------------------GAG 588

Qy        183 AsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeu 201
                 ||||||   |||::::::          |||:::   |||   |||   |||::::::
Db        589 AATAGTGACCTCAAGGATGCAGCAGCGTACAGAATCAAGTTCAAGCAATGCTTGATC 645

RESULT 9
US-10-953-349-3750/c
; Sequence 3750, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3750
;   LENGTH: 1647
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-3750

Alignment Scores:
Pred. No.:              2.21          Length:        1647
Score:                  83.00         Matches:       31
Percent Similarity:     44.8%         Conservative:  12
Best Local Similarity:  32.3%         Mismatches:    31
Query Match:            7.4%          Indels:        22
DB:                     6             Gaps:          5

US-10-821-670A-33 (1-222) x US-10-953-349-3750 (1-1647)

Qy         67 CysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu 86
Db       1098 TGCCTCCTTAGTGAATGTTTTTGGGAAGATATCCTTAAGGAT-----------ATTGAG 1051

Qy         87 AlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu------ 104
Db       1050 GCTACTGTCCCATCTTGGCTGAGTCAGATAGATAGTTGTGTCGCTGGCAAATCCAAGCTT 991

Qy        105 --------------------IleSerLeuIleThrAsnGlySerCysLeuAlaSerArg 117
Db        990 TCTCAAGAATAAAGCAATCTCTTGAGCGTTGTAACA---------TGTCTTGGACCCTAC 940

Qy        118 LysThrSerPheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyr 137
Db        939 TACACCAGTTGTATGGCAATTTTTCTTCTCAAG------TATGTCGATTCTAAGGTCTAC 886

Qy        138 GlnValGlu------------PheLysAlaMetAsnAlaLysLeuLeu 149
Db        885 TGCTATGAAACGGCCACCGGATTTACGGCTATGAGTCCTCAACCGCTC 838

RESULT 10
US-10-505-928-342
; Sequence 342, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
;  APPLICANT: Ludwig Institute for Cancer Research et al.
;  TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
;  FILE REFERENCE: 28967/39178
;  CURRENT APPLICATION NUMBER: US/10/505,928
;  CURRENT FILING DATE:  2004-08-27
;  PRIOR APPLICATION NUMBER: US 60/363,019
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: PatentIn 3.2
; SEQ ID NO 342
;   LENGTH: 5198
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-505-928-342

Alignment Scores:
Pred. No.:              12.2          Length:        5198
Score:                  83.00         Matches:       58
Percent Similarity:     39.1%         Conservative:  41
Best Local Similarity:  22.9%         Mismatches:    87
Query Match:            7.4%          Indels:        67
DB:                     6             Gaps:          14

US-10-821-670A-33 (1-222) x US-10-505-928-342 (1-5198)

Qy         10 ValThrIleLeuValLeuLeuAsnHisLeuAspHisLeuSerLeuAlaArgAsnLeuPro 29
Db        657 GTAACATTGACAGTA--------------GATCGCTTTGATCCTGGTCGAGAAGTACCT 701

Qy         30 --------------ThrProThrProSer---ProGlyMetPhe------GlnCysLeu 41
Db        702 GAATGCCTAGAAATAACCCCTACTGCTTCTCTTCCTGGGGACTTTTTGATTCCATGCAAA 761

Qy         42 AsnHisSerGlnThrLeu-----------------LeuArgAlaIleSerAsnThrLeu 55
Db        762 GTTCATACTCAAGAACTTTGTTCAAGAGAAATGATAGTTCACAGTGTAGATGAC---TTC 818

Qy         56 GlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGluIleAspHisGlu 75
Db        819 AGTTCAGCTTTAAAGGCTCTACAGTGCCATATATGTAGCAAAGATTCCTTGGACTGTGGT 878

Qy         76 AspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMet 95
Db        879 AAGCTGCTTTCC--------------------------CTAAGAGTTCATATCACTTCC 911

Qy         96 AsnGluSerCysLeuAlaSerArgGlu--------------------IleSerLeuIle 108
Db        912 AGGGAGAGT---TTGGACAGTGTGGAATTTGACTTGCATTGGGCAGCAGTAACTCTAGCA 968

Qy        109 ThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCysLeuSer 128
Db        969 AATAACTTTAAATGCACACCTGTGAAGCCCATCCCCATTATTCCAACAGCTCTGGCAAGA 1028

Qy        129 SerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAlaLysLeu 148
Db       1029 AACTTGAGCAGTAATCTGAATATTTCTCAAGTTCAAGGGACTTATAAATATGGATATCTT 1088

Qy        149 LeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGlu 168
Db       1089 ACCATGGATGAAACACGCAAATTGTTACTT------------TTGTTGGAATCTGATCCC 1136

Qy        169 LeuLeuGlnAlaLeu-----------------------AsnValAsnSerValThrVal 180
Db       1137 AAGGTTTATTCTCTACCATTGGTGGGAATTTGGCTGTCTGGAATTACACATATCTATAGT 1196

Qy        181 ProGln----------------------------AsnSerSerLeuGluGluProAsp 190
Db       1197 CCTCAGGTATGGGCTTGCTGTTTGCGATACATATTCAATTCTTCTGTTCAAGAAAGGGTT 1256

Qy        191 PheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe-ArgIleArgAlaVa 210
Db       1257 TTTTCAGAATCTGGA---AATTTCATCATAGTTCTCTATTCTATGACACATA-------- 1305

Qy        210 lThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
Db       1306 ----------AGGAACCTGAGTTTTATGAATGCTTCC 1332

RESULT 11
US-11-122-986-339
; Sequence 339, Application US/11122986
; Publication No. US20060104989A1
; GENERAL INFORMATION:
;  APPLICANT: EDWARDS, ALED
;  APPLICANT:  DHARAMSI, AKIL
;  APPLICANT:  VEDADI, MASOUD
;  TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
;  FILE REFERENCE: IPT-330.01
;  CURRENT APPLICATION NUMBER: US/11/122,986
;  CURRENT FILING DATE:  2005-05-05
;  PRIOR APPLICATION NUMBER: 60/423,875
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/423,832
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/423,915
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/423,757
;  PRIOR FILING DATE: 2002-11-05
```

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;  PRIOR APPLICATION NUMBER: 60/423,758
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/424,367
;  PRIOR FILING DATE: 2002-11-06
;  PRIOR APPLICATION NUMBER: 60/424,376
;  PRIOR FILING DATE: 2002-11-06
;  PRIOR APPLICATION NUMBER: 60/424,370
;  PRIOR FILING DATE: 2002-11-06
;  PRIOR APPLICATION NUMBER: 60/424,362
;  PRIOR FILING DATE: 2002-11-06
;  PRIOR APPLICATION NUMBER: 60/424,373
;  PRIOR FILING DATE: 2002-11-06
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 844
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 339
;   LENGTH: 2289
;   TYPE: DNA
;   ORGANISM: Streptococcus pneumoniae
US-11-122-986-339

Alignment Scores:
Pred. No.:              4.13          Length:        2289
Score:                  82.50         Matches:       43
Percent Similarity:     39.2%         Conservative:  42
Best Local Similarity:  19.8%         Mismatches:    111
Query Match:            7.3%          Indels:        21
DB:                     7             Gaps:          5

US-10-821-670A-33 (1-222) x US-11-122-986-339 (1-2289)

Qy         12 IleLeuValLeuLeuAsnHisLeuAspHisLeuSerLeuAlaArgAsnLeuProThrPro 31
              :::|||   |||         |||||||||||||||:::         :::   :::
Db       1387 ATGCTTGATTTGCGGGAGCAGCTAGACCACTTAAGCATTACAGAGTTGGTTGAGTCCGTC 1446

Qy         32 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 51
                      |||           ||||||         ||||||
Db       1447 CTAGAAAAAACAGGTTATGTCGATATTCTTAACTCCCAAGCGACTCTA---------- 1494

Qy         52 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 71
                    :::       :::                 ||||||   |||   |||
Db       1495 ---GAAAGCAAGGCACGGGTTGAAAATATCGAAGAGTTTCTTTCTGTTACGAAGAACTTT 1551

Qy         72 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 91
              |||       |||:::|||:::::::::|||          :::             |||
Db       1552 GATGACACCACGGATGTGACAGAAGAGGAAACTGGTCTGGACAAA-----------CTG 1599

Qy         92 GluLeuThrMetAsnGluSerCysLeu-----------------AlaSerArgGluIle 105
                    :::|||:::      |||                  |||:::|||
Db       1600 AGTCGTTTCTTAAATGACTTGGCTTTGATTGCCGACACAGATTCAGGTAGTCAGGAGACA 1659

Qy        106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
              |||   :::|||      :::      |||::::::         |||
Db       1660 TCAGAAGTGACCTTGATGACCCTGCATGCTGCCAAAGGTCTCGAATTTCCAGTTGTCTTT 1719

Qy        126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
                 :::                 :::      ::::::   :::                :::
Db       1720 TTGATTGGGATG---------GAAGAAAATGTCTTTCCACTTAGTCGTGCGACTGAAGAT 1770

Qy        146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
              :::      |||   :::   :::|||      ::::::          :::|||
Db       1771 TCAGATGAATTAGAAGAAGAGCGCCGTCTAGCCTATGTAGGT---------ATCACGCGT 1821

Qy        166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
                 :::::::::|||         |||   ||||||      :::         ::::::
Db       1822 GCAGAGAAAATTCTCTATCTGACCAATGCCAACTCACGCTTGCTTTTTGGTCGTACCAAT 1881

Qy        186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
                    |||      :::      :::|||         :::|||   :::
Db       1882 TATAACCGTCCGACTCGTTTTATTAACGAAATCAGTTCAGACTTGCTTGAGTATCAAGGT 1941

Qy        206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
                  |||            :::         ||||||   :::   |||
Db       1942 CTGGCTCGTCCTGCAAATACAAGCTTTAAGGCATCATATAGCAGTGGTAGT 1992

RESULT 12
US-11-122-986-337
; Sequence 337, Application US/11122986
; Publication No. US20060104989A1
; GENERAL INFORMATION:
;  APPLICANT: EDWARDS, ALED
;  APPLICANT:  DHARAMSI, AKIL
;  APPLICANT:  VEDADI, MASOUD
;  TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
;  FILE REFERENCE: IPT-330.01
;  CURRENT APPLICATION NUMBER: US/11/122,986
;  CURRENT FILING DATE:  2005-05-05
;  PRIOR APPLICATION NUMBER: 60/423,875
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/423,832
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/423,915
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/423,757
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/423,758
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/424,367
;  PRIOR FILING DATE: 2002-11-06
;  PRIOR APPLICATION NUMBER: 60/424,376
;  PRIOR FILING DATE: 2002-11-06
;  PRIOR APPLICATION NUMBER: 60/424,370
;  PRIOR FILING DATE: 2002-11-06
;  PRIOR APPLICATION NUMBER: 60/424,362
;  PRIOR FILING DATE: 2002-11-06
;  PRIOR APPLICATION NUMBER: 60/424,373
;  PRIOR FILING DATE: 2002-11-06
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 844
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 337
;   LENGTH: 2292
;   TYPE: DNA
;   ORGANISM: Streptococcus pneumoniae
US-11-122-986-337

Alignment Scores:
Pred. No.:              4.14          Length:        2292
Score:                  82.50         Matches:       43
Percent Similarity:     39.2%         Conservative:  42
Best Local Similarity:  19.8%         Mismatches:    111
Query Match:            7.3%          Indels:        21
DB:                     7             Gaps:          5

US-10-821-670A-33 (1-222) x US-11-122-986-337 (1-2292)

Qy         12 IleLeuValLeuLeuAsnHisLeuAspHisLeuSerLeuAlaArgAsnLeuProThrPro 31
              :::|||   |||         |||||||||||||||:::         :::   :::
Db       1387 ATGCTTGATTTGCGGGAGCAGCTAGACCACTTAAGCATTACAGAGTTGGTTGAGTCCGTC 1446

Qy         32 ThrProSerProGlyMetPheGlnCysLeuAsnHisSerGlnThrLeuLeuArgAlaIle 51
                      |||           ||||||         ||||||
Db       1447 CTAGAAAAAACAGGTTATGTCGATATTCTTAACTCCCAAGCGACTCTA---------- 1494

Qy         52 SerAsnThrLeuGlnLysAlaArgGlnThrLeuGluPheTyrSerCysThrSerGluGlu 71
                    :::       :::                 ||||||   |||   |||
Db       1495 ---GAAAGCAAGGCACGGGTTGAAAATATCGAAGAGTTTCTTTCTGTTACGAAGAACTTT 1551

Qy         72 IleAspHisGluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeu 91
              |||       |||:::|||:::::::::|||          :::             |||
Db       1552 GATGACACCACGGATGTGACAGAAGAGGAAACTGGTCTGGACAAA-----------CTG 1599

Qy         92 GluLeuThrMetAsnGluSerCysLeu-----------------AlaSerArgGluIle 105
                    :::|||:::      |||                  |||:::|||
Db       1600 AGTCGTTTCTTAAATGACTTGGCTTTGATTGCCGACACAGATTCAGGTAGTCAGGAGACA 1659
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Qy        106 SerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeu 125
Db       1660 TCAGAAGTGACCTTGATGACCCTGCATGCTGCCAAAGGTCTCGAATTTCCAGTTGTCTTT 1719

Qy        126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
Db       1720 TTGATTGGGATG---------GAAGAAAATGTCTTTCCACTTAGTCGTGCGACTGAAGAT 1770

Qy        146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
Db       1771 TCAGATGAATTAGAAGAAGAGCGCCGTCTAGCCTATGTAGGT---------ATCACGCGT 1821

Qy        166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
Db       1822 GCAGAGAAAATTCTCTATCTGACCAATGCCAACTCACGCTTGCTTTTTGGTCGTACCAAT 1881

Qy        186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
Db       1882 TATAACCGTCCGACTCGTTTTATTAACGAAATCAGTTCAGACTTGCTTGAGTATCAAGGT 1941

Qy        206 ArgIleArgAlaValThrIleAsnArgMetMetSerTyrLeuAsnAlaSer 222
Db       1942 CTGGCTCGTCCTGCAAATACAAGCTTTAAGGCATCATATAGCAGTGGTAGT 1992

RESULT 13
US-10-505-928-101
; Sequence 101, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
;  APPLICANT: Ludwig Institute for Cancer Research et al.
;  TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
;  FILE REFERENCE: 28967/39178
;  CURRENT APPLICATION NUMBER: US/10/505,928
;  CURRENT FILING DATE:  2004-08-27
;  PRIOR APPLICATION NUMBER: US 60/363,019
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: PatentIn 3.2
; SEQ ID NO 101
;   LENGTH: 9588
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-505-928-101

Alignment Scores:
Pred. No.:              39.8          Length:         9588
Score:                  82.00         Matches:        48
Percent Similarity:     40.6%         Conservative:   40
Best Local Similarity:  22.1%         Mismatches:     81
Query Match:            7.3%          Indels:         49
DB:                     6             Gaps:           8

US-10-821-670A-33 (1-222) x US-10-505-928-101 (1-9588)

Qy          6 GlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAspHisLeuSerLeuAla 25
Db       2945 GGAATTATCGTGATAACTATCAGGCTTTCTGCAAGTGGCTCTATGATCGTAAACGCCGCC 3004

Qy         26 Arg-----------------AsnLeuProThrProThrProSerProGlyMetPheGln 39
Db       3005 AGGATTCCTTAGAATCCATGAAATTTGGAGATTCCAACACAGTCATGCGGTTT------- 3057

Qy         40 CysLeuAsnHisSerGlnThrLeuLeuArgAlaIleSerAsnThrLeuGlnLysAlaArg 59
Db       3058 ---TTGAATGAGCAGAAGAACTTGCACAGTGAAATATCTGGCAAACGAGACAAATCAGAG 3114

Qy         60 GlnThrLeuGluPheTyrSer---CysThrSerGluGluIleAspHisGluAspIleThr 78
Db       3115 GAAGTACAAAAAATTGCTGAACTTTGCGCCAATTCAATTAAGGATTATGAGCTCCAGCTG 3174

Qy         79 LysAspLysThrSerThrValGluAlaCysLeu------ProLeuGluLeuThrMetAsn 96
Db       3175 GCCTCATACACCTCAGGACTGGAAACTCTGCTGAACATACCTATCAAGAGGACCATGATT 3234

Qy         97 GluSer-----------------------------CysLeuAlaSerArgGluIleSer 106
Db       3235 CAGTCCCCTTCTGGGGTGATTCTGCAAGAGGCTGCAGATGTTCATGCTCGGTACATTGAA 3294

Qy        107 LeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThrLeuCys 126
Db       3295 CTACTTACAAGATCTGGAGACTATTACAGGTTCTTAAGTGAGATGCTGAAGAGTTTG--- 3351

Qy        127 LeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsnAla 146
Db       3352 --------------GAAGATCTGAAGCTGAAAAATACCAAGATCGAAGTTTTGGAAGAG 3396

Qy        147 LysLeuLeuMet--------------------AspProLysArgGlnIlePheLeuAsp 159
Db       3397 GAGCTCAGACTGGCCCGAGATGCCAACTCGGAAAACTGTAATAAGAACAAATTCCTGGAT 3456

Qy        160 GlnAsnMet-----------------------------------LeuThrAlaIle 166
Db       3457 CAGAACCTGCAGAAATACCAGGCAGAGTGTTCCCAGTTCAAAGCGAAGCTTGCGAGCCTG 3516

Qy        167 AspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsn 183
Db       3517 GAGGAGCTGAAGAGACAGGCTGAGCTGGATGGGAAGTCGGCTAAGCAAAAT 3567

RESULT 14
US-10-953-349-5587/c
; Sequence 5587, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5587
;   LENGTH: 1798
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-5587

Alignment Scores:
Pred. No.:              5.63          Length:         1798
Score:                  80.00         Matches:        34
Percent Similarity:     42.0%         Conservative:   26
Best Local Similarity:  23.8%         Mismatches:     57
Query Match:            7.1%          Indels:         26
DB:                     6             Gaps:           5

US-10-821-670A-33 (1-222) x US-10-953-349-5587 (1-1798)

Qy         83 SerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAla--- 101
Db       1271 TCCTCTGCTGCCTTTTGCCTACCACTCTCAGTTTTGTTCCGCGCCTGCGAGCTGAGTCTG 1212

Qy        102 ----------------------------------------SerArgGluIleSerLeu 107
Db       1211 TATCGTCCTACTAAGTCGATGTAATATGGAATTAGCGCCACCAACCGGACAATATCATCC 1152

Qy        108 IleThrAsnGlySerCysLeuAlaSerArgLysThrSerPheMetThrThr------Leu 125
Db       1151 ATA-----------TGTTTAGCATCAGGTAAAGAAAACTTGAAAAGCATCATCTTCTTG 1104

Qy        126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGluPheLysAlaMetAsn 145
Db       1103 TGCTTGCCAGGGTGTTGGTCAGATATATGCATCGACATGAAATTCTTCCCATACTTATCC 1044

Qy        146 AlaLysLeuLeuMetAspProLys---------ArgGlnIlePheLeuAspGlnAsnMet 162
Db       1043 ACAGCCTTG------TCACCAAAAACCTGATCAAGAACAGTGTCAGTGATCAAATCCGCA 990
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Qy        163 LeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGln 182
              |||::::::|||      ::::::|||   :::   ::::::      :::|||
Db        989 GCAACTTCCTTGGATTCAGAGATCAAGGCGAACTCCTCCGACACCCATTTCCTTCCAGCA 930

Qy        183 AsnSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeu 202
                          :::      |||:::   |||      ||||||:::
Db        929 GGAGGAGACACAATCCCAGCAAATCTTTGCAAATCCCTCATCTCCTTTTGCATAGTTTTT 870

Qy        203 HisAlaPhe 205
              ||||||
Db        869 GCAGCCTTC 861

RESULT 15
US-11-217-529-76747
; Sequence 76747, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76747
;   LENGTH: 1956
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-76747

Alignment Scores:
Pred. No.:              6.38          Length:         1956
Score:                  80.00         Matches:        48
Percent Similarity:     39.6%         Conservative:   42
Best Local Similarity:  21.1%         Mismatches:     89
Query Match:            7.1%          Indels:         48
DB:                     7             Gaps:           9

US-10-821-670A-33 (1-222) x US-11-217-529-76747 (1-1956)

Qy          5 ArgGlyLeuLeuLeuValThrIleLeuValLeuLeuAsnHisLeuAspHisLeuSerLeu 24
              :::   |||:::      :::||||||:::|||   :::||||||   |||      :::
Db        799 AAAGACCTTATTCATCCGTCGATATTATTATTAACTTCTCATCTAGCACACTATAAAATA 858

Qy         25 AlaArgAsnLeuPro------------------------------------------- 29
                    ::::::|||
Db        859 GTAGGATCCATCCCACGTTGCATAGCCATGCTAGAGGTTTTCCAAATTGTTATCAAAGAC 918

Qy         30 ------ThrPro---------ThrProSerProGlyMetPheGlnCysLeuAsnHisSer 44
                  ||||||         |||   |||      :::        |||:::|||
Db        919 TATCAAACGCCTAAGGGAACTACCTTGTCACGTAACTTAACAAGTTATTTGTCACACCAG 978

Qy         45 GlnThrLeuLeu---------ArgAlaIleSerAsnThrLeuGlnLysAlaArgGlnThr 61
                 ||||||         |||   :::|||   |||:::      |||   :::
Db        979 ATTGATCTTTTGAAAAAAGCTAGACCTTTAAGTGTTACTATGGGTAATGCTATCAGATGG 1038

Qy         62 LeuGluPheTyrSerCysThrSerGluGluIleAspHisGluAsp---IleThrLysAsp 80
              |||:::                  :::||||||         |||      |||   |||
Db       1039 TTAAAG-----------------CAAGAAATTTCATTAATTGACCCATCTACCCCCGAC 1080

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              |||   :::      :::   |||      :::                |||
Db       1081 AAAGCCGCCAAAAAAGACCTTTGTGAGAAAATTGGGCAGTTTGCTAAAGAAAAAATCGAA 1140

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerArgLysThrSer 120
                    :::   ::::::   :::|||   |||   |||                  |||:::
Db       1141 CTGGCTGATCAACTA---ATTATAGACAATGCCTCTACACAAATTGAAGAATCTACTACT 1197

Qy        121 PheMetThrThrLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnValGlu 140
                 :::   |||          |||   :::      :::|||   ::::::
Db       1198 ---ATTGTGACATATGGTTCATCAAAGGTTCTAACTGAACTGTTACTGCATAATGCAATC 1254

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
                       |||   |||:::::::::          |||   :::|||      :::
Db       1255 AGTTTAAAGAAAAACATCAAAGTGATTGTCATCGATTCGAGACCACTATTTGAAGGGCGG 1314

Qy        161 AsnMet----------------------------------------------LeuThrAla 165
              |||                                                 :::|||:::
Db       1315 AAAATGGCCGAAACTTTAAGAAATGCTGGTGTCAATGTTATGTATGCACTTATTACAAGT 1374

Qy        166 IleAspGluLeuLeuGlnAlaLeuAsnValAsnSerValThrValProGlnAsnSerSer 185
              :::|||   :::          ::::::|||:::   |||   :::      :::|||
Db       1375 TTGGATACGATATTCAAT---ATGGATGTGGACTATGTGTTTTTAGGAGCCCATTCTATC 1431

Qy        186 LeuGluGluProAspPheTyr 192
              |||                 |||
Db       1432 CTATCTAATGGGTTCCTATAT 1452


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Job time : 20.5501 secs
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

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Sequence: 1 atgtgcccgccgcgtggcct.....tgagctatctgaatgcttcc 666

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_pat:*
3: gb_ph:*
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5: gb_pr:*
6: gb_ro:*
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13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	666	100.0	666	2	AR595952	AR595952 Sequence
c	2	666	100.0	666	2	AR595953	AR595953 Sequence
	3	664.4	99.8	669	14	FCIL12P35	Y07761 Felis catus
	4	661.2	99.3	669	14	FCU83185	U83185 Felis catus
	5	661.2	99.3	1441	2	AR242438	AR242438 Sequence
	6	661.2	99.3	1441	2	AR280206	AR280206 Sequence
	7	661.2	99.3	1441	2	AR322421	AR322421 Sequence
	8	651.6	97.8	669	2	AX076201	AX076201 Sequence
	9	651.6	97.8	669	2	AX076483	AX076483 Sequence
	10	651.6	97.8	4201	2	AX076477	AX076477 Sequence
	11	642	96.4	689	2	AR242451	AR242451 Sequence
	12	642	96.4	689	2	AR280219	AR280219 Sequence
	13	642	96.4	689	2	AR322434	AR322434 Sequence
	14	602	90.4	669	2	AR151072	AR151072 Sequence
	15	602	90.4	669	2	E15018	E15018 Canine mRNA
	16	602	90.4	669	2	AR316471	AR316471 Sequence
	17	600.4	90.2	666	2	AR595961	AR595961 Sequence
c	18	600.4	90.2	666	2	AR595962	AR595962 Sequence
	19	600.4	90.2	669	2	BD014664	BD014664 Process f
	20	600.4	90.2	1282	2	BD171283	BD171283 Novel can
	21	600.4	90.2	1455	2	AR596009	AR596009 Sequence
c	22	600.4	90.2	1455	2	AR596010	AR596010 Sequence
	23	592.4	88.9	669	14	CFU49085	U49085 Canis famil
	24	589.4	88.5	591	2	AR595954	AR595954 Sequence
c	25	589.4	88.5	591	2	AR595955	AR595955 Sequence
	26	587.6	88.2	669	2	AR151062	AR151062 Sequence
	27	587.6	88.2	669	2	BD014654	BD014654 Process f
	28	587.6	88.2	669	2	AR316461	AR316461 Sequence
	29	586.2	88.0	591	2	AR242439	AR242439 Sequence
	30	586.2	88.0	591	2	AR280207	AR280207 Sequence
	31	586.2	88.0	591	2	AR322422	AR322422 Sequence
	32	572.2	85.9	1533	2	AR595959	AR595959 Sequence
c	33	572.2	85.9	1533	2	AR595960	AR595960 Sequence
	34	572.2	85.9	1599	2	AR595956	AR595956 Sequence
c	35	572.2	85.9	1599	2	AR595957	AR595957 Sequence
	36	570.8	85.7	660	2	AX154619	AX154619 Sequence
	37	564.4	84.7	657	8	AY191828	AY191828 Synthetic
	38	564.4	84.7	660	2	AX154617	AX154617 Sequence
	39	562.8	84.5	660	2	AX154614	AX154614 Sequence
	40	562.8	84.5	660	2	AX154615	AX154615 Sequence
	41	562.8	84.5	660	2	AX154621	AX154621 Sequence
	42	561.2	84.3	660	2	AX154618	AX154618 Sequence
	43	559.6	84.0	660	2	AX154616	AX154616 Sequence
	44	559.4	84.0	561	2	AR596007	AR596007 Sequence
c	45	559.4	84.0	561	2	AR596008	AR596008 Sequence

ALIGNMENTS

RESULT 1
AR595952
LOCUS AR595952 666 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 32 from patent US 6818444.
ACCESSION AR595952
VERSION AR595952.1 GI:56646933
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 666)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 32 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .666
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 100.0%; Score 666; DB 2; Length 666;
Best Local Similarity 100.0%; Pred. No. 4.8e-185;
Matches 666; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120.
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
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Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        661 GCTTCC 666
              ||||||
Db        661 GCTTCC 666
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RESULT 2
AR595953/c
LOCUS       AR595953                 666 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 34 from patent US 6818444.
ACCESSION   AR595953
VERSION     AR595953.1  GI:56646934
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 34 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 666;  DB 2;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-185;
  Matches  666;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 607

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 547

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 427
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Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 307

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 247

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 187

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 127

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 7

Qy        661 GCTTCC 666
              ||||||
Db          6 GCTTCC 1
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RESULT 3
FCIL12P35
LOCUS       FCIL12P35                669 bp    mRNA    linear   MAM 18-APR-2005
DEFINITION  Felis catus mRNA for interleukin-12 p35 chain.
ACCESSION   Y07761
VERSION     Y07761.1  GI:2102662
KEYWORDS    interleukin-12 subunit p35.
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1
  AUTHORS   Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
  TITLE     Molecular cloning of cat interleukin-12
  JOURNAL   Immunogenetics 45 (6), 462-463 (1997)
   PUBMED   9089110
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Schijns,V.E.C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
            Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
            Utrecht, NETHERLANDS
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
                     /cell_type="lymphocyte"
                     /tissue_type="peripheral blood"
     gene            1. .669
                     /gene="IL-12.p35"
     CDS             1. .669
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ORIGIN

  Query Match             99.8%;  Score 664.4;  DB 14;  Length 669;
  Best Local Similarity   99.8%;  Pred. No. 1.4e-184;
  Matches  665;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
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Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
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Db        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
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Db        541 CCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        661 GCTTCC 666
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Db        661 GCTTCC 666


RESULT 4
FCU83185
LOCUS       FCU83185                669 bp    mRNA    linear   MAM 16-JUL-1999
DEFINITION  Felis catus interleukin-12 p35 subunit (IL-12) mRNA, complete cds.
ACCESSION   U83185
VERSION     U83185.1  GI:2735052
KEYWORDS    .
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Nucleotide and predicted peptide sequence of feline interleukin-12
            (IL-12)
  JOURNAL   DNA Seq. 8 (1-2), 77-82 (1997)
   PUBMED   9522125
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal
            Veterinary Medicine, University of Zurich, Winterthurerstrasse 260,
            Zurich, ZH 8057, Switzerland
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Felis catus"
                     /mol_type="mRNA"
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     CDS             1. .669
                     /note="cytokine"
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                     /protein_id="AAB93836.1"
                     /db_xref="GI:2735053"
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                     QTLLRAISNTLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
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                     LNSS"
ORIGIN

  Query Match             99.3%;  Score 661.2;  DB 14;  Length 669;
  Best Local Similarity   99.5%;  Pred. No. 1.3e-183;
  Matches  663;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
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Db        181 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
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Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
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Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
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Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
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Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
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Db        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        661 GCTTCC 666
              ||||||
Db        661 TCTTCC 666


RESULT 5
AR242438
LOCUS       AR242438               1441 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 8 from patent US 6472509.
ACCESSION   AR242438
VERSION     AR242438.1  GI:27288855
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1441)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 8 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .1441
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ORIGIN

  Query Match             99.3%;  Score 661.2;  DB 2;  Length 1441;
  Best Local Similarity   99.5%;  Pred. No. 1.4e-183;
  Matches  663;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
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Db        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
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Db        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
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Db        623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
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Db        743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

Qy        661 GCTTCC 666
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Db        803 TCTTCC 808


RESULT 6
AR280206
LOCUS       AR280206               1441 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 8 from patent US 6518045.
ACCESSION   AR280206
VERSION     AR280206.1  GI:29715596
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1441)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 8 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .1441
                     /organism="unknown"
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ORIGIN

  Query Match             99.3%;  Score 661.2;  DB 2;  Length 1441;
  Best Local Similarity   99.5%;  Pred. No. 1.4e-183;
  Matches  663;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
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Db        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
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Db        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562
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Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
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Db        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
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Db        623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
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Db        743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

Qy        661 GCTTCC 666
              ||||||
Db        803 TCTTCC 808


RESULT 7
AR322421
LOCUS       AR322421               1441 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 8 from patent US 6566097.
ACCESSION   AR322421
VERSION     AR322421.1  GI:33708174
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1441)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 8 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             99.3%;  Score 661.2;  DB 2;  Length 1441;
  Best Local Similarity   99.5%;  Pred. No. 1.4e-183;
  Matches  663;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
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Db        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
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Db        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
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Db        623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
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Db        683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
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Db        743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

Qy        661 GCTTCC 666
              ||||||
Db        803 TCTTCC 808


RESULT 8
AX076201
LOCUS       AX076201               669 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 2 from Patent WO0104155.
ACCESSION   AX076201
VERSION     AX076201.1  GI:12710826
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 2 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="feline IL-12 p35"
ORIGIN

  Query Match             97.8%;  Score 651.6;  DB 2;  Length 669;
  Best Local Similarity   98.6%;  Pred. No. 8.5e-181;
  Matches  657;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
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Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
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Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
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Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
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Db        181 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
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Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTG 300
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Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
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Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
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Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
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Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
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Db        481 AACATGCTGACAGCTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
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Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
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Qy        661 GCTTCC 666
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Db        661 GCTTCC 666
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RESULT 9
AX076483
LOCUS       AX076483                669 bp    DNA     linear   PAT 07-FEB-2001
DEFINITION  Sequence 9 from Patent WO0104280.
ACCESSION   AX076483
VERSION     AX076483.1  GI:12711035
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 9 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Sequence coding for SEQ ID NO 3, IL-12 p35"
ORIGIN

  Query Match             97.8%;  Score 651.6;  DB 2;  Length 669;
  Best Local Similarity   98.6%;  Pred. No. 8.5e-181;
  Matches  657;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
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Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
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Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
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Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
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Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
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Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
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Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
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Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
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Db        481 AACATGCTGACAGCTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
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Db        541 CCACAGAACTCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
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Db        601 CTTCTTCATGCTTTCAGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        661 GCTTCC 666
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Db        661 GCTTCC 666
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RESULT 10
AX076477
LOCUS       AX076477                4201 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 3 from Patent WO0104280.
ACCESSION   AX076477
VERSION     AX076477.1  GI:12711029
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 3 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .4201
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="IL-12p35 (pMOLfIL-12p35 (e-,_e31-)clone61)"
ORIGIN

  Query Match             97.8%;  Score 651.6;  DB 2;  Length 4201;
  Best Local Similarity   98.6%;  Pred. No. 1.1e-180;
  Matches  657;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
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Db       3047 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 3106

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3107 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 3166

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
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Db       3167 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 3226

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
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Db       3227 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 3286

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
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Db       3287 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTG 3346

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              |||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db       3347 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCT 3406

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
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Db       3407 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 3466

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3467 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 3526

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
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Db       3527 AACATGCTGACAGCTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTG 3586

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
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Db       3587 CCACAGAACTCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 3646

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
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Db       3647 CTTCTTCATGCTTTCAGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 3706

Qy        661 GCTTCC 666
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Db       3707 GCTTCC 3712
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RESULT 11
AR242451
LOCUS       AR242451                689 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 26 from patent US 6472509.
ACCESSION   AR242451
VERSION     AR242451.1  GI:27288868
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 26 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .689
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ORIGIN

  Query Match             96.4%;  Score 642;  DB 2;  Length 689;
  Best Local Similarity   97.7%;  Pred. No. 5.9e-178;
  Matches  651;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
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Db          7 ATGTGCCCCCCCCGTGGCCTCCTCCTGGTGACCATCCTGGTCCTGCTGAACCACCTGGAC 66

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 126
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Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 186

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
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Db        187 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 246

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
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Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 366

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
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Db        367 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 426

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
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Db        427 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 486

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
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Db        487 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 546

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
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Db        547 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 606

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
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Db        607 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666

Qy        661 GCTTCC 666
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Db        667 TCTTCC 672
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RESULT 12
AR280219
LOCUS       AR280219                689 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 26 from patent US 6518045.
ACCESSION   AR280219
VERSION     AR280219.1  GI:29715609
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 26 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             96.4%;  Score 642;  DB 2;  Length 689;
  Best Local Similarity   97.7%;  Pred. No. 5.9e-178;
  Matches  651;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
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Db          7 ATGTGCCCCCCCCGTGGCCTCCTCCTGGTGACCATCCTGGTCCTGCTGAACCACCTGGAC 66
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Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
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Db          67 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 126

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
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Db        127 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 186

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 246

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
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Db        247 AAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTG 306

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 366

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 426

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
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Db        427 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 486

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
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Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        547 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 606

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
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Db        607 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666

Qy        661 GCTTCC 666
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Db        667 TCTTCC 672
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RESULT 13
AR322434
LOCUS AR322434 689 bp mRNA linear PAT 17-AUG-2003
DEFINITION Sequence 26 from patent US 6566097.
ACCESSION AR322434
VERSION AR322434.1 GI:33708187
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 689)
AUTHORS Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
TITLE Feline cytokine protein
JOURNAL Patent: US 6566097-A 26 20-MAY-2003;
Juridical Foundation The Chemo-Sero-Therapeutic Research
Institute;;
EPX;
FEATURES Location/Qualifiers
source 1. .689
/organism="unknown"
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ORIGIN

Query Match 96.4%; Score 642; DB 2; Length 689;
Best Local Similarity 97.7%; Pred. No. 5.9e-178;
Matches 651; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
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Db          7 ATGTGCCCCCCCCGTGGCCTCCTCCTGGTGACCATCCTGGTCCTGCTGAACCACCTGGAC 66

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 126

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
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Db        127 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 186

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 246

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              |||||||||||||||||||||| | ||||||||| | ||||||||||||||||||||||
Db        247 AAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTG 306

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 366

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 426

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              |||||||||||||||||||||| | ||||||||||||||||||||||||||||||||||
Db        427 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 486

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 546

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        547 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 606

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666

Qy        661 GCTTCC 666
              ||||||
Db        667 TCTTCC 672
```

RESULT 14
AR151072
LOCUS AR151072 669 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 12 from patent US 6231850.
ACCESSION AR151072
VERSION AR151072.1 GI:15117122
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 669)
AUTHORS Okano,F., Satoh,M. and Yamada,K.
TITLE Canine interleukin 12
JOURNAL Patent: US 6231850-A 12 15-MAY-2001;
FEATURES Location/Qualifiers
source 1. .669
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Query Match 90.4%; Score 602; DB 2; Length 669;
Best Local Similarity 94.0%; Pred. No. 3.8e-166;
Matches 626; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

```
Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
```

```
                ||||||||||||||| |||||||||||||| |||||||||||||||| ||| ||||||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
                ||||| | || |||||||| |||||||||| || |||||||||||||||| |||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
                |||||||||||||||| ||||||| ||||| ||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
                |||||||||| || ||||||||||||||||||||||||||||||||||||||||| |||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
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Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
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Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
                |||||||||  |||||||||||||||| |||||||||||||||||||||||||||| ||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
                |||||||||||||| |||||||| |||||||||| || ||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
                |||||||||||||||||| |||||||||||||||||||||||| ||||||||||||||||||
Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
                |||||||| |||||||| ||||| ||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
                |||||||||||||||||||||| ||||||||| |||||||||||||| |||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        661 GCTTCC 666
                ||||||
Db        661 TCTTCC 666


RESULT 15
E15018
LOCUS       E15018                    669 bp    DNA     linear   PAT 28-JUL-1999
DEFINITION  Canine mRNA for interleukin 12 35kDa subunit,complete cds.
ACCESSION   E15018
VERSION     E15018.1  GI:5709701
KEYWORDS    JP 1998036397-A/2.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F.
  TITLE     CANINE INTERLEUKIN 12 AND ITS PRODUCTION
  JOURNAL   Patent: JP 1998036397-A 2 10-FEB-1998;
            TORAY IND INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 1998036397-A/2
            PD   10-FEB-1998
            PF   08-NOV-1996 JP 1996296789
            PR   08-NOV-1995 JP 95P   289729, 23-MAY-1996 JP 96P   128104 PI
            OKANO FUMIYOSHI
            PC   C07K14/54,C07H21/04,C12N5/10,C12N15/09,C12P21/02,(C12N5/10, PC
              C12R1:91),
            PC   (C12P21/02,C12R1:91);
            CC   strandedness: Double;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .669
            FT                   /organism='Canis sp.'
            FT                   /tissue_type='liver'
            FT   CDS             1. .669
            FT                   /product='interleukin12 35kDa subunit'.
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Canis sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9616"
ORIGIN

  Query Match             90.4%;  Score 602;  DB 2;  Length 669;
  Best Local Similarity   94.0%;  Pred. No. 3.8e-166;
  Matches  626;  Conservative    0;  Mismatches   40;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
                |||||||||||||| |||||||||||||| |||||||||||||||| ||| ||||||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
                ||||| | || |||||||| |||||||||| || |||||||||||||||| |||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
                |||||||||||||||| |||||||| ||||| ||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
                |||||||||| || ||||||||||||||||||||||||||||||||||||||||| |||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
                |||||||||||||||||| |||||||||| |||||||||||||||||  ||||| |||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
                |||||||||  |||||||||||||||| |||||||||||||||||||||||||||| ||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
                |||||||||||||| |||||||| |||||||||| || ||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
                |||||||||||||||||| |||||||||||||||||||||||| ||||||||||||||||||
Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
                |||||||| |||||||| ||||| ||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
                |||||||||||||||||||||| ||||||||| |||||||||||||| |||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        661 GCTTCC 666
                ||||||
Db        661 TCTTCC 666


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OM nucleic - nucleic search, using sw model

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Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	666	100.0	666	6	ABK98947	Abk98947 Feline in
	2	666	100.0	666	6	ABK98946	Abk98946 Feline in
	3	666	100.0	666	14	ADV34685	Adv34685 Feline si
c	4	666	100.0	666	14	ADV34687	Adv34687 Feline si
	5	661.2	99.3	1441	2	AAV56628	Aav56628 Feline FL
	6	653.2	98.1	679	4	AAF26097	Aaf26097 Feline fi
	7	651.6	97.8	669	4	AAF26083	Aaf26083 Feline IL
	8	651.6	97.8	669	4	AAF26086	Aaf26086 Feline IL
	9	651.6	97.8	4201	4	AAF26077	Aaf26077 Feline IL
	10	642	96.4	689	2	AAV56641	Aav56641 Feline FL
	11	602	90.4	669	2	AAV13819	Aav13819 Canine IL
	12	600.4	90.2	666	6	ABK98955	Abk98955 Canine in
c	13	600.4	90.2	666	6	ABK98956	Abk98956 Canine in
c	14	600.4	90.2	666	14	ADV34700	Adv34700 Canine si
	15	600.4	90.2	666	14	ADV34698	Adv34698 Canine si
	16	600.4	90.2	669	2	AAX03163	Aax03163 Nucleic a
	17	600.4	90.2	669	2	AAX35626	Aax35626 Nucleic a
	18	600.4	90.2	669	4	AAI64389	Aai64389 Canine co
	19	600.4	90.2	1282	2	AAX18178	Aax18178 Canine fu
	20	600.4	90.2	1455	6	ABK99003	Abk99003 Canine in
c	21	600.4	90.2	1455	6	ABK99004	Abk99004 Canine in
c	22	600.4	90.2	1455	14	ADV34756	Adv34756 Canine si
	23	600.4	90.2	1455	14	ADV34754	Adv34754 Canine si
	24	597	89.6	639	4	AAF26098	Aaf26098 Plasmid p
	25	592.4	88.9	669	13	ADT04852	Adt04852 Canine in
	26	589.4	88.5	591	6	ABK98948	Abk98948 Feline in
c	27	589.4	88.5	591	6	ABK98949	Abk98949 Feline in
	28	589.4	88.5	591	14	ADV34688	Adv34688 Feline si
c	29	589.4	88.5	591	14	ADV34690	Adv34690 Feline si
	30	587.6	88.2	669	2	AAV13818	Aav13818 Canine IL
	31	587.6	88.2	669	2	AAX03153	Aax03153 Nucleic a
	32	587.6	88.2	669	2	AAX35616	Aax35616 Nucleic a
	33	587.6	88.2	669	4	AAI64379	Aai64379 Canine co
	34	587.6	88.2	669	11	ADZ25701	Adz25701 Canine in
	35	586.2	88.0	591	2	AAV56629	Aav56629 Feline FL
c	36	572.2	85.9	1533	6	ABK98954	Abk98954 Feline in
	37	572.2	85.9	1533	6	ABK98953	Abk98953 Feline in
c	38	572.2	85.9	1533	14	ADV34697	Adv34697 Feline si
	39	572.2	85.9	1533	14	ADV34695	Adv34695 Feline si
	40	572.2	85.9	1599	6	ABK98950	Abk98950 Feline in
c	41	572.2	85.9	1599	6	ABK98951	Abk98951 Feline in
	42	572.2	85.9	1599	14	ADV34691	Adv34691 Feline si
c	43	572.2	85.9	1599	14	ADV34693	Adv34693 Feline si
	44	570.8	85.7	660	5	AAD15218	Aad15218 Modified
	45	564.4	84.7	660	5	AAD15216	Aad15216 Modified

ALIGNMENTS

RESULT 1
ABK98947/c
ID ABK98947 standard; cDNA; 666 BP.
XX
AC ABK98947;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p35-666 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Example 3; Page 56; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,

```
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 666 BP; 160 A; 138 C; 179 G; 189 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 666;  DB 6;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-195;
  Matches  666;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 607

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 547

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 427

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 307

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 247

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 187

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 127

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 7

Qy        661 GCTTCC 666
              ||||||
Db          6 GCTTCC 1


RESULT 2
ABK98946
ID   ABK98946 standard; cDNA; 666 BP.
XX
AC   ABK98946;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p35-666 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69304.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 54-55; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 666 BP; 189 A; 179 C; 138 G; 160 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 666;  DB 6;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-195;
  Matches  666;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
```

```
Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        661 GCTTCC 666
              ||||||
Db        661 GCTTCC 666
```

RESULT 3
ADV34685
ID ADV34685 standard; cDNA; 666 BP.
XX
AC ADV34685;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain IL-12p35 full-length cDNA, nFeIL-12p35 666.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; gene; ss.
XX
OS Felis catus.
XX
FH Key   Location/Qualifiers
FT CDS   1. .666
FT   /*tag= a
FT   /product= "PFeIL-12p35 222 protein "
FT   /partial
FT   /note= "No stop codon"
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
DR P-PSDB; ADV34686.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Claim 23; SEQ ID NO 32; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain IL-12p35 subunit protein
CC encoding full-length cDNA.
XX
SQ Sequence 666 BP; 189 A; 179 C; 138 G; 160 T; 0 U; 0 Other;

  Query Match   100.0%; Score 666; DB 14; Length 666;
  Best Local Similarity 100.0%; Pred. No. 1.7e-195;
  Matches 666; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        661 GCTTCC 666
              ||||||
Db        661 GCTTCC 666
```

RESULT 4
ADV34687/c
ID ADV34687 standard; DNA; 666 BP.
XX
AC ADV34687;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain IL-12p35 complementary DNA, nFeIL-12p35 666.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;

```
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 34; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12p35 subunit full-length
CC   complementary DNA.
XX
SQ   Sequence 666 BP; 160 A; 138 C; 179 G; 189 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 666;  DB 14;  Length 666;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-195;
  Matches  666;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 607

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 547

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 427

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 307

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 247

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 187

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 127

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 7

Qy        661 GCTTCC 666
              ||||||
Db          6 GCTTCC 1


RESULT 5
AAV56628
ID   AAV56628 standard; cDNA; 1441 BP.
XX
AC   AAV56628;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp35 cDNA.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             133. .811
FT                   /*tag=  a
FT   sig_peptide     133. .217
FT                   /*tag=  b
FT   mat_peptide     218. .808
FT                   /*tag=  c
FT                   /product= "FLAFp35"
FT                   /note= "feline cytokine"
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP001824.
XX
PR   04-JUN-1996;   96JP-00165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76175.
XX
PT   Novel feline cytokine protein - useful for treating feline auto:immune
PT   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS   Claim 22; Page 57-58; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine protein, FLAFp35. This
CC   protein can be used in the production of a FLAFp35/FLAFp40 heterodimer
CC   which can potentiate the cytotoxic activity of feline cytotoxic T
CC   lymphocyte cells. Such proteins are used for treatment of feline
CC   autoimmune diseases e.g. as caused by feline herpes virus or feline
CC   calcivirus
XX
SQ   Sequence 1441 BP; 451 A; 325 C; 258 G; 407 T; 0 U; 0 Other;

  Query Match           99.3%;  Score 661.2;  DB 2;  Length 1441;
  Best Local Similarity  99.5%;  Pred. No. 7.9e-194;
```

```
  Matches  663;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

Qy        661 GCTTCC 666
              ||||||
Db        803 TCTTCC 808


RESULT 6
AAF26097
ID   AAF26097 standard; DNA; 679 BP.
XX
AC   AAF26097;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline fil12p35a DNA.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS   Felis sp.
XX
PN   WO200104155-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002263.
XX
PR   08-JUL-1999;   99CH-00001259.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Lutz H,  Leutenegger C,  Pedersen N,  Schroff M,  Wittig B;
XX
DR   WPI; 2001-147178/15.
XX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs.
XX
PS   Disclosure; Fig 2; 35pp; German.
XX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
CC   following: (i) as immunostimulant, for preventative or therapeutic use;
CC   and (ii) treating tumors and autoimmune diseases, or diseases associated
CC   with a Th1 defect, especially pre-existing infections by feline immune
CC   deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ   Sequence 679 BP; 196 A; 180 C; 140 G; 163 T; 0 U; 0 Other;

  Query Match             98.1%;  Score 653.2;  DB 4;  Length 679;
  Best Local Similarity   98.8%;  Pred. No. 1.6e-191;
  Matches  658;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGGCTGGCCTCCAGAAAGACCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
                ||||||||  |||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAACCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
                |||||||||||||||||||||||||||||||||||||| | ||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAAAGTGATGAGCTATCTGAAT 660

Qy        661 GCTTCC 666
                |||||
Db        661 TCTTCC 666


RESULT 7
AAF26083
ID   AAF26083 standard; DNA; 669 BP.
XX
AC   AAF26083;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p35 encoding DNA SEQ ID 4.
XX
KW   Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW   interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS   Felis sp.
XX
PN   WO200104280-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002262.
XX
PR   08-JUL-1999;   99CH-00001258.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
XX
PI   Leutenegger C,  Schroff M,  Wittig B,  Lutz H;
XX
DR   WPI; 2001-147190/15.
XX
PT   Vaccine for treating or preventing lentivirus infection in cats, contains
PT   nucleic acid sequence encoding viral protein under control of eukaryotic
PT   promoter.
XX
PS   Claim 14; Page 37; 37pp; German.
XX
CC   This invention describes a novel vaccine (A) for prevention or treatment
CC   of lentivirus infection in felines which comprises an immunizing nucleic
CC   acid sequence (I) that contains, or comprises, at least part of a gene
CC   encoding a protein (II) of the virus, under control of a eukaryotic
CC   promoter functional in the relevant animal. (II) is especially the
CC   envelope (env) protein. The invention also describes (1) vaccine (A)
CC   containing an immunizing protein, or fragment, from a lentivirus plus at
CC   least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC   lentivirus protein, or fragment, especially derived from feline immune
CC   deficiency virus (FIV), by expressing the corresponding nucleic acid
CC   sequence in a host cell. The products of the invention have antiviral
CC   activity. The vaccine (A) and related protein-based vaccines, are
CC   particularly used to treat or prevent lentivirus infections in domestic
CC   cats, especially feline immune deficiency virus (FIV). Vaccination with
CC   (A) allows differentiation between vaccinated and infected animals, from
CC   the antibody status. The vaccines may be formulated with an adjuvant
CC   (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC   immune response, particularly a Th1 response
XX
SQ   Sequence 669 BP; 189 A; 179 C; 140 G; 161 T; 0 U; 0 Other;

  Query Match             97.8%;  Score 651.6;  DB 4;  Length 669;
  Best Local Similarity   98.6%;  Pred. No. 5.1e-191;
  Matches  657;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              |||||||||||||||||||||||||| | |||||||||||| ||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        661 GCTTCC 666
              ||||||
Db        661 GCTTCC 666


RESULT 8
AAF26086
ID   AAF26086 standard; DNA; 669 BP.
XX
AC   AAF26086;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p35 encoding DNA.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS   Felis sp.
XX
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PN WO200104155-A2.
XX
PD 18-JAN-2001.
XX
PF 08-JUL-2000; 2000WO-DE002263.
XX
PR 08-JUL-1999; 99CH-00001259.
XX
PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA (UYZU-) UNIV ZUERICH.
PA (REGC) UNIV CALIFORNIA.
XX
PI Lutz H, Leutenegger C, Pedersen N, Schroff M, Wittig B;
XX
DR WPI; 2001-147178/15.
XX
PT Recombinant feline interleukin-12, useful as immunostimulant and for
PT treating e.g. viral infections in cats, and related nucleic acid
PT constructs.
XX
PS Claim 3; Page 31; 35pp; German.
XX
CC This invention describes a novel feline interleukin-12 (fIL-12)
CC polypeptide (I) that is expressed, by recombinant gene expression in
CC eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC of subunits p35 and p40. These proteins are formed so that, in equimolar
CC concentrations and in presence of an immunizing antigen, they can be
CC administered to carnivores, particularly domestic cats. The invention
CC also describes a nucleic acid construct (II) encoding fIL-12 containing
CC sequences at least 95% identical with the p40- and p35-encoding sequences
CC (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC as immunostimulants for immunization against infectious diseases and/or
CC for treating infections or tumors in felines, especially domestic cats.
CC The products of the invention have immunostimulatory, antiviral and
CC antitumor activity. Nucleic acid constructs that encode (II) are useful
CC as adjuvants for prophylactic immunization against viral diseases and for
CC treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC is useful for carnivores, and particularly domestic cats in the
CC following: (i) as immunostimulant, for preventative or therapeutic use;
CC and (ii) treating tumors and autoimmune diseases, or diseases associated
CC with a Th1 defect, especially pre-existing infections by feline immune
CC deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ Sequence 669 BP; 189 A; 179 C; 140 G; 161 T; 0 U; 0 Other;

Query Match 97.8%; Score 651.6; DB 4; Length 669;
Best Local Similarity 98.6%; Pred. No. 5.1e-191;
Matches 657; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              |||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              |||||||||||||||||||||||||| | |||||||||||| ||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        661 GCTTCC 666
              ||||||
Db        661 GCTTCC 666
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RESULT 9
AAF26077
ID AAF26077 standard; DNA; 4201 BP.
XX
AC AAF26077;
XX
DT 24-APR-2001 (first entry)
XX
DE Feline IL-12p35 encoding DNA SEQ ID 3.
XX
KW Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS Felis sp.
XX
PN WO200104280-A2.
XX
PD 18-JAN-2001.
XX
PF 08-JUL-2000; 2000WO-DE002262.
XX
PR 08-JUL-1999; 99CH-00001258.
XX
PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA (UYZU-) UNIV ZUERICH.
XX
PI Leutenegger C, Schroff M, Wittig B, Lutz H;
XX
DR WPI; 2001-147190/15.
XX
PT Vaccine for treating or preventing lentivirus infection in cats, contains
PT nucleic acid sequence encoding viral protein under control of eukaryotic
PT promoter.
XX
PS Disclosure; Page 31-33; 37pp; German.
XX
CC This invention describes a novel vaccine (A) for prevention or treatment
CC of lentivirus infection in felines which comprises an immunizing nucleic
CC acid sequence (I) that contains, or comprises, at least part of a gene
CC encoding a protein (II) of the virus, under control of a eukaryotic
CC promoter functional in the relevant animal. (II) is especially the
CC envelope (env) protein. The invention also describes (1) vaccine (A)
CC containing an immunizing protein, or fragment, from a lentivirus plus at
CC least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC lentivirus protein, or fragment, especially derived from feline immune
CC deficiency virus (FIV), by expressing the corresponding nucleic acid
CC sequence in a host cell. The products of the invention have antiviral

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CC   activity. The vaccine (A) and related protein-based vaccines, are
CC   particularly used to treat or prevent lentivirus infections in domestic
CC   cats, especially feline immune deficiency virus (FIV). Vaccination with
CC   (A) allows differentiation between vaccinated and infected animals, from
CC   the antibody status. The vaccines may be formulated with an adjuvant
CC   (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC   immune response, particularly a Th1 response
XX
SQ   Sequence 4201 BP; 1086 A; 1055 C; 999 G; 1061 T; 0 U; 0 Other;

  Query Match             97.8%;  Score 651.6;  DB 4;  Length 4201;
  Best Local Similarity   98.6%;  Pred. No. 1.3e-190;
  Matches  657;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3047 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 3106

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3107 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 3166

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3167 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 3226

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       3227 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 3286

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       3287 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTG 3346

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       3347 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCT 3406

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3407 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 3466

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3467 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 3526

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              |||||||||||||||||||||||||| | |||||||||||| ||||||||||||||||||
Db       3527 AACATGCTGACAGCTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTG 3586

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       3587 CCACAGAACTCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 3646

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       3647 CTTCTTCATGCTTTCAGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 3706

Qy        661 GCTTCC 666
              ||||||
Db       3707 GCTTCC 3712


RESULT 10
AAV56641
ID   AAV56641 standard; DNA; 689 BP.
XX
AC   AAV56641;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp35 DNA fragment.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ss.
XX
OS   Felis catus.
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP001824.
XX
PR   04-JUN-1996;   96JP-00165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
XX
PT   Novel feline cytokine protein - useful for treating feline auto:immune
PT   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS   Claim 24; Page 67; 94pp; Japanese.
XX
CC   This sequence encodes a fragment of a novel feline cytokine protein,
CC   FLAFp35. This protein can be used in the production of a FLAFp35/FLAFp40
CC   heterodimer which can potentiate the cytotoxic activity of feline
CC   cytotoxic T lymphocyte cells. Such proteins are used for treatment of
CC   feline autoimmune diseases e.g. as caused by feline herpes virus or
CC   feline calcivirus
XX
SQ   Sequence 689 BP; 192 A; 193 C; 145 G; 159 T; 0 U; 0 Other;

  Query Match             96.4%;  Score 642;  DB 2;  Length 689;
  Best Local Similarity   97.7%;  Pred. No. 4.9e-188;
  Matches  651;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              |||||||| || |||||||||||||| || |||||||||||||| | ||||||||||||
Db          7 ATGTGCCCCCCCCGTGGCCTCCTCCTGGTGACCATCCTGGTCCTGCTGAACCACCTGGAC 66

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 126

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 186

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 246

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              |||||||||||||||||||||||| | ||||||||| | ||||||||||||||||||||
Db        247 AAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTG 306

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 366

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 426

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||| | ||||||||||||||||||||||||||||||||
Db        427 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 486

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 546
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Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        547 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 606

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        607 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666

Qy        661 GCTTCC 666
              ||||||
Db        667 TCTTCC 672


RESULT 11
AAV13819
ID   AAV13819 standard; cDNA to mRNA; 669 BP.
XX
AC   AAV13819;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P35 subunit cDNA.
XX
KW   Canine; interleukin-12 P35 subunit; IL-12 P35 subunit; antitumour;
KW   antiviral; vaccine adjuvant; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .669
FT                   /*tag= a
FT                   /product= "interleukin-12_P35_subunit"
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-00296789.
XX
PR   08-NOV-1995;   95JP-00289729.
PR   23-MAY-1996;   96JP-00128104.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   P-PSDB; AAW41793.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected.
XX
PS   Claim 11; Page 11-12; 12pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin-12 (IL-12) P35 subunit.
CC   A canine IL-12 comprising a P40 and P35 subunit is capable of inducing an
CC   antiviral activating factor and the expression of class II MHC molecules
CC   in canine tumour cells, stimulating proliferation of canine blastogenic
CC   lymphocytes and activating canine leukocytes to inhibit canine tumour
CC   cells. The canine IL-12 can be used in veterinary medicines, e.g.
CC   antitumour, antivirus and vaccine adjuvant activities are expected
XX
SQ   Sequence 669 BP; 185 A; 177 C; 144 G; 163 T; 0 U; 0 Other;

  Query Match             90.4%;  Score 602;  DB 2;  Length 669;
  Best Local Similarity   94.0%;  Pred. No. 1.2e-175;
  Matches  626;  Conservative    0;  Mismatches   40;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              |||||||||||||| |||||||||||||| |||||||||||||| ||| ||||||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||| | || |||||||| |||||||||| || ||||||||||||||| |||||||||

Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              |||||||||||||||| ||||||| ||||| ||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              |||||||||||| || ||||||||||||||||||||||||||||||||||||||||| |||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              |||||||||||||||||| |||||||||| ||||||||||||||||  ||||| |||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              |||||||||  |||||||||||||| |||||||||||||||||||||||||||| ||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||| |||||||| |||||||||| || ||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              |||||||||||||||| |||||||||||||||||||||| ||||||||||||||||||
Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||| |||||||| ||||| ||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              |||||||||||||||||||||||||| ||||||||| |||||||||||| |||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        661 GCTTCC 666
              ||||||
Db        661 TCTTCC 666


RESULT 12
ABK98955
ID   ABK98955 standard; cDNA; 666 BP.
XX
AC   ABK98955;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p35-666 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
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DR   P-PSDB; ABG69308.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 67-68; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 666 BP; 182 A; 177 C; 145 G; 162 T; 0 U; 0 Other;

  Query Match             90.2%;  Score 600.4;  DB 6;  Length 666;
  Best Local Similarity   93.8%;  Pred. No. 3.8e-175;
  Matches  625;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||| ||||||||||||||| |||||||||||||| ||| ||||||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||| | || |||||||| |||||||||| || |||| |||||||||||| |||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||| ||||||| ||||| ||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              |||||||||| || ||||||||||||||||||||||||||||||||||||||||||| |||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              |||||||||||||||||| |||||||| |||||||||||||||||  ||||| |||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              |||||||||  |||||||||||||| |||||||||||||||||||||||| ||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              |||||||||||||| |||||||| |||||||||| || ||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||| |||||||||||||||||||||||||| ||||||||||||||||
Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||| |||||||| ||||| ||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              |||||||||||||||||||||||||| ||||||||| |||||||||||| |||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        661 GCTTCC 666
              ||||||
Db        661 TCTTCC 666


RESULT 13
ABK98956/c
ID   ABK98956 standard; cDNA; 666 BP.
XX
AC   ABK98956;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p35-66 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Disclosure; Page 68-69; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 666 BP; 162 A; 145 C; 177 G; 182 T; 0 U; 0 Other;

  Query Match             90.2%;  Score 600.4;  DB 6;  Length 666;
  Best Local Similarity   93.8%;  Pred. No. 3.8e-175;
  Matches  625;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||| ||||||||||||||| |||||||||||||| ||| ||||||||||
Db        666 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 607

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||| | || |||||||| |||||||||| || |||| |||||||||||| |||||||||
Db        606 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 547

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||| ||||||| ||||| ||||||||||||||||||||||||||||||
Db        546 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 487
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Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              |||||||||||  || ||||||||||||||||||||||||||||||||||||||||| |||
Db        486 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 427

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              |||||||||||||||||  ||||||||| ||||||||||||||||   ||||| |||||
Db        366 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 307

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              |||||||||  ||||||||||||||| ||||||||||||||||||||||||||| ||||
Db        306 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 247

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              |||||||||||||| |||||||| |||||||||| || ||||||||||||||||||||||
Db        246 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 187

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              |||||||||||||||| ||||||||||||||||||||| ||||||||||||||||||||
Db        186 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 127

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||| |||||||| ||||| ||||||||||||||||||||||||||||||||||||
Db        126 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              |||||||||||||||||||||||||| ||||||||| |||||||||||| |||||||||
Db         66 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 7

Qy        661 GCTTCC 666
              ||||||
Db          6 TCTTCC 1


RESULT 14
ADV34700/c
ID   ADV34700 standard; DNA; 666 BP.
XX
AC   ADV34700;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p35 complementary DNA, nCaIL-12p35 666.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 48; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p35 subunit full-length
CC   complementary DNA.
XX
SQ   Sequence 666 BP; 162 A; 145 C; 177 G; 182 T; 0 U; 0 Other;

  Query Match            90.2%;  Score 600.4;  DB 14;  Length 666;
  Best Local Similarity   93.8%;  Pred. No. 3.8e-175;
  Matches  625;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              |||||||||||||| |||||||||||||| |||||||||||||| ||| ||||||||||
Db        666 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 607

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||| | || |||||||| |||||||||| || |||| |||||||||||| |||||||||
Db        606 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 547

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||| ||||||| |||| ||||||||||||||||||||||||||||
Db        546 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              |||||||||||  || ||||||||||||||||||||||||||||||||||||||||| |||
Db        486 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 427

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              |||||||||||||||||  ||||||||| ||||||||||||||||   ||||| |||||
Db        366 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 307

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              |||||||||  ||||||||||||||| ||||||||||||||||||||||||||| ||||
Db        306 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 247

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              |||||||||||||| |||||||| |||||||||| || ||||||||||||||||||||||
Db        246 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 187

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              |||||||||||||||| ||||||||||||||||||||| ||||||||||||||||||||
Db        186 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 127

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||| |||||||| ||||| ||||||||||||||||||||||||||||||||||||
Db        126 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              |||||||||||||||||||||||||| ||||||||| |||||||||||| |||||||||
Db         66 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 7

Qy        661 GCTTCC 666
              ||||||
Db          6 TCTTCC 1


RESULT 15
ADV34698
ID   ADV34698 standard; cDNA; 666 BP.
XX
AC   ADV34698;
XX
DT   24-FEB-2005  (first entry)
XX
```

```
DE   Canine single chain IL-12p35 full-length cDNA, nCaIL-12p35 666.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .666
FT                   /*tag=  a
FT                   /product= "PCaIL-12p222 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34699.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 46; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p35 subunit protein
CC   encoding full-length cDNA.
XX
SQ   Sequence 666 BP; 182 A; 177 C; 145 G; 162 T; 0 U; 0 Other;

  Query Match             90.2%;  Score 600.4;  DB 14;  Length 666;
  Best Local Similarity   93.8%;  Pred. No. 3.8e-175;
  Matches  625;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
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Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              |||||||||||||||| ||||||| ||||| ||||||||||||||||||||||||||||
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Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
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Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
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Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
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Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
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Qy        661 GCTTCC 666
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Db        661 TCTTCC 666


Search completed: June 10, 2006, 04:50:49
Job time : 493.979 secs
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 10, 2006, 03:16:38 ; Search time 3889.4 Seconds
(without alignments)
9575.336 Million cell updates/sec

Title: US-10-821-670A-32
Perfect score: 666
Sequence: 1 atgtgcccgccgcgtggcct.....tgagctatctgaatgcttcc 666

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	2	532.4	79.9	762	14	DQ033873	DQ033873 Pan trogl
	3	449.6	67.5	935	4	CD013914	CD013914 90138124
	4	449	67.4	1136	4	CD013915	CD013915 90138132
	5	332.8	50.0	863	4	CD013916	CD013916 90138296
	6	266	39.9	812	2	BG702253	BG702253 602683459
	7	259.6	39.0	1938	6	BC035571	BC035571 Homo sapi
c	8	216.6	32.5	1099	2	BI523344	BI523344 603175938
	9	216.4	32.5	589	1	AI050362	AI050362 ub30a07.r
	10	214.2	32.2	563	3	BU698113	BU698113 LL2in1206
c	11	209.2	31.4	778	1	AJ820622	AJ820622 AJ820622
	12	200	30.0	373	7	BF552757	BF552757 UI-R-C0-i
	13	193.2	29.0	832	2	BI523569	BI523569 603175938
	14	192.8	28.9	581	3	BP260963	BP260963 BP260963
	15	190	28.5	561	3	BU699383	BU699383 LL2in1157
c	16	175.4	26.3	777	4	CB168830	CB168830 CWI602769
	17	175.2	26.3	412	4	CB801533	CB801533 AMGNNUC:S
	18	173	26.0	427	10	DT930939	DT930939 S13.1784
	19	166.8	25.0	456	10	DT913216	DT913216 S13.1426
	20	165	24.8	371	3	BU699957	BU699957 B4-79 Hem
	21	164.2	24.7	571	3	BP261459	BP261459 BP261459
	22	157.8	23.7	354	4	BY230958	BY230958 BY230958
	23	154	23.1	1299	6	AK153729	AK153729 Mus muscu
	24	145.2	21.8	342	2	BM257856	BM257856 521721 MA
	25	129.4	19.4	777	14	CT080894	CT080894 Sus scrof
	26	117.8	17.7	551	10	DT919655	DT919655 PCRS30821
	27	111.2	16.7	373	3	BU695376	BU695376 B1-30 Hem
	28	102	15.3	508	9	DA505380	DA505380 DA505380
	29	101	15.2	692	5	CJ137697	CJ137697 CJ137697
	30	95.2	14.3	463	9	DR007201	DR007201 TC124111
	31	86.2	12.9	592	12	CE159257	CE159257 tigr-gss-
	32	77.6	11.7	840	11	BZ261813	BZ261813 CH230-420
	33	76	11.4	447	2	BI824638	BI824638 603033580
c	34	74.6	11.2	940	14	BX963061	BX963061 Forward s
	35	69.6	10.5	382	4	CB809298	CB809298 AMGNNUC:T
	36	69	10.4	558	9	CX570753	CX570753 RVL1941 W
	37	62.2	9.3	361	3	BU694675	BU694675 B2-56 Hem
	38	61.6	9.2	344	14	BX537236	BX537236 INRA porc
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	42	44.6	6.7	840	8	CN228296	CN228296 RJB052F11
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ALIGNMENTS

RESULT 1
DQ033872
LOCUS DQ033872 762 bp DNA linear GSS 02-JUN-2005
DEFINITION Homo sapiens IL12A gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION DQ033872
VERSION DQ033872.1 GI:66885081
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 762)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 762)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.
FEATURES Location/Qualifiers
source 1. .762
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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gene <1. .>762
/gene="IL12A"
/locus_tag="HC3464"
ORIGIN

Query Match 80.4%; Score 535.6; DB 14; Length 762;
Best Local Similarity 89.0%; Pred. No. 8.8e-146;
Matches 593; Conservative 0; Mismatches 64; Indels 9; Gaps 1;

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Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
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Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
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Db        214 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 273

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
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Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
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Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
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Db        514 TTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAA 573

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
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Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
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Db        694 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAAT 753

Qy        661 GCTTCC 666
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Db        754 GCTTCC 759
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RESULT 2
DQ033873
LOCUS DQ033873 762 bp DNA linear GSS 02-JUN-2005
DEFINITION Pan troglodytes IL12A gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION DQ033873
VERSION DQ033873.1 GI:66885082
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 762)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 762)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.
FEATURES Location/Qualifiers
source 1. .762
/organism="Pan troglodytes"
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ORIGIN

Query Match 79.9%; Score 532.4; DB 14; Length 762;
Best Local Similarity 88.7%; Pred. No. 7.7e-145;
Matches 591; Conservative 0; Mismatches 66; Indels 9; Gaps 1;

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Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
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Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
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Qy        661 GCTTCC 666
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Db        754 GCTTCC 759
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RESULT 3
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LOCUS       CD013914                935 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION  90138124 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD013914
VERSION     CD013914.1  GI:37777444
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 935)
  AUTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
            Au-Young,J. and Stuve,L.L.
  TITLE     PCR isolation and cloning of novel splice variant mRNAs from known
            drug target genes
  JOURNAL   Genomics 83 (4), 566-571 (2004)
   PUBMED   15028279
COMMENT     Contact: Jin, P.
            Incyte Corporation
            3160 Porter Drive, Palo Alto, CA 94304, USA
            Tel: 650 621 8639
            Fax: 650 621 8965
            Email: pjin@incyte.com.
FEATURES             Location/Qualifiers
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                     /note="Vector: pDrive Cloning Vector; RT-PCR was performed
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                     frame. PCR products were subcloned into pDrive Cloning
                     Vector and sequenced completely using M13 forward and
                     reverse primers. Sequencing gaps were closed by
                     re-sequencig using primers flanking the gapped areas."
ORIGIN

  Query Match            67.5%;  Score 449.6;  DB 4;  Length 935;
  Best Local Similarity  83.5%;  Pred. No. 1.9e-120;
  Matches  556;  Conservative    0;  Mismatches   59;  Indels   51;  Gaps    2;

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              ||||| || |||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        695 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 754

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              |||||||||||||||||||||| |||||||  ||  ||||| ||||||||||||||||
Db        755 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAAT 814

Qy        661 GCTTCC 666
              ||||||
Db        815 GCTTCC 820


RESULT 4
CD013915
LOCUS       CD013915                1136 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION  90138132 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD013915
VERSION     CD013915.1  GI:37777445
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1136)
  AUTHORS   Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
            Au-Young,J. and Stuve,L.L.
  TITLE     PCR isolation and cloning of novel splice variant mRNAs from known
            drug target genes
  JOURNAL   Genomics 83 (4), 566-571 (2004)
   PUBMED   15028279
COMMENT     Contact: Jin, P.
            Incyte Corporation
            3160 Porter Drive, Palo Alto, CA 94304, USA
            Tel: 650 621 8639
            Fax: 650 621 8965
            Email: pjin@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .1136
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Single gene library"
                     /note="Vector: pDrive Cloning Vector; RT-PCR was performed
                     using gene-specific primers flanking the open-reading
                     frame. PCR products were subcloned into pDrive Cloning
                     Vector and sequenced completely using M13 forward and
                     reverse primers. Sequencing gaps were closed by
                     re-sequencig using primers flanking the gapped areas."
ORIGIN

  Query Match            67.4%;  Score 449;  DB 4;  Length 1136;
  Best Local Similarity  79.9%;  Pred. No. 3e-120;
  Matches  592;  Conservative    0;  Mismatches   65;  Indels   84;  Gaps    2;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||| ||  ||||  |||||||||||||  | | |||||||||        |||||||
Db        290 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCT---------CCTGGAC 340

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||  ||||||||    |||| |||  ||||||||||||||  |||
Db        341 CACCTCAGTTTGGCCAGAGACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 400

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||  |||||||||||| ||||||| | ||| |||||||| ||| ||||||||||||||||
```

```
Db        401 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 460

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              |||||||||||||||| | |||||||| ||||||||||||||||||||||||||||||||
Db        461 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 520

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              |||||||||||||||||||||| |||||| |||||||||||| ||||||||||||||||
Db        521 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTA 580

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACT-------------------------------- 327
                |||||||||||| |||| | ||||||
Db        581 AATTCCAGAGAGACCTCTTTCATAACTGTAAGTCAAAAAATGAAAAGTTTCAGCCTGTAT 640

Qy        328 ----------------------------------------AATGGGAGTTGCCTGGCC 345
                                                       ||||||||||||||||||
Db        641 GATGAATTCATATCACTGATGTCTGATTATTTTTTCCTCTAGAATGGGAGTTGCCTGGCC 700

Qy        346 TCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAG 405
              |||||||||||||||||||| | |||||||||||| ||||| ||||| |||||||||
Db        701 TCCAGAAAGACCTCTTTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAG 760

Qy        406 ATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAG 465
              |||||||||||||||||||| |||||||||||||||  | ||||||||||| ||||||
Db        761 ATGTACCAGGTGGAGTTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAG 820

Qy        466 ATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTC 525
              |||||||| |||||||||||||| ||| |||||||||||| | |||||||||||| ||
Db        821 ATCTTTCTAGATCAAAACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTC 880

Qy        526 AACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 585
              ||||||| |||||||||||| || |||||||| ||||||||||||||||||||||||||
Db        881 AACAGTGAGACTGTGCCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAA 940

Qy        586 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATG 645
              |||||||||||||||||||||||||||||||||||||||| |||||||| ||  ||||| ||
Db        941 ATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTG 1000

Qy        646 ATGAGCTATCTGAATGCTTCC 666
              |||||||||||||||||||||
Db       1001 ATGAGCTATCTGAATGCTTCC 1021
```

RESULT 5
CD013916
LOCUS CD013916 863 bp mRNA linear EST 21-OCT-2003
DEFINITION 90138296 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION CD013916
VERSION CD013916.1 GI:37777446
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 863)
AUTHORS Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R., Au-Young,J. and Stuve,L.L.
TITLE PCR isolation and cloning of novel splice variant mRNAs from known drug target genes
JOURNAL Genomics 83 (4), 566-571 (2004)
PUBMED 15028279
COMMENT Contact: Jin, P.
Incyte Corporation
3160 Porter Drive, Palo Alto, CA 94304, USA
Tel: 650 621 8639
Fax: 650 621 8965
Email: pjin@incyte.com.
FEATURES Location/Qualifiers
source 1. .863
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Single gene library"
/note="Vector: pDrive Cloning Vector; RT-PCR was performed using gene-specific primers flanking the open-reading frame. PCR products were subcloned into pDrive Cloning Vector and sequenced completely using M13 forward and reverse primers. Sequencing gaps were closed by re-sequencig using primers flanking the gapped areas."
ORIGIN

Query Match 50.0%; Score 332.8; DB 4; Length 863;
Best Local Similarity 91.7%; Pred. No. 4.1e-86;
Matches 352; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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Qy        283 ATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTG 342
              | |||||||||||||||   |||||||||| |||| | ||||||||||||||||||||||
Db        365 AAGAATGAGAGTTGCCTAAATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTG 424

Qy        343 GCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTG 402
              |||||||||||||||||||||||| | |||||||||||| ||||| ||||| ||||||
Db        425 GCCTCCAGAAAGACCTCTTTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTG 484

Qy        403 AAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGG 462
              |||||||||||||||||||| |||||||||||||||||  | |||||||||| |||
Db        485 AAGATGTACCAGGTGGAGTTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGG 544

Qy        463 CAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAAT 522
              |||||||||| |||||||||||||| ||| |||||||||||| | ||||||||||||
Db        545 CAGATCTTTCTAGATCAAAACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAAT 604

Qy        523 GTCAACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACT 582
              |||||||| |||||||||||| || |||||||| ||||||||||||||||||||||||||
Db        605 TTCAACAGTGAGACTGTGCCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACT 664

Qy        583 AAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGA 642
              |||||||||||||||||||||||||||||||||||||||| |||||||| ||  ||||| 
Db        665 AAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGA 724

Qy        643 ATGATGAGCTATCTGAATGCTTCC 666
              |||||||||||||||||||||||
Db        725 GTGATGAGCTATCTGAATGCTTCC 748
```

RESULT 6
BG702253
LOCUS BG702253 812 bp mRNA linear EST 07-MAY-2001
DEFINITION 602683459F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4816118 5', mRNA sequence.
ACCESSION BG702253
VERSION BG702253.1 GI:13973409
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 812)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10714 row: e column: 15
High quality sequence stop: 804.
FEATURES Location/Qualifiers
source 1. .812

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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4816118"
                     /tissue_type="hippocampus"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_95"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
                     (gtcgag); Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTTTTVN-3', size-selected for  average
                     insert size 2.5 kb and normalized to ROT 5. This is a
                     primary library enriched for  full-length clones and
                     constructed using the Cap-trapper method (Carninci, in
                     preparation).  Library constructed by M. Brownstein
                     (NIMH/NHGRI, National Institutes of Health).  Note: this
                     is a NIH_MGC Library."
ORIGIN

  Query Match             39.9%;  Score 266;  DB 2;  Length 812;
  Best Local Similarity   83.6%;  Pred. No. 1.8e-66;
  Matches  341;  Conservative    0;  Mismatches   55;  Indels   12;  Gaps    3;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||| ||  ||||  |||||||||||||  | | |||||||||       |||||||
Db        417 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCT---------CCTGGAC 467

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              |||||||||||||||| |||||||||    |||| |||  ||||||||||||  |||
Db        468 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 527

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||  |||||||||||| ||||||| | ||| |||||||||  ||| ||||||||||||||
Db        528 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 587

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              |||||||||||||| | |||||||| |||||||| ||||||||||||||||||||||||
Db        588 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATCGATCATGAAGATATCACAAAAGAT 647

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              |||||||||||||||||||||| |||||| |||||||||| ||||||||||||
Db        648 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGC--T 705

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
                 |||||||||| |||| | ||||||||||||||||||||| ||||||||||||||||
Db        706 AAATCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGG-CTCCAGAAAGACCTCT 764

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              |||||||  |  |||||||||||| |||||     ||   |  ||||||
Db        765 TTTATGATGTGCCTGTGCCTTAGTAGTATTATGAAGACTTGAAAGATG 812


RESULT 7
BC035571
LOCUS       BC035571               1938 bp    mRNA    linear   HTC 04-MAR-2003
DEFINITION  Homo sapiens, clone IMAGE:5240216, mRNA.
ACCESSION   BC035571
VERSION     BC035571.1  GI:23958681
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1938)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 69 Row: b Column: 15
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 4504638
            This clone has the following problem: retained intron.
FEATURES             Location/Qualifiers
     source          1. .1938
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240216"
                     /tissue_type="Brain, fetal, whole pooled"
                     /clone_lib="NIH_MGC_121"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
ORIGIN

  Query Match             39.0%;  Score 259.6;  DB 6;  Length 1938;
  Best Local Similarity   91.9%;  Pred. No. 1.8e-64;
  Matches  274;  Conservative    0;  Mismatches   24;  Indels    0;  Gaps    0;

Qy        369 GACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGC 428
              | |||||||||||||| ||||| ||||| ||||||||||||||||||||||||||||| |
Db       1145 GGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGAC 1204

Qy        429 CATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCT 488
              ||||||||||||||  | |||||||||| |||||||||||||| ||||||||||||||
Db       1205 CATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCT 1264

Qy        489 GACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAA 548
              | ||| |||||||||||| | |||||||||||| ||||||||| |||||||||||  ||
Db       1265 GGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAA 1324

Qy        549 CTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCA 608
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1325 ATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCA 1384

Qy        609 TGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666
              |||||||||||||| |||||||| ||  ||||| ||||||||||||||||||||||
Db       1385 TGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTCC 1442


RESULT 8
BI523344/c
LOCUS       BI523344               1099 bp    mRNA    linear   EST 29-AUG-2001
DEFINITION  603175938T1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 3',
            mRNA sequence.
ACCESSION   BI523344
VERSION     BI523344.1  GI:15348136
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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           Hominidae; Homo.
REFERENCE  1  (bases 1 to 1099)
  AUTHORS  NIH-MGC http://mgc.nci.nih.gov/.
  TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL  Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Life Technologies, Inc.
           cDNA Library Preparation: Life Technologies, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM11605  row: 1  column: 09
           High quality sequence start: 40
           High quality sequence stop: 727.
FEATURES             Location/Qualifiers
     source          1. .1099
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240216"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_121"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 017. Note:
                     this is a NIH_MGC Library."
ORIGIN

  Query Match             32.5%;  Score 216.6;  DB 2;  Length 1099;
  Best Local Similarity   89.0%;  Pred. No. 6.7e-52;
  Matches  268;  Conservative    0;  Mismatches   29;  Indels    4;  Gaps    3;

Qy        369 GACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGC 428
              | |||||||| |||| ||||| ||||| ||| |||||||||||||||||||||||||| |
Db        741 GGCCCTGTGCTTTAGTAGTATTTATGAAGAC-TGAAGATGTACCAGGTGGAGTTCAAGAC 683

Qy        429 CATGAATGCAAAGC-TGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGC 487
              ||||||||||||| |   | |||||||||| |||||||||||||| ||||||||||||
Db        682 CATGAATGCAAAGCTTCCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGC 623

Qy        488 TGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGA 547
              || ||| |||||||||||||| | |||||||||||| |||||||| ||||||||||| |
Db        622 TGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAA 563

Qy        548 ACTCCTCCCTGGAAGAACCGGAT--TTTTATAAAACTAAAATCAAGCTCTGCATACTTCT 605
              | |||||||| ||||||||||||   |||   |||||| ||||||||||||||||||||
Db        562 AATCCTCCCTTGAAGAACCGGATTGTTTATCAAAACTGAAATCAAGCTCTGCATACTTCT 503

Qy        606 TCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTC 665
              ||||||||||||||||| |||||||| ||  ||||| ||||||||||||||||||||||
Db        502 TCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTC 443

Qy        666 C 666
              |
Db        442 C 442


RESULT 9
AI050362
LOCUS       AI050362                589 bp    mRNA    linear   EST 09-JUL-1998
DEFINITION  ub30a07.r1 Soares_thymus_2NbMT Mus musculus cDNA clone
            IMAGE:1379220 5' similar to gb:M65291 INTERLEUKIN-12 ALPHA CHAIN
            PRECURSOR (HUMAN); gb:M86672 Mus musculus interleukin 12 p35
            subunit, complete cds (MOUSE);, mRNA sequence.
ACCESSION   AI050362
VERSION     AI050362.1  GI:3299479
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 589)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:901688
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 60.
FEATURES             Location/Qualifiers
     source          1. .589
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1379220"
                     /sex="male"
                     /tissue_type="Thymus"
                     /dev_stage="4 weeks"
                     /lab_host="DH10B"
                     /clone_lib="Soares_thymus_2NbMT"
                     /note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI;
                     1st strand cDNA was primed with a Not I - oligo(dT) primer
                     [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGTTTTTTTTTTTTTTTTTTTTTTTT
                     3']; double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. RNA
                     provided by Dr. Bertrand Jordan. Library went through two
                     rounds of normalization, and was constructed by Bento
                     Soares and M.Fatima Bonaldo."
ORIGIN

  Query Match             32.5%;  Score 216.4;  DB 1;  Length 589;
  Best Local Similarity   72.5%;  Pred. No. 6.2e-52;
  Matches  280;  Conservative    0;  Mismatches  106;  Indels    0;  Gaps    0;

Qy        170 AGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATA 229
              |||||||| |||  ||  ||  ||| ||||||||| | ||||| || |||||||||| |
Db        109 AGGCCAGAGAAAAACTGAAACATTATTCCTGCACTGCTGAAGACATCGATCATGAAGACA 168

Qy        230 TCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATG 289
              |||||   ||  |||||||||| || || |||| |||||||||||| ||  || ||| |
Db        169 TCACACGGGACCAAACCAGCACATTGAAGACCTGTTTACCACTGGAACTACACAAGAACG 228

Qy        290 AGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCA 349
              |||||||||||||| | |||||||  |||   | ||| |  ||||| |||||| || |
Db        229 AGAGTTGCCTGGCTACTAGAGAGACTTCTTCCACAACAAGAGGGAGCTGCCTGCCCCCAC 288

Qy        350 GAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGT 409
              |||||  ||||| |||| |||||||||||||| | || ||||||||||||||||||||
Db        289 AGAAGACGTCTTTGATGATGACCCTGTGCCTTGGTAGCATCTATGAGGACTTGAAGATGT 348

Qy        410 ACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCT 469
```

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                ||||||   |||||| ||||||| || |||   ||    |   |     |   |||||||
Db        349 ACCAGACAGAGTTCCAGGCCATCAACGCAGCACTTCAGAATCACAACCATCAGCAGATCA 408

Qy        470 TTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACA 529
                |||| ||  |   |||||||   |  || |||||||| | ||| | ||||||   ||
Db        409 TTCTAGACAAGGGCATGCTGGGTGGCATCGATGAGCTGATGCAGTCTCTGAATCATAATG 468

Qy        530 GTGTGACTGTGCCACAGAACTCCTCC 555
                | | |||| |||  |||||  |  ||
Db        469 GCGAGACTCTGCGCCAGAAACCTCCC 494


RESULT 10
BU698113
LOCUS       BU698113                563 bp    mRNA    linear   EST 09-OCT-2002
DEFINITION  LL2in12067T7 Hematopoietic Stem Cell Subtracted Library Mus
            musculus cDNA 5' similar to interleukin 12 p35 subunit, mRNA
            sequence.
ACCESSION   BU698113
VERSION     BU698113.1  GI:23610620
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 563)
  AUTHORS   Phillips,R.L., Ernst,R.E., Brunk,B.P., Ivanova,N., Mahan,M.A.,
            Deanehan,J.K., Moore,K.A., Overton,G.C. and Lemischka,I.R.
  TITLE     The genetic program of hematopoietic stem cells
  JOURNAL   Science 288 (5471), 1635-1640 (2000)
   PUBMED   10834841
COMMENT     Contact: Lemischka, Ihor R.
            Department of Molecular Biology
            Princeton University
            Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544, USA
            Tel: 609 258 2838
            Fax: 609 258 2759
            Email: ilemischka@molbio.princeton.edu
            These ESTs are derived from a subtracted cDNA library enriched for
            gene products expressed in day 14-14.5 fetal liver hematopoietic
            stem cells defined as Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E
            (Sca-1)pos
            Seq primer: M13Reverse or T7.
FEATURES             Location/Qualifiers
     source          1. .563
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /tissue_type="Hematopoietic"
                     /cell_type="Stem Cells; Lineageneg/lo, AA4.1pos, cKitpos,
                     Ly6A/E (Sca-1)pos"
                     /dev_stage="Embryonic day 14-14.5"
                     /lab_host="DH10B"
                     /clone_lib="Hematopoietic Stem Cell Subtracted Library"
                     /note="Organ: Fetal Liver; Vector: Sport 1; Site_1: Sal I;
                     Site_2: Not I; Two directionally cloned cDNA libraries
                     were made from fetal liver hematopoietic stem cells
                     enriched to be Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E
                     (Sca-1)pos called Scapos and from AA4.1neg fetal liver
                     cells. Subtractive hybridization was performed by
                     hybridization of the target, Scapos, single stranded cDNA
                     library in pSport1 to biotinylated RNA transcribed from
                     the driver, AA4.1neg cDNA library in pSport2 with inserts
                     cloned in the complementary orientation. For detailed
                     protocols and additional information please see our
                     website at http://stemcell.princeton.edu."
ORIGIN

  Query Match           32.2%;  Score 214.2;  DB 3;  Length 563;
  Best Local Similarity  69.6%;  Pred. No. 2.7e-51;
  Matches  305;  Conservative    0;  Mismatches  129;  Indels    4;  Gaps    1;

Qy        170 AGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATA 229
                |||||||| |||  ||  ||  ||| ||||||||| | ||||| || ||||||||||| |
Db        100 AGGCCAGAGAAAAACTGAAACATTATTCCTGCACTGCTGAAGACATCGATCATGAAGACA 159

Qy        230 TCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATG 289
                |||||   ||  |||||||||| || || |||| |||||||||||| ||  || ||| |
Db        160 TCACACGGGACCAAACCAGCACATTGAAGACCTGTTTACCACTGGAACTACACAAGAACG 219

Qy        290 AGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCA 349
                |||||||||||||| | |||||||  |||   | ||| |  ||||| |||||| || |
Db        220 AGAGTTGCCTGGCTACTAGAGAGACTTCTTCCACAACAAGAGGGAGCTGCCTGCCCCCAC 279

Qy        350 GAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGT 409
                |||||  ||||| |||| |||||||||||||| | || ||||||||||||||||||||
Db        280 AGAAGACGTCTTTGATGATGACCCTGTGCCTTGGTAGCATCTATGAGGACTTGAAGATGT 339

Qy        410 ACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCT 469
                |||||   |||||| ||||||| || |||   ||    |   |     |   |||||||
Db        340 ACCAGACAGAGTTCCAGGCCATCAACGCAGCACTTCAGAATCACAACCATCAGCAGATCA 399

Qy        470 TTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACA 529
                |||| ||  |   |||||||   || || ||||||||| | ||| | ||||||   ||
Db        400 TTCTAGACAAGGGCATGCTGGTGGCCATCGATGAGCTGATGCAGTCTCTGAATCATAATG 459

Qy        530 GTG----TGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAA 585
                |          || |||| | | || |     |||  | | |||   ||| | |   |||
Db        460 GGNGAGACTCTTGCGCCAGAAACCTTCCTGTGGGAGAAGCAGGACCCTTACAGAGTGAAA 519

Qy        586 ATCAAGCTCTGCATACTT 603
                || |||||||  || | |
Db        520 ATGAAGCTCTTGATTCCT 537


RESULT 11
AJ820622/c
LOCUS       AJ820622                778 bp    mRNA    linear   EST 12-MAY-2005
DEFINITION  AJ820622 KN206 Bos sp. cDNA clone C0006020h12, mRNA sequence.
ACCESSION   AJ820622
VERSION     AJ820622.1  GI:51888098
KEYWORDS    EST.
SOURCE      Bos sp.
  ORGANISM  Bos sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 778)
  AUTHORS   McGuire,K. and Glass,E.J.
  TITLE     The expanding role of microarrays in the investigation of
            macrophage responses to pathogens
  JOURNAL   Vet. Immunol. Immunopathol. 105 (3-4), 259-275 (2005)
COMMENT     Contact: McGuire K
            Genomics and Genetics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
            Single pass sequencing. Bases called and trimmed with phred
            v0.020425.c. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options. Vector:pBluescriptII(SK+) R. Site
            1:EcoRV(lost) R. Site 2:NotI Seq Primer: T7 Normalised library
            constructed from pooled monocytes from Bos taurus (Holstein) and
            Bos indicus (Sahiwals) cattle subjected to various stimuli,
            including infection with the protozoan parasite Theileria annulata.
FEATURES             Location/Qualifiers
     source          1. .778
                     /organism="Bos sp."
                     /mol_type="mRNA"
                     /db_xref="taxon:29061"
                     /clone="C0006020h12"
                     /tissue_type="blood"
                     /cell_type="bovine monocyte"
                     /clone_lib="KN206"
                     /note="Vector: pBluescriptII(SK+); Site_1: EcoRV(lost);
                     Site_2: NotI; Normalised library constructed from pooled
```

monocytes from Bos taurus (Holstein) and Bos indicus (Sahiwals) cattle subjected to various stimuli, including infection with the protozoan parasite Theileria annulata"

ORIGIN

Query Match 31.4%; Score 209.2; DB 1; Length 778;
Best Local Similarity 87.4%; Pred. No. 9e-50;
Matches 229; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

```
Qy        405 GATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCA 464
              ||||||||| |||||||| |||||||||||||||||  | ||||||||||| |||||
Db        778 GATGTACCACGTGGAGTTCCAGGCCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCA 719

Qy        465 GATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGT 524
              |||||||| || || ||||||||| |||||||| ||||||| | ||||||||||||  |
Db        718 AATCTTTCTAGACCAGAACATGCTGGCAGCTATTGCTGAGCTGATGCAGGCCCTGAATTT 659

Qy        525 CAACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAA 584
              | |||||| ||||||||||||||||  |||||||| |||||| ||||||||| || || ||
Db        658 CGACAGTGAGACTGTGCCACAGAAACCCTCCCTGAAAGAACTGGATTTTTACAAGACAAA 599

Qy        585 AATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAAT 644
              | |||||||||||| |||||||| || |||||||||||| ||||||||| | |||||
Db        598 AGTCAAGCTCTGCATCCTTCTTCACGCCTTCAGAATTCGTGCGGTGACCATCGACAGAAT 539

Qy        645 GATGAGCTATCTGAATGCTTCC 666
              ||||||||||||| | |||||
Db        538 GATGAGCTATCTGAGTTCTTCC 517
```

RESULT 12
BF552757
LOCUS BF552757 373 bp mRNA linear EST 12-DEC-2000
DEFINITION UI-R-C0-iz-d-02-0-UI.r1 UI-R-C0 Rattus norvegicus cDNA clone UI-R-C0-iz-d-02-0-UI 5', mRNA sequence.
ACCESSION BF552757
VERSION BF552757.1 GI:11662487
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 373)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) This clone is also available through the I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE ID= 1782759
Seq primer: M13 Forward.
FEATURES Location/Qualifiers
source 1. .373
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-C0-iz-d-02-0-UI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-C0"
/note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI; The UI-R-C0 library is a subtracted library derived from the UI-R-A1 and UI-R-E1 libraries. The UI-R-A1 library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, and muscle. The UI-R-E1 library consisted of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-C0) was constructed as follows: PCR amplified cDNA inserts from a pool of UI-R-A1 and UI-R-E1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the pooled UI-R-A1 and UI-R-E1 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C0 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996)"

ORIGIN

Query Match 30.0%; Score 200; DB 7; Length 373;
Best Local Similarity 71.5%; Pred. No. 3.6e-47;
Matches 263; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

```
Qy        291 GAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAG 350
              ||| ||||||||| | | |||||  |||   ||||  |  ||||| ||||||  |  |
Db          4 GAGGTGCCTGGCTACTAAAGAGACTTCTTCCATAATAAGAGGGAGCTGCCTGCCTCCACA 63

Qy        351 AAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTA 410
              |||||| ||||| |||| |||||||||||||| | || |||||||||||||||||||||||
Db         64 AAAGACTTCTTTGATGATGACCCTGTGCCTTGGTAGCATCTATGAGGACTTGAAGATGTA 123

Qy        411 CCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTT 470
              ||||   |||||| ||||||| ||||||   ||     |   | |   |||||||
Db        124 CCAGTCAGAGTTCCAGGCCATAAATGCAGCACTTCAGAGCCACAATCATCAGCAGATCAC 183

Qy        471 TCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAG 530
              ||||||   ||||||||||| ||||||||||||||  | | | | ||||||  || | |
Db        184 TCTGGACAGAAACATGCTGATGGCTATTGATGAGCTAATGCGGTCTCTGAATCACAGCGG 243

Qy        531 TGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAA 590
              | || | |||  |||||  |  || ||| |||| | |||  ||| | |   || || ||
Db        244 CGAGATTCTGCACCAGAAAGCTCCCATGGGAGAAGCAGATCCTTACAGAGTGAAGATGAA 303

Qy        591 GCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAG 650
              |||||| || || || ||||| |||||  |  || |   |||| |||||  ||  ||||||
Db        304 GCTCTGTATCCTGCTCCATGCCTTCAGCACACGCGTCATGACTATCAACAGGGTGATGAA 363

Qy        651 CTATCTGA 658
              ||||||||
Db        364 CTATCTGA 371
```

RESULT 13
BI523569
LOCUS BI523569 832 bp mRNA linear EST 29-AUG-2001
DEFINITION 603175938F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 5', mRNA sequence.
ACCESSION BI523569
VERSION BI523569.1 GI:15348361
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 832)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

```
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11605  row: l  column: 09
            High quality sequence start: 23
            High quality sequence stop: 821.
FEATURES             Location/Qualifiers
     source          1. .832
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240216"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_121"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 017. Note:
                     this is a NIH_MGC Library."
ORIGIN

  Query Match            29.0%;  Score 193.2;  DB 2;  Length 832;
  Best Local Similarity  85.0%;  Pred. No. 4.7e-45;
  Matches  243;  Conservative    0;  Mismatches   33;  Indels   10;  Gaps    2;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||| ||  ||||  |||||||||||||  | | |||||||||         |||||||
Db        321 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCT---------CCTGGAC 371

Qy         61 CACCTCAGTTTGGCCAGG-AACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTG 119
              |||||||||||||||| | |||||||||     |||| |||  ||||||||||||||  ||
Db        372 CACCTCAGTTTGGCCATGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATG 431

Qy        120 CCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACA 179
              |||  |||||||||||| ||||||| | ||| |||||||||| ||| ||||||||||||
Db        432 CCTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACA 491

Qy        180 AACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGA 239
              |||||||||||||||| | |||||||| ||||||||||||||||||||||||||||||
Db        492 AACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGA 551

Qy        240 TAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATG 285
              |||||||||||||||||||||| |||||| |||||||||||| |
Db        552 TAAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAG 597


RESULT 14
BP260963
LOCUS       BP260963                 581 bp    mRNA    linear   EST 16-SEP-2004
DEFINITION  BP260963 Sugano cDNA library, small intestine Homo sapiens cDNA
            clone HSI02082, mRNA sequence.
ACCESSION   BP260963
VERSION     BP260963.1  GI:52176194
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 581)
  AUTHORS   Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
            Mizushima-Sugano,J., Nakai,K. and Sugano,S.
  TITLE     Sequence comparison of human and mouse genes reveals a homologous
            block structure in the promoter regions
  JOURNAL   Genome Res. 14 (9), 1711-1718 (2004)
   PUBMED   15342556
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Tel: 81-3-5449-5343
            Fax: 81-3-5449-5416
            Email: ysuzuki@hgc.jp.
FEATURES             Location/Qualifiers
     source          1. .581
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HSI02082"
                     /tissue_type="small intestine"
                     /clone_lib="Sugano cDNA library, small intestine"
ORIGIN

  Query Match            28.9%;  Score 192.8;  DB 3;  Length 581;
  Best Local Similarity  84.9%;  Pred. No. 5.4e-45;
  Matches  231;  Conservative    0;  Mismatches   32;  Indels    9;  Gaps    1;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||| ||  ||||  |||||||||||||  | | |||||||||         |||||||
Db        319 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCT---------CCTGGAC 369

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              |||||||||||||||| |||||||||     |||| |||  ||||||||||||||  |||
Db        370 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 429

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||  |||||||||||| ||||||| | ||| ||||||||| ||| ||||||||||||||||
Db        430 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 489

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              |||||||||||||| | |||||||| ||||||||||||||||||||||||||||||||||
Db        490 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 549

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACT 272
              |||||||||||||||||||||| |||||| |
Db        550 AAAACCAGCACAGTGGAGGCCTGTTTACCATT 581


RESULT 15
BU699383
LOCUS       BU699383                 561 bp    mRNA    linear   EST 09-OCT-2002
DEFINITION  LL2in11573T7 Hematopoietic Stem Cell Subtracted Library Mus
            musculus cDNA 5' similar to interleukin 12 p35 subunit, mRNA
            sequence.
ACCESSION   BU699383
VERSION     BU699383.1  GI:23615967
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 561)
  AUTHORS   Phillips,R.L., Ernst,R.E., Brunk,B.P., Ivanova,N., Mahan,M.A.,
            Deanehan,J.K., Moore,K.A., Overton,G.C. and Lemischka,I.R.
  TITLE     The genetic program of hematopoietic stem cells
  JOURNAL   Science 288 (5471), 1635-1640 (2000)
   PUBMED   10834841
COMMENT     Contact: Lemischka, Ihor R.
            Department of Molecular Biology
            Princeton University
            Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544, USA
            Tel: 609 258 2838
            Fax: 609 258 2759
```

```
            Email: ilemischka@molbio.princeton.edu
            These ESTs are derived from a subtracted cDNA library enriched for
            gene products expressed in day 14-14.5 fetal liver hematopoietic
            stem cells defined as Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E
            (Sca-1)pos
            Seq primer: M13Reverse or T7.
FEATURES              Location/Qualifiers
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                      Ly6A/E (Sca-1)pos"
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                      /lab_host="DH10B"
                      /clone_lib="Hematopoietic Stem Cell Subtracted Library"
                      /note="Organ: Fetal Liver; Vector: Sport 1; Site_1: Sal I;
                      Site_2: Not I; Two directionally cloned cDNA libraries
                      were made from fetal liver  hematopoietic stem cells
                      enriched to be Lineageneg/lo, AA4.1pos, cKitpos, Ly6A/E
                      (Sca-1)pos called Scapos and from AA4.1neg fetal liver
                      cells. Subtractive hybridization was  performed by
                      hybridization of the target, Scapos, single stranded cDNA
                      library in pSport1 to  biotinylated RNA transcribed from
                      the driver, AA4.1neg cDNA library in pSport2 with  inserts
                      cloned in the complementary orientation. For detailed
                      protocols and additional  information please see our
                      website at http://stemcell.princeton.edu."
ORIGIN

  Query Match             28.5%;  Score 190;  DB 3;  Length 561;
  Best Local Similarity   68.2%;  Pred. No. 3.6e-44;
  Matches  275;  Conservative    0;  Mismatches  125;  Indels    3;  Gaps    1;

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Qy        455 CTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGG 514
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Job time : 3893.4 secs
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 10, 2006, 04:51:14 ; Search time 143.768 Seconds
(without alignments)
8667.862 Million cell updates/sec

Title: US-10-821-670A-32
Perfect score: 666
Sequence: 1 atgtgcccgccgcgtggcct.....tgagctatctgaatgcttcc 666

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	2	666	100.0	666	3	US-09-917-265A-34	Sequence 34, Appl
	3	661.2	99.3	1441	3	US-09-011-143-8	Sequence 8, Appli
	4	661.2	99.3	1441	3	US-09-302-495-8	Sequence 8, Appli
	5	661.2	99.3	1441	3	US-10-079-616-8	Sequence 8, Appli
	6	642	96.4	689	3	US-09-011-143-26	Sequence 26, Appl
	7	642	96.4	689	3	US-09-302-495-26	Sequence 26, Appl
	8	642	96.4	689	3	US-10-079-616-26	Sequence 26, Appl
	9	602	90.4	669	3	US-09-079-984A-12	Sequence 12, Appl
	10	602	90.4	669	3	US-09-390-729-12	Sequence 12, Appl
	11	600.4	90.2	666	3	US-09-917-265A-46	Sequence 46, Appl
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	19	586.2	88.0	591	3	US-09-011-143-9	Sequence 9, Appli
	20	586.2	88.0	591	3	US-09-302-495-9	Sequence 9, Appli
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ALIGNMENTS

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; Sequence 32, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(666)
US-09-917-265A-32

Query Match 100.0%; Score 666; DB 3; Length 666;
Best Local Similarity 100.0%; Pred. No. 2e-209;
Matches 666; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        661 GCTTCC 666


RESULT 2
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; Sequence 34, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-34

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Db          6 GCTTCC 1


RESULT 3
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; Sequence 8, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
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;       TELEPHONE:  202-628-5197
;       TELEFAX:  202-737-3528
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1441 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-09-011-143-8

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Db        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

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Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
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Db        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

Qy        661 GCTTCC 666
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Db        803 TCTTCC 808


RESULT 4
US-09-302-495-8
; Sequence 8, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/302,495
;            FILING DATE: 30-Apr-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1441 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-302-495-8

  Query Match             99.3%;  Score 661.2;  DB 3;  Length 1441;
  Best Local Similarity   99.5%;  Pred. No. 1.3e-207;
  Matches  663;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
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Db        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
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Db        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
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Db        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

Qy        661 GCTTCC 666
              ||||||
Db        803 TCTTCC 808


RESULT 5
US-10-079-616-8
; Sequence 8, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1441 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-10-079-616-8

  Query Match             99.3%;  Score 661.2;  DB 3;  Length 1441;
  Best Local Similarity   99.5%;  Pred. No. 1.3e-207;
  Matches  663;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
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Db        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

Qy        661 GCTTCC 666
              ||||||
Db        803 TCTTCC 808


RESULT 6
US-09-011-143-26
; Sequence 26, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
```

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;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  26:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  689 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-26

  Query Match             96.4%;  Score 642;  DB 3;  Length 689;
  Best Local Similarity   97.7%;  Pred. No. 1.8e-201;
  Matches  651;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
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Db          7 ATGTGCCCCCCCCGTGGCCTCCTCCTGGTGACCATCCTGGTCCTGCTGAACCACCTGGAC 66

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
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Db         67 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 126

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 186

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 246

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||| | |||||||||  | ||||||||||||||||||||||
Db        247 AAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTG 306

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 366

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 426

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
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Db        427 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 486

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 546

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db        547 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 606

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
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Db        607 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666

Qy        661 GCTTCC 666
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Db        667 TCTTCC 672


RESULT 7
US-09-302-495-26
; Sequence 26, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/302,495
;            FILING DATE: 30-Apr-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 26:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 689 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-302-495-26

  Query Match             96.4%;  Score 642;  DB 3;  Length 689;
  Best Local Similarity   97.7%;  Pred. No. 1.8e-201;
  Matches  651;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
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Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          67 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 126

Qy         121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
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Db         127 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 186

Qy         181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
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Db         187 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 246

Qy         241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
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Db         247 AAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTG 306

Qy         301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
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Db         307 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 366

Qy         361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         367 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 426

Qy         421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
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Db         427 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 486

Qy         481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
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Db         487 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 546

Qy         541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
                |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db         547 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 606

Qy         601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db         607 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666

Qy         661 GCTTCC 666
                ||||||
Db         667 TCTTCC 672


RESULT 8
US-10-079-616-26
; Sequence 26, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 26:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 689 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-079-616-26

  Query Match             96.4%;  Score 642;  DB 3;  Length 689;
  Best Local Similarity   97.7%;  Pred. No. 1.8e-201;
  Matches  651;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy           1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
                |||||||| || ||||||||||||||| || |||||||||||||||| | ||||||||||||
Db           7 ATGTGCCCCCCCCGTGGCCTCCTCCTGGTGACCATCCTGGTCCTGCTGAACCACCTGGAC 66

Qy          61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          67 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 126

Qy         121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         127 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 186

Qy         181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         187 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 246

Qy         241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
                |||||||||||||||||||||||| | ||||||||| | ||||||||||||||||||||||
Db         247 AAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTG 306

Qy         301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         307 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 366

Qy         361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         367 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 426

Qy         421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
                |||||||||||||||||||||||| | ||||||||||||||||||||||||||||||||
Db         427 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 486

Qy         481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         487 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 546

Qy         541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
                |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db         547 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 606

Qy         601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db         607 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666

Qy         661 GCTTCC 666
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Db        667 TCTTCC 672


RESULT 9
US-09-079-984A-12
; Sequence 12, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,984A
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  669 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 666
;      IDENTIFICATION METHOD:  Similarity
US-09-079-984A-12

  Query Match             90.4%;  Score 602;  DB 3;  Length 669;
  Best Local Similarity   94.0%;  Pred. No. 2.9e-188;
  Matches  626;  Conservative    0;  Mismatches   40;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||| ||||||||||||| ||||||||||||| ||| ||||||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||| | || |||||||| |||||||||| || ||||||||||||||| |||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              |||||||||||||||| ||||||| ||||| ||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              |||||||||| || ||||||||||||||||||||||||||||||||||||||||| |||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||| |||||||||| |||||||||||||||  ||||| |||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              |||||||||  |||||||||||||||| |||||||||||||||||||||||| ||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||| |||||||| |||||||||| || ||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              |||||||||||||||| ||||||||||||||||||||||||| ||||||||||||||||
Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||| |||||||| ||||| ||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              |||||||||||||||||||||||| ||||||||| |||||||||||| |||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        661 GCTTCC 666
              ||||||
Db        661 TCTTCC 666


RESULT 10
US-09-390-729-12
; Sequence 12, Application US/09390729
; Patent No. 6562334
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/390,729
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/079,984
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  669 base pairs
;      TYPE:  nucleic acid
```

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;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 666
;      IDENTIFICATION METHOD:  Similarity
US-09-390-729-12

  Query Match             90.4%;  Score 602;  DB 3;  Length 669;
  Best Local Similarity   94.0%;  Pred. No. 2.9e-188;
  Matches  626;  Conservative    0;  Mismatches   40;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||| ||||||||||||||| |||||||||||||||| ||| ||||||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||| | || |||||||| |||||||||| || ||||||||||||||| |||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              |||||||||||||||| ||||||| ||||| ||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              |||||||||| || |||||||||||||||||||||||||||||||||||||||||||| |||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              |||||||||||||||||| |||||||||| ||||||||||||||||||  ||||| |||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              |||||||||  |||||||||||||||| |||||||||||||||||||||||||||| ||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||| |||||||| |||||||||| || ||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              |||||||||||||||||| |||||||||||||||||||||||| ||||||||||||||||||
Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||| |||||||| ||||| ||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              |||||||||||||||||||||||||| ||||||||| |||||||||||| |||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        661 GCTTCC 666
              ||||||
Db        661 TCTTCC 666


RESULT 11
US-09-917-265A-46
; Sequence 46, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
US-09-917-265A-46

  Query Match             90.2%;  Score 600.4;  DB 3;  Length 666;
  Best Local Similarity   93.8%;  Pred. No. 9.7e-188;
  Matches  625;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||| ||||||||||||||| |||||||||||||||| ||| ||||||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||| | || |||||||| |||||||||| || |||| |||||||||| ||||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              |||||||||||||||| ||||||| ||||| ||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              |||||||||| || |||||||||||||||||||||||||||||||||||||||||||| |||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              |||||||||||||||||| |||||||||| ||||||||||||||||||  ||||| |||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              |||||||||  |||||||||||||||| |||||||||||||||||||||||||||| ||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||| |||||||| |||||||||| || ||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              |||||||||||||||||| |||||||||||||||||||||||| ||||||||||||||||||
Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||| |||||||| ||||| ||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              |||||||||||||||||||||||||| ||||||||| |||||||||||| |||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        661 GCTTCC 666
              ||||||
Db        661 TCTTCC 666


RESULT 12
US-09-917-265A-48/c
; Sequence 48, Application US/09917265A
; Patent No. 6818444
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; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-48

  Query Match            90.2%;  Score 600.4;  DB 3;  Length 666;
  Best Local Similarity   93.8%;  Pred. No. 9.7e-188;
  Matches  625;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||| |||||||||||||| |||||||||||||||| ||| ||||||||||
Db        666 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 607

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||| | || |||||||| |||||||||| || |||| |||||||||| |||||||||
Db        606 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 547

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              |||||||||||||||| ||||||| ||||| ||||||||||||||||||||||||||||
Db        546 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              |||||||||||| || ||||||||||||||||||||||||||||||||||||||| |||
Db        486 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 427

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              |||||||||||||||| |||||||||| |||||||||||||||||  ||||| |||||
Db        366 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 307

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              |||||||||  |||||||||||||||| |||||||||||||||||||||||||| ||||
Db        306 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 247

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||| |||||||| |||||||||| || ||||||||||||||||||||||
Db        246 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 187

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              |||||||||||||||| ||||||||||||||||||||||||| ||||||||||||||||
Db        186 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 127

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
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Db        126 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
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Db         66 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 7

Qy        661 GCTTCC 666
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Db          6 TCTTCC 1


RESULT 13
US-09-917-265A-104
; Sequence 104, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 104
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (232)..(897)
US-09-917-265A-104

  Query Match            90.2%;  Score 600.4;  DB 3;  Length 1455;
  Best Local Similarity   93.8%;  Pred. No. 1.6e-187;
  Matches  625;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
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Db        232 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 291

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||| | || |||||||| |||||||||| || |||| |||||||||| |||||||||
Db        292 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 351

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              |||||||||||||||| ||||||| ||||| ||||||||||||||||||||||||||||
Db        352 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 411

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              |||||||||||| || ||||||||||||||||||||||||||||||||||||||| |||
Db        412 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 471

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
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Db        472 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 531

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
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Db        532 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 591

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              |||||||||  |||||||||||||||| |||||||||||||||||||||||||| ||||
Db        592 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 651

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
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Db        652 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 711

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
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Db        712 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 771

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||| |||||||| ||||| ||||||||||||||||||||||||||||||||||||
Db        772 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 831

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              |||||||||||||||||||||||| ||||||||| |||||||||||| |||||||||
Db        832 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 891

Qy        661 GCTTCC 666
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Db        892 TCTTCC 897


RESULT 14
US-09-917-265A-106/c
; Sequence 106, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 106
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-106

  Query Match             90.2%;  Score 600.4;  DB 3;  Length 1455;
  Best Local Similarity   93.8%;  Pred. No. 1.6e-187;
  Matches  625;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||| ||||||||||||||| |||||||||||||||| ||| ||||||||||
Db       1224 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 1165

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||| | || |||||||| |||||||||| || |||| |||||||||| ||||||||||
Db       1164 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 1105

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||| ||||||| ||||| ||||||||||||||||||||||||||||||
Db       1104 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 1045

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              |||||||||| || ||||||||||||||||||||||||||||||||||||||||| |||
Db       1044 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 985

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
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Db        984 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 925

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              |||||||||||||||| ||||||||| |||||||||||||||  ||||| |||||
Db        924 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 865

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              |||||||||  |||||||||||||||| |||||||||||||||||||||||||| ||||
Db        864 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 805

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
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Db        804 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 745

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
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Db        744 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 685

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||| |||||||| ||||| ||||||||||||||||||||||||||||||||||||
Db        684 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 625

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              |||||||||||||||||||||||| ||||||||| |||||||||| |||||||||
Db        624 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 565

Qy        661 GCTTCC 666
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Db        564 TCTTCC 559


RESULT 15
US-09-917-265A-35
; Sequence 35, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(591)
US-09-917-265A-35

  Query Match             88.5%;  Score 589.4;  DB 3;  Length 591;
  Best Local Similarity   99.8%;  Pred. No. 3.9e-184;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195
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Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315
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Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555
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Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

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Db        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666
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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	2	666	100.0	666	3	US-09-917-265-34	Sequence 34, Appl
	3	666	100.0	666	9	US-10-821-670-32	Sequence 32, Appl
c	4	666	100.0	666	9	US-10-821-670-34	Sequence 34, Appl
	5	661.2	99.3	1441	6	US-10-079-616-8	Sequence 8, Appli
	6	651.6	97.8	669	7	US-10-041-672C-2	Sequence 2, Appli
	7	642	96.4	689	6	US-10-079-616-26	Sequence 26, Appl
	8	600.4	90.2	666	3	US-09-917-265-46	Sequence 46, Appl
c	9	600.4	90.2	666	3	US-09-917-265-48	Sequence 48, Appl
	10	600.4	90.2	666	9	US-10-821-670-46	Sequence 46, Appl
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	12	600.4	90.2	1455	3	US-09-917-265-104	Sequence 104, App
c	13	600.4	90.2	1455	3	US-09-917-265-106	Sequence 106, App
	14	600.4	90.2	1455	9	US-10-821-670-104	Sequence 104, App
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	16	589.4	88.5	591	3	US-09-917-265-35	Sequence 35, Appl
c	17	589.4	88.5	591	3	US-09-917-265-37	Sequence 37, Appl
	18	589.4	88.5	591	9	US-10-821-670-35	Sequence 35, Appl
c	19	589.4	88.5	591	9	US-10-821-670-37	Sequence 37, Appl
	20	586.2	88.0	591	6	US-10-079-616-9	Sequence 9, Appli
	21	572.2	85.9	1533	3	US-09-917-265-43	Sequence 43, Appl
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	25	572.2	85.9	1599	3	US-09-917-265-38	Sequence 38, Appl
c	26	572.2	85.9	1599	3	US-09-917-265-40	Sequence 40, Appl
	27	572.2	85.9	1599	9	US-10-821-670-38	Sequence 38, Appl
c	28	572.2	85.9	1599	9	US-10-821-670-40	Sequence 40, Appl
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	31	559.4	84.0	561	9	US-10-821-670-101	Sequence 101, App
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	33	536.6	80.6	591	3	US-09-917-265-49	Sequence 49, Appl
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	35	536.6	80.6	591	9	US-10-821-670-49	Sequence 49, Appl
c	36	536.6	80.6	591	9	US-10-821-670-51	Sequence 51, Appl
	37	535.6	80.4	762	3	US-09-826-025-21	Sequence 21, Appl
	38	535.6	80.4	762	9	US-10-785-577-21	Sequence 21, Appl
	39	535.6	80.4	762	9	US-10-688-845-57	Sequence 57, Appl
	40	535.6	80.4	1316	9	US-10-476-960-3	Sequence 3, Appli
	41	535.6	80.4	1316	15	US-11-089-191-3	Sequence 3, Appli
	42	535.6	80.4	1395	3	US-09-924-703-5	Sequence 5, Appli
	43	535.6	80.4	1395	8	US-10-358-395-5	Sequence 5, Appli
	44	535.6	80.4	1444	7	US-10-429-802-43	Sequence 43, Appl
	45	535.6	80.4	1444	7	US-10-430-503-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-09-917-265-32
; Sequence 32, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(666)
; OTHER INFORMATION:
US-09-917-265-32

Query Match 100.0%; Score 666; DB 3; Length 666;
Best Local Similarity 100.0%; Pred. No. 5e-203;
Matches 666; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
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Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
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Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
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Db        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
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Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        661 GCTTCC 666
              ||||||
Db        661 GCTTCC 666
```

RESULT 2
US-09-917-265-34/c
; Sequence 34, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265-34

Query Match 100.0%; Score 666; DB 3; Length 666;
Best Local Similarity 100.0%; Pred. No. 5e-203;
Matches 666; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 607

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 547

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 427

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 307

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 247

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 187

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 127

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 7

Qy        661 GCTTCC 666
              ||||||
Db          6 GCTTCC 1
```

RESULT 3
US-10-821-670-32
; Sequence 32, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(666)
US-10-821-670-32

Query Match 100.0%; Score 666; DB 9; Length 666;
Best Local Similarity 100.0%; Pred. No. 5e-203;
Matches 666; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
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Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        661 GCTTCC 666
              ||||||
Db        661 GCTTCC 666
```

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RESULT 4
US-10-821-670-34/c
; Sequence 34, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-34

  Query Match           100.0%;  Score 666;  DB 9;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 5e-203;
  Matches  666;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 607
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Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 547

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 427

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 307

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 247

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 187

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 127

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 7

Qy        661 GCTTCC 666
              ||||||
Db          6 GCTTCC 1
```

```
RESULT 5
US-10-079-616-8
; Sequence 8, Application US/10079616
; Publication No. US20020107366A1
;  GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
```

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;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1441 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-079-616-8

  Query Match             99.3%;  Score 661.2;  DB 6;  Length 1441;
  Best Local Similarity   99.5%;  Pred. No. 2.7e-201;
  Matches  663;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

Qy        661 GCTTCC 666
              ||||||
Db        803 TCTTCC 808


RESULT 6
US-10-041-672C-2
; Sequence 2, Application US/10041672C
; Publication No. US20030157059A1
; GENERAL INFORMATION:
;  APPLICANT: Mologen Forschungs-, Entwicklungs- und Vetriebs GmbH
;  APPLICANT:  Universitat Zurich
;  TITLE OF INVENTION: FELINE INTERLEUKIN-12 AS IMMUNOSTIMULANT
;  FILE REFERENCE: NHL-NP-36
;  CURRENT APPLICATION NUMBER: US/10/041,672C
;  CURRENT FILING DATE:  2002-01-08
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 669
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: feline IL-12 p35
US-10-041-672C-2

  Query Match             97.8%;  Score 651.6;  DB 7;  Length 669;
  Best Local Similarity   98.6%;  Pred. No. 2.2e-198;
  Matches  657;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              |||||||||||||||||||||||| | |||||||||||| ||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
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Qy        661 GCTTCC 666
              ||||||
Db        661 GCTTCC 666


RESULT 7
US-10-079-616-26
; Sequence 26, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 26:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 689 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-079-616-26

  Query Match             96.4%;  Score 642;  DB 6;  Length 689;
  Best Local Similarity   97.7%;  Pred. No. 2.7e-195;
  Matches  651;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              |||||||| || ||||||||||||| || |||||||||||||| | ||||||||||||
Db          7 ATGTGCCCCCCCCGTGGCCTCCTCCTGGTGACCATCCTGGTCCTGCTGAACCACCTGGAC 66

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 126

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 186

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 246

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              |||||||||||||||||||||||| | ||||||||| | ||||||||||||||||||||
Db        247 AAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTG 306

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 366

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 426

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              |||||||||||||||||||||| | ||||||||||||||||||||||||||||||||||
Db        427 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 486

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 546

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        547 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 606

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        607 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666

Qy        661 GCTTCC 666
              ||||||
Db        667 TCTTCC 672


RESULT 8
US-09-917-265-46
; Sequence 46, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
;   OTHER INFORMATION:
US-09-917-265-46

  Query Match             90.2%;  Score 600.4;  DB 3;  Length 666;
  Best Local Similarity   93.8%;  Pred. No. 6.6e-182;
  Matches  625;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||| |||||||||||||| |||||||||||||| ||| ||||||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||| | || |||||||| |||||||||| || |||| |||||||||||| |||||||||
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Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              |||||||||||||||| ||||||| ||||| ||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              |||||||||| || ||||||||||||||||||||||||||||||||||||||||||| |||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              |||||||||||||||||| |||||||||| |||||||||||||||||  ||||| |||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              |||||||||  ||||||||||||||| ||||||||||||||||||||||||||| ||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              |||||||||||||| |||||||| |||||||||| || ||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              |||||||||||||||||| |||||||||||||||||||| ||||||||||||||||||||
Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||| |||||||| ||||| ||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              |||||||||||||||||||||||||||| ||||||||| |||||||||||| |||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        661 GCTTCC 666
              ||||||
Db        661 TCTTCC 666


RESULT 9
US-09-917-265-48/c
; Sequence 48, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-48

  Query Match            90.2%;  Score 600.4;  DB 3;  Length 666;
  Best Local Similarity   93.8%;  Pred. No. 6.6e-182;
  Matches  625;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              |||||||||||||| |||||||||||||| ||||||||||||||| ||| ||||||||||
Db        666 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 607

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||| | || |||||||| |||||||||| || |||| |||||||||| |||||||||
Db        606 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 547

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              |||||||||||||||| ||||||| ||||| ||||||||||||||||||||||||||||||
Db        546 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              |||||||||| || ||||||||||||||||||||||||||||||||||||||||||| |||
Db        486 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 427

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              |||||||||||||||||| |||||||||| |||||||||||||||||  ||||| |||||
Db        366 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 307

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              |||||||||  ||||||||||||||| ||||||||||||||||||||||||||| ||||
Db        306 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 247

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              |||||||||||||| |||||||| |||||||||| || ||||||||||||||||||||||
Db        246 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 187

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              |||||||||||||||||| |||||||||||||||||||| ||||||||||||||||||||
Db        186 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 127

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||| |||||||| ||||| ||||||||||||||||||||||||||||||||||||
Db        126 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              |||||||||||||||||||||||||||| ||||||||| |||||||||||| |||||||||
Db         66 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 7

Qy        661 GCTTCC 666
              ||||||
Db          6 TCTTCC 1


RESULT 10
US-10-821-670-46
; Sequence 46, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
US-10-821-670-46

  Query Match            90.2%;  Score 600.4;  DB 9;  Length 666;
  Best Local Similarity   93.8%;  Pred. No. 6.6e-182;
  Matches  625;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;
```

```
Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||| ||||||||||||||| ||||||||||||||| ||| ||||||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||| | || |||||||| |||||||||| || |||| |||||||||| |||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              |||||||||||||||| ||||||| ||||| ||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              |||||||||| || ||||||||||||||||||||||||||||||||||||||||||| |||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              |||||||||||||||||| |||||||||| |||||||||||||||||  ||||| |||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              |||||||||  |||||||||||||||| ||||||||||||||||||||||||||||| ||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||| |||||||| |||||||||| || ||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              |||||||||||||||| |||||||||||||||||||||||||||| ||||||||||||||||
Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||| |||||||| ||||| ||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              |||||||||||||||||||||||||| ||||||||| |||||||||||| |||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        661 GCTTCC 666
                |||||
Db        661 TCTTCC 666
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RESULT 11
US-10-821-670-48/c
; Sequence 48, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-821-670-48

Query Match 90.2%; Score 600.4; DB 9; Length 666;
Best Local Similarity 93.8%; Pred. No. 6.6e-182;

Matches 625; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

```
Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||| ||||||||||||||| ||||||||||||||| ||| ||||||||||
Db        666 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 607

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||| | || |||||||| |||||||||| || |||| |||||||||| |||||||||
Db        606 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 547

Qy        121 CTCAACCACTCCCAAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              |||||||||||||||| ||||||| ||||| ||||||||||||||||||||||||||||||
Db        546 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              |||||||||| || ||||||||||||||||||||||||||||||||||||||||||| |||
Db        486 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 427

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              |||||||||||||||||| |||||||||| |||||||||||||||||  ||||| |||||
Db        366 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 307

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              |||||||||  |||||||||||||||| ||||||||||||||||||||||||||||| ||||
Db        306 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 247

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||| |||||||| |||||||||| || ||||||||||||||||||||||
Db        246 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 187

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              |||||||||||||||| |||||||||||||||||||||||||||| ||||||||||||||||
Db        186 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 127

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||| |||||||| ||||| ||||||||||||||||||||||||||||||||||||||
Db        126 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              |||||||||||||||||||||||||| ||||||||| |||||||||||| |||||||||
Db         66 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 7

Qy        661 GCTTCC 666
                |||||
Db          6 TCTTCC 1
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RESULT 12
US-09-917-265-104
; Sequence 104, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(897)

; OTHER INFORMATION:
US-09-917-265-104

  Query Match 90.2%; Score 600.4; DB 3; Length 1455;
  Best Local Similarity 93.8%; Pred. No. 1e-181;
  Matches 625; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

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Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
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Db        232 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 291

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
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Db        292 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 351

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
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Db        352 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 411

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
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Db        412 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 471

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
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Db        472 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 531

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
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Db        532 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 591

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
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Db        592 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 651

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
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Db        652 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 711

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Db        712 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 771

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
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Db        772 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 831

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Db        832 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 891

Qy        661 GCTTCC 666
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Db        892 TCTTCC 897
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RESULT 13
US-09-917-265-106/c
; Sequence 106, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 106
; LENGTH: 1455

; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-917-265-106

  Query Match 90.2%; Score 600.4; DB 3; Length 1455;
  Best Local Similarity 93.8%; Pred. No. 1e-181;
  Matches 625; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

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              ||||||||||||||| ||||||||||||||| |||||||||||||||| ||| ||||||||||
Db       1224 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 1165

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
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Db       1164 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 1105

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
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Db       1104 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 1045

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
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Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
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Db        984 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 925

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
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Db        924 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 865

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              |||||||||  |||||||||||||||| |||||||||||||||||||||||||| ||||
Db        864 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 805

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              |||||||||||||| |||||||| |||||||||| || ||||||||||||||||||||||
Db        804 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 745

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
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Db        744 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 685

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
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Db        684 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 625

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
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Db        624 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 565

Qy        661 GCTTCC 666
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Db        564 TCTTCC 559
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RESULT 14
US-10-821-670-104
; Sequence 104, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2

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; SEQ ID NO 104
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (232)..(897)
US-10-821-670-104

  Query Match            90.2%;  Score 600.4;  DB 9;  Length 1455;
  Best Local Similarity  93.8%;  Pred. No. 1e-181;
  Matches  625;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

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Db        232 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 291

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
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Db        352 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 411

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Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
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Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
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Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
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Db        652 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 711

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
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Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
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Qy        661 GCTTCC 666
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Db        892 TCTTCC 897


RESULT 15
US-10-821-670-106/c
; Sequence 106, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 106
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-106

  Query Match            90.2%;  Score 600.4;  DB 9;  Length 1455;
  Best Local Similarity  93.8%;  Pred. No. 1e-181;
  Matches  625;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
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Db       1224 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 1165

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
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Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
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Qy        661 GCTTCC 666
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Db        564 TCTTCC 559


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GenCore version 5.1.9
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Perfect score: 666
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Searched: 253354 seqs, 63461778 residues

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	3	33.2	5.0	1710	7	US-11-217-529-79541	Sequence 79541, A
	4	33	5.0	905	6	US-10-953-349-3742	Sequence 3742, Ap
	5	32.4	4.9	2338	7	US-11-293-697-1600	Sequence 1600, Ap
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c	29	28.6	4.3	683	6	US-10-953-349-4301	Sequence 4301, Ap
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	38	28.2	4.2	807	6	US-10-468-193-16	Sequence 16, Appl
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	44	28	4.2	1463	6	US-10-953-349-31591	Sequence 31591, A
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ALIGNMENTS

RESULT 1
US-10-471-571A-3681
; Sequence 3681, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 3681
; LENGTH: 2487
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-471-571A-3681

Query Match 5.3%; Score 35; DB 6; Length 2487;
Best Local Similarity 46.2%; Pred. No. 0.18;
Matches 116; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

```
Qy        403 AAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGG 462
              || ||  | | | || |   || |    ||||   |||| |  ||| | | | ||  |
Db       2144 AATATAAAACGGTTGAATCACAGGAATCTGAAGCTAAAGATAGTAAGGAAACATACGACA 2203

Qy        463 CAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAAT 522
              ||    ||   | ||    ||| | ||  |   ||  ||         | ||   | |
Db       2204 CAACCTTTAAAGTATATCCACAAGGTGCAACAAATGTATCGAAACATCAAGATGCACATG 2263

Qy        523 GTCAACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACT 582
              | ||| |   ||    | | | || |||     |  ||  |  | ||| |   || |
Db       2264 GGCAAGATGATGCACATTCAATAGTACTAGATGATAAAACGATGGCATTGTACCAAGAAG 2323

Qy        583 AAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGA 642
                || ||          | ||| |  | |||  |  || | |  |  ||  ||||| | |
Db       2324 TGAAACAGCAATCAGCAAGTTCATTGTTCTTATATGATGCTTTAATAGATTATCAAAACA 2383

Qy        643 ATGATGAGCTA 653
              |  || | |||
Db       2384 AGCATCAACTA 2394
```

RESULT 2
US-10-953-349-35671
; Sequence 35671, Application US/10953349

```
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35671
;   LENGTH: 814
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (463)..(463)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (509)..(509)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-35671

  Query Match             5.0%;  Score 33.4;  DB 6;  Length 814;
  Best Local Similarity   55.7%;  Pred. No. 0.29;
  Matches   64;  Conservative    0;  Mismatches   51;  Indels    0;  Gaps    0;

Qy         56 TGGACCACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCC 115
              || |  ||||| | ||   | | || |      |   |||  |||  ||  |||    |||
Db        239 TGAAGTACCTCCGCTTTCTCCGCAAGCGGATGAACACCAAGCCATCCCATGGACCCATCC 298

Qy        116 AGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAA 170
              | | || |  ||  ||| | | |||| |||  ||||| ||   | | ||| | |
Db        299 ACTTCCGCGCCCCGTCCAAGATCCTGTGGCGCACCATCCGCGGGATGATTCCGCA 353


RESULT 3
US-11-217-529-79541
; Sequence 79541, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79541
;   LENGTH: 1710
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (1692)..(1692)
;   OTHER INFORMATION: a, c, g, t, unknown, or other
US-11-217-529-79541

  Query Match             5.0%;  Score 33.2;  DB 7;  Length 1710;
  Best Local Similarity   55.1%;  Pred. No. 0.53;
  Matches   65;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy        152 TCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAG 211
              |||  |||   ||||| ||   ||   | | | ||| |||| ||     ||    |||||
Db        290 TCAAGAACGATCTTCAAAATTTCATGAAGAATGTAGGATTTGACCAACACAAACTCGAAG 349

Qy        212 AGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACC 269
              |  | ||  |||| |||||   | ||||    || ||| |    ||  |     ||||
Db        350 ATGTAGACGATGACGATATAGAAGAAGAATCCACTAGCTCCAAAGAATCTAAAATACC 407


RESULT 4
US-10-953-349-3742
; Sequence 3742, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3742
;   LENGTH: 905
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-3742

  Query Match             5.0%;  Score 33;  DB 6;  Length 905;
  Best Local Similarity   53.5%;  Pred. No. 0.42;
  Matches   69;  Conservative    0;  Mismatches   60;  Indels    0;  Gaps    0;

Qy          6 CCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGACCACCT 65
              || ||| |      | || |||| |      ||| ||  ||  ||   |||| | | |||||
Db        471 CCGGCCACTCCCACGCCACCTTCTTCAACTCCGGGAACTCCTACCACACCGGAATCACCT 530

Qy         66 CAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAA 125
              | || ||||      |||  | | ||||     |||  ||  |    | | ||    |||
Db        531 CCGTCTGGCGGATCACCCACACCCACCACACCCACACCTGGTGCAGGTTCAACTTCTCCT 590

Qy        126 CCACTCCCA 134
              ||  |  |||
Db        591 CCTCCTCCA 599


RESULT 5
US-11-293-697-1600
; Sequence 1600, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1600
;   LENGTH: 2338
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1600

  Query Match             4.9%;  Score 32.4;  DB 7;  Length 2338;
  Best Local Similarity   49.4%;  Pred. No. 1.2;
  Matches   84;  Conservative    0;  Mismatches   86;  Indels    0;  Gaps    0;

Qy        379 CTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCA 438
              || ||  | | | | | |  | |  ||||||||||  | || |         || | |
Db       1001 CTCAGGCGGAGCAAAGTGTCCATTGAGATGTACCAGTCGCAGGTGGCAAAGCTGGAGGAT 1060

Qy        439 AAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATT 498
              |  | |  |  ||  |  ||  | ||  | | ||| |  |   | ||  |
Db       1061 GATATCTACAAAGAGGCCGAAGAGAAGGCCCTGCTGAAGGAGGCCCTGGAGCGCATGGAG 1120
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Qy        499 GATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAA 548
              |  ||||||  ||||    ||  |||||||| |  |    ||  |||||
Db       1121 CACCAGCTGTGCCAGGAGAAGAGGGTCAACAGGGCCATCCGGCAGCAGAA 1170
```

RESULT 6
US-11-217-529-80999
; Sequence 80999, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80999
; LENGTH: 1287
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-80999

Query Match 4.8%; Score 32.2; DB 7; Length 1287;
Best Local Similarity 52.6%; Pred. No. 0.95;
Matches 70; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

```
Qy        513 GGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTT 572
              | || |||||          ||||  | |  ||    ||| |||  |  | ||| ||| |||
Db        327 GCCCATGAATAGATCAGATGTGGATTTAACAATATACTACTCTTTTAATGAAACGGTTTT 386

Qy        573 TTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGAC 632
              | ||  | || ||    |   |   | || |||| | |  |   || |  ||| |  |
Db        387 AGAGAACCCAAATATAGGTCAAAGTGCAGTTTTTCAGGATGGCTACATCCAAGCATTAGC 446

Qy        633 CATCAATAGAATG 645
              ||||| |  | ||
Db        447 CATCAGTCCAGTG 459
```

RESULT 7
US-10-488-619-2605/c
; Sequence 2605, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2605
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2605

Query Match 4.7%; Score 31.4; DB 6; Length 654;
Best Local Similarity 51.0%; Pred. No. 1.1;
Matches 74; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

```
Qy        302 CTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTT 361
              |||| | ||  | ||    |||  |   |  |  || || |||| |   || | |  ||
Db        476 CTTCAAAAGTCACCTTCACGATCTCCTCTCTGCCTTCCCGGGCCACGTAAAGGGCGACTC 417

Qy        362 TTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGT 421
              |  |    || ||||||  || ||  ||| || | | |||| |  |   |   || |
Db        416 TGTCGTTCTCCTTGTGCCGCAGGAGGTTCTCTGCGTAGTTGAGGCGGCTGCCTCTGAACC 357

Qy        422 TCAAGGCCATGAATGCAAAGCTGTT 446
              |  ||  |    |||||  |  ||
Db        356 ACTCGGGGACATCTGCAATCCCTTT 332
```

RESULT 8
US-10-196-749-121/c
; Sequence 121, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 121
; LENGTH: 1532
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-196-749-121

Query Match 4.7%; Score 31.2; DB 6; Length 1532;
Best Local Similarity 49.4%; Pred. No. 2.2;
Matches 81; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

```
Qy        245 CCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTT 304
              ||| |  || | |   | |||  ||     ||  ||| ||     ||   || ||||
Db        633 CCAACGGAGGGTACATCGACTTCACAACATCATCCACCCTGGGGCTGATCCGCTTGGCCA 574

Qy        305 CCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTA 364
              ||| |  ||| || |||| |     ||     | | |     ||  | || ||  | | |
Db        573 CCACAATGATGTCGCTGACACTGGCTGAAGTCTTCATCTTGGCCCCAGAGCCCATTGTCA 514

Qy        365 TGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
```

```
                 || | ||    | |  |  |||  | |    |   ||| ||||||
Db        513 TGGCAACAAGCTTCTCTGTCAGAGTGTGACAAATCTTCAAGATG 470
```

RESULT 9
US-10-471-571A-4253
; Sequence 4253, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 4253
; LENGTH: 1212
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-471-571A-4253

Query Match 4.6%; Score 30.8; DB 6; Length 1212;
Best Local Similarity 50.7%; Pred. No. 2.6;
Matches 74; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

```
Qy        402 GAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAG 461
              | ||||| |  ||||    ||   |   ||| | |  ||  ||||   | | | | || |
Db         25 GCAGATGAATTAGGTTTCTTTGGTGAATATGGAGGGCAATATGTTCCAGAAACATTAATG 84

Qy        462 GCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAA 521
              |||   ||  ||  |  ||| | ||| | |   |   |  ||| |   |||    | ||
Db         85 CCAGCAATTATTGAGTTGAAAAAAGCTTATAAAGAGGCAAAAGCAGACCCAGAGTTTCAA 144

Qy        522 TGTCAACAGTGTGACTGTGCCACAGA 547
              |  ||| |    ||| |    ||||
Db        145 AGAGAACTGGAATACTATTTATCAGA 170
```

RESULT 10
US-11-293-697-683/c
; Sequence 683, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 683
; LENGTH: 2920
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-683

Query Match 4.6%; Score 30.8; DB 7; Length 2920;
Best Local Similarity 53.3%; Pred. No. 4.4;
Matches 65; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

```
Qy        160 ACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGAT 219
              | | || ||| |   || | ||  |  |   | || ||| | ||||     |  || |||
Db       1411 AGGATTGAGACGCTGAGCCCAATGCAGGTGATGTAGTCCAGAACTTTGTCGGTCATCGAT 1352

Qy        220 CATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 279
              || || || | ||  || ||| || |||       ||  |  |||| | | | ||
Db       1351 TTGGAGGACATGAGAATGGAAAAAGACATCACCACACTGGTGTAGTTACAGCGGCATTTC 1292

Qy        280 AC 281
              ||
Db       1291 AC 1290
```

RESULT 11
US-10-505-928-330
; Sequence 330, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 330
; LENGTH: 6826
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-330

Query Match 4.6%; Score 30.4; DB 6; Length 6826;
Best Local Similarity 53.3%; Pred. No. 10;
Matches 64; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

```
Qy        486 GCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACA 545
              ||  || |  |||| ||||  |      ||  |  |||   |   |  ||   || | ||
Db       3630 GCCTACGGTCATTGGTGAGAGGAAGTGGGGACAAAATTGAAGGGGGTGGAGCATGACTCA 3689

Qy        546 GAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCT 605
              | || ||||||||||   |  || | |||| |  |    |   | ||| ||| | | | ||
Db       3690 AAGCTTCTCCCTGGAGAGAGAGGGTATTTAGACCAGGCATTCCTAGCCCTGAAAATTCCT 3749
```

RESULT 12
US-10-953-349-31587/c
; Sequence 31587, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31587
; LENGTH: 1422
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-953-349-31587

Query Match 4.5%; Score 30.2; DB 6; Length 1422;
Best Local Similarity 49.7%; Pred. No. 4.5;
Matches 77; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

```
Qy        322 ATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTT 381
              || || |  | ||| ||| | | |  |||||  ||||| || | |  ||   |||
Db        430 ATGACGATGGCGAGATGCGTCGGCGTCAGAATAACCTCCTTGAAGCGGATGATGTTGGGA 371

Qy        382 AGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAG 441
              || | | |  |   |||| ||| |  |       ||||    | ||      |   |
Db        370 TGCCGCAGCGACCTGTGGTTGATGATCTCTCTCTGCACGTTCTCATCGATCTTCTCGCCG 311

Qy        442 CTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGA 476
              | ||  ||| |    | |  |  || ||  | |||
Db        310 CGGTCGATGTACTTGACAGCGACGAGCTCGCCGGA 276
```

```
RESULT 13
US-10-953-349-10993
; Sequence 10993, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10993
;   LENGTH: 1491
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-10993

  Query Match             4.5%;  Score 30.2;  DB 6;  Length 1491;
  Best Local Similarity   51.9%;  Pred. No. 4.6;
  Matches   68;  Conservative    0;  Mismatches   63;  Indels    0;  Gaps    0;

Qy        379 CTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCA 438
              || |  || |   | | ||    ||||| | |  | || ||   || |  || |||| |
Db        929 CTGAAGAGGAAAGAGGCGGCAAAGAAGAGGAAGAAAGTCGATCCCATGATCAAGAATCCT 988

Qy        439 AAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATT 498
               ||   |   | |||  |   | | | |||  | | ||   |||| ||  ||      |
Db        989 GAGAGATACCTCGATGATCCTAAGAATATCCATTTCGAGACAAACGTGAAGAATAGGTTA 1048

Qy        499 GATGAGCTGTT 509
              | ||||||||
Db       1049 TACGAGCTGTT 1059


RESULT 14
US-11-291-668-48
; Sequence 48, Application US/11291668
; Publication No. US20060117394A1
; GENERAL INFORMATION:
;  APPLICANT: Robl, James M.
;  APPLICANT:  Goldsby, Richard A.
;  APPLICANT:  Ferguson, Stacy E.
;  APPLICANT:  Kuroiwa, Yoshima
;  APPLICANT:  Tomizuka, Kazuma
;  APPLICANT:  Ishida, Isao
;  TITLE OF INVENTION: Expression of Xenogenous (Human)
;  TITLE OF INVENTION:  Immunoglobulins in Cloned, Transgenic Ungulates
;  FILE REFERENCE: 50195/008003
;  CURRENT APPLICATION NUMBER: US/11/291,668
;  CURRENT FILING DATE:  2005-12-01
;  PRIOR APPLICATION NUMBER: US/09/988,115
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,625
;  PRIOR FILING DATE: 2001-08-09
;  PRIOR APPLICATION NUMBER: US 60/256,458
;  PRIOR FILING DATE: 2000-12-20
;  PRIOR APPLICATION NUMBER: US 09/714,185
;  PRIOR FILING DATE: 2000-11-17
;  PRIOR APPLICATION NUMBER: US 60/166,410
;  PRIOR FILING DATE: 1999-11-19
;  NUMBER OF SEQ ID NOS: 68
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
;   LENGTH: 3120
;   TYPE: DNA
;   ORGANISM: Bovine
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(3120)
;   OTHER INFORMATION: n=a, t, c, g or no nucleotide
US-11-291-668-48

  Query Match             4.5%;  Score 30;  DB 7;  Length 3120;
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  Matches   83;  Conservative    0;  Mismatches   70;  Indels    1;  Gaps    1;

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Db       1648 CCAGCCCAGCCCAGCTCACACACTTGGCCCACCTCAGCCACTCCATTCAGCTCAGCCCAG 1707

Qy         92 CCACACCAAGCCCAGGAATGTTCCA-GTGCCTCAACCACTCCCAAACCCTGCTGCGAGCC 150
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RESULT 15
US-11-292-164-48
; Sequence 48, Application US/11292164
; Publication No. US20060117395A1
; GENERAL INFORMATION:
;  APPLICANT: Robl, James M.
;  APPLICANT:  Goldsby, Richard A.
;  APPLICANT:  Ferguson, Stacy E.
;  APPLICANT:  Kuroiwa, Yoshima
;  APPLICANT:  Tomizuka, Kazuma
;  APPLICANT:  Ishida, Isao
;  TITLE OF INVENTION: Expression of Xenogenous (Human)
;  TITLE OF INVENTION:  Immunoglobulins in Cloned, Transgenic Ungulates
;  FILE REFERENCE: 50195/008003
;  CURRENT APPLICATION NUMBER: US/11/292,164
;  CURRENT FILING DATE:  2005-12-01
;  PRIOR APPLICATION NUMBER: US/09/988,115
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,625
;  PRIOR FILING DATE: 2001-08-09
;  PRIOR APPLICATION NUMBER: US 60/256,458
;  PRIOR FILING DATE: 2000-12-20
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;  PRIOR FILING DATE: 2000-11-17
;  PRIOR APPLICATION NUMBER: US 60/166,410
;  PRIOR FILING DATE: 1999-11-19
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; SEQ ID NO 48
;   LENGTH: 3120
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;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(3120)
;   OTHER INFORMATION: n=a, t, c, g or no nucleotide
US-11-292-164-48

  Query Match             4.5%;  Score 30;  DB 7;  Length 3120;
  Best Local Similarity   53.9%;  Pred. No. 8.4;
  Matches   83;  Conservative    0;  Mismatches   70;  Indels    1;  Gaps    1;

Qy         32 CCATCCTGGTCCTGTTAAACCACCTGGACCACCTCAGTTTGGCCAGGAACCTCCCCACAC 91
              ||| ||  | || | | |  ||| ||| |||||||||     |||   | |||  | ||
Db       1648 CCAGCCCAGCCCAGCTCACACACTTGGCCCACCTCAGCCACTCCATTCAGCTCAGCCCAG 1707

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Search completed: June 10, 2006, 18:18:54
Job time : 12.5452 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2006, 22:33:03 ; Search time 4218.94 Seconds
(without alignments)
10094.706 Million cell updates/sec

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Perfect score: 666
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 6366136 seqs, 31973710525 residues

Word size : 1

Total number of hits satisfying chosen parameters: 12730834

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 200 summaries

Database : GenEmbl:*
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2: gb_pat:*
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10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	4	602	90.4	1441	2	AR242438	AR242438 Sequence
	5	602	90.4	1441	2	AR280206	AR280206 Sequence
	6	602	90.4	1441	2	AR322421	AR322421 Sequence
	7	558	83.8	561	2	AR596007	AR596007 Sequence
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	12	527	79.1	591	2	AR242439	AR242439 Sequence
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	15	507	76.1	1533	2	AR595959	AR595959 Sequence
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	17	507	76.1	1599	2	AR595956	AR595956 Sequence
c	18	507	76.1	1599	2	AR595957	AR595957 Sequence
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	22	253	38.0	285	14	AF054605	AF054605 Felis cat
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	24	248	37.2	689	2	AR280219	AR280219 Sequence
	25	248	37.2	689	2	AR322434	AR322434 Sequence
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	27	120	18.0	660	2	AX154616	AX154616 Sequence
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	76	65	9.8	1026	2	AR091390	AR091390 Sequence
	77	65	9.8	1026	2	AR380496	AR380496 Sequence
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	79	65	9.8	1287	2	AR393790	AR393790 Sequence
	80	65	9.8	1287	2	AX084108	AX084108 Sequence
	81	65	9.8	1316	2	AR050785	AR050785 Sequence
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	88	65	9.8	1395	2	AR309637	AR309637 Sequence
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	91	65	9.8	1444	2	CS143811	CS143811 Sequence

	92	65	9.8	1560	2	AR091395 AR091395 Sequence
	93	65	9.8	1623	2	AR091394 AR091394 Sequence
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ACCESSION   AR595952
VERSION     AR595952.1  GI:56646933
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 32 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
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ORIGIN

  Query Match             100.0%;  Score 666;  DB 2;  Length 666;
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  Matches  666;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
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Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
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Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
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Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
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Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
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Db        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
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Db        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        661 GCTTCC 666
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Db        661 GCTTCC 666
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RESULT 2
AR595953/c
LOCUS       AR595953                 666 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 34 from patent US 6818444.
ACCESSION   AR595953
VERSION     AR595953.1  GI:56646934
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 34 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="unknown"
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ORIGIN

  Query Match           100.0%;  Score 666;  DB 2;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  666;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
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Db        666 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 607

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
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Db        606 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 547

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 427

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
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Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 307

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
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Db        306 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 247

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
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Db        246 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 187

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
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Db        186 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 127

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
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Db        126 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
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Db         66 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 7

Qy        661 GCTTCC 666
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Db          6 GCTTCC 1
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RESULT 3
FCIL12P35
LOCUS       FCIL12P35                669 bp    mRNA    linear   MAM 18-APR-2005
DEFINITION  Felis catus mRNA for interleukin-12 p35 chain.
ACCESSION   Y07761
VERSION     Y07761.1  GI:2102662
KEYWORDS    interleukin-12 subunit p35.
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1
  AUTHORS   Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
  TITLE     Molecular cloning of cat interleukin-12
  JOURNAL   Immunogenetics 45 (6), 462-463 (1997)
   PUBMED   9089110
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Schijns,V.E.C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
            Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
            Utrecht, NETHERLANDS
FEATURES             Location/Qualifiers
     source          1. .669
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                     /cell_type="lymphocyte"
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                    /protein_id="CAA69067.1"
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                    /db_xref="UniProtKB/Swiss-Prot:O02743"
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                    LNAS"
ORIGIN

  Query Match             92.3%;  Score 615;  DB 14;  Length 669;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches  665;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        661 GCTTCC 666
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Db        661 GCTTCC 666
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RESULT 4
AR242438
LOCUS       AR242438               1441 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 8 from patent US 6472509.
ACCESSION   AR242438
VERSION     AR242438.1  GI:27288855
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1441)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 8 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .1441
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                     /mol_type="mRNA"
ORIGIN

  Query Match             90.4%;  Score 602;  DB 2;  Length 1441;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches  652;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
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Db        683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTA 653
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Db        743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTA 795


RESULT 5
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AR280206
LOCUS       AR280206               1441 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 8 from patent US 6518045.
ACCESSION   AR280206
VERSION     AR280206.1  GI:29715596
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1441)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 8 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .1441
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                     /mol_type="mRNA"
ORIGIN

  Query Match             90.4%;  Score 602;  DB 2;  Length 1441;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches  652;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
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Db        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
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Db        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
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Db        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTA 653
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTA 795


RESULT 6
AR322421
LOCUS       AR322421               1441 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 8 from patent US 6566097.
ACCESSION   AR322421
VERSION     AR322421.1  GI:33708174
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1441)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 8 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .1441
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             90.4%;  Score 602;  DB 2;  Length 1441;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches  652;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
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Db        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
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Db        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTA 653
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTA 795


RESULT 7
AR596007
LOCUS       AR596007               561 bp    DNA     linear   PAT 15-DEC-2004
```

```
DEFINITION  Sequence 101 from patent US 6818444.
ACCESSION   AR596007
VERSION     AR596007.1  GI:56646988
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 561)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 101 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .561
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             83.8%;  Score 558;  DB 2;  Length 561;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-296;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 63

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 123

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 183

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 243

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 303

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 363

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 423

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 483

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 543

Qy        649 AGCTATCTGAATGCTTCC 666
              ||||||||||||||||||
Db        544 AGCTATCTGAATGCTTCC 561


RESULT 8
AR596008/c
LOCUS       AR596008                561 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 103 from patent US 6818444.
ACCESSION   AR596008
VERSION     AR596008.1  GI:56646989
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 561)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 103 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .561
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             83.8%;  Score 558;  DB 2;  Length 561;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-296;
  Matches  558;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
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Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        649 AGCTATCTGAATGCTTCC 666
              ||||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1


RESULT 9
FCU83185
LOCUS       FCU83185                669 bp    mRNA    linear   MAM 16-JUL-1999
DEFINITION  Felis catus interleukin-12 p35 subunit (IL-12) mRNA, complete cds.
ACCESSION   U83185
VERSION     U83185.1  GI:2735052
KEYWORDS    .
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Nucleotide and predicted peptide sequence of feline interleukin-12
            (IL-12)
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  JOURNAL   DNA Seq. 8 (1-2), 77-82 (1997)
   PUBMED   9522125
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal
            Veterinary Medicine, University of Zurich, Winterthurerstrasse 260,
            Zurich, ZH 8057, Switzerland
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Felis catus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
     CDS             1. .669
                     /note="cytokine"
                     /codon_start=1
                     /product="interleukin-12 p35 subunit"
                     /protein_id="AAB93836.1"
                     /db_xref="GI:2735053"
                     /translation="MCPPRGLLLVTILVLLNHLDHLSLARNLPTPTPSPGMFQCLNHS
                     QTLLRAISNTLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
                     REISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAMNAKLLMDPKRQIFLDQ
                     NMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSY
                     LNSS"
ORIGIN

  Query Match             83.8%;  Score 558;  DB 14;  Length 669;
  Best Local Similarity   99.7%;  Pred. No. 2.5e-296;
  Matches  658;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660


RESULT 10
AR595954
LOCUS       AR595954                591 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 35 from patent US 6818444.
ACCESSION   AR595954
VERSION     AR595954.1  GI:56646935
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 35 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             81.1%;  Score 540;  DB 2;  Length 591;
  Best Local Similarity   99.8%;  Pred. No. 2.2e-286;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 591


RESULT 11
AR595955/c
LOCUS       AR595955                591 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 37 from patent US 6818444.
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ACCESSION   AR595955
VERSION     AR595955.1  GI:56646936
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 37 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             81.1%;  Score 540;  DB 2;  Length 591;
  Best Local Similarity   99.8%;  Pred. No. 2.2e-286;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 532

Qy        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 472

Qy        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 412

Qy        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 292

Qy        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 232

Qy        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 112

Qy        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1


RESULT 12
AR242439
LOCUS       AR242439                 591 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 9 from patent US 6472509.
ACCESSION   AR242439
VERSION     AR242439.1  GI:27288856
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 9 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             79.1%;  Score 527;  DB 2;  Length 591;
  Best Local Similarity   99.8%;  Pred. No. 3.4e-279;
  Matches  577;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTA 653
              |||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTA 578


RESULT 13
AR280207
LOCUS       AR280207                 591 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 9 from patent US 6518045.
ACCESSION   AR280207
VERSION     AR280207.1  GI:29715597
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 9 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
```

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            EPX;
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             79.1%;  Score 527;  DB 2;  Length 591;
  Best Local Similarity   99.8%;  Pred. No. 3.4e-279;
  Matches  577;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTA 653
              |||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTA 578


RESULT 14
AR322422
LOCUS       AR322422                591 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 9 from patent US 6566097.
ACCESSION   AR322422
VERSION     AR322422.1  GI:33708175
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 9 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             79.1%;  Score 527;  DB 2;  Length 591;
  Best Local Similarity   99.8%;  Pred. No. 3.4e-279;
  Matches  577;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        556 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTA 653
              |||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTA 578


RESULT 15
AR595959
LOCUS       AR595959                1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 43 from patent US 6818444.
ACCESSION   AR595959
VERSION     AR595959.1  GI:56646940
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 43 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             76.1%;  Score 507;  DB 2;  Length 1533;
  Best Local Similarity   99.8%;  Pred. No. 3.6e-268;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
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Db        976 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 1035

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228

Db       1036 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 1095

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288

Db       1096 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 1155

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348

Db       1156 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 1215

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408

Db       1216 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 1275

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468

Db       1276 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 1335

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528

Db       1336 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 1395

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588

Db       1396 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 1455

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648

Db       1456 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 1515

Qy        649 AGCTATCTGAATGCTTCC 666

Db       1516 AGCTATCTGAATGCTTCC 1533
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RESULT 16
AR595960/c
LOCUS AR595960 1533 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 45 from patent US 6818444.
ACCESSION AR595960
VERSION AR595960.1 GI:56646941
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1533)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 45 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .1533
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

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  Query Match            76.1%;  Score 507;  DB 2;  Length 1533;
  Best Local Similarity  99.8%;  Pred. No. 3.6e-268;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168

Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228

Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288

Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348

Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408

Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468

Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528

Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588

Db        138 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648

Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        649 AGCTATCTGAATGCTTCC 666

Db         18 AGCTATCTGAATGCTTCC 1
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RESULT 17
AR595956
LOCUS AR595956 1599 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 38 from patent US 6818444.
ACCESSION AR595956
VERSION AR595956.1 GI:56646937
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1599)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 38 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .1599
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

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  Query Match            76.1%;  Score 507;  DB 2;  Length 1599;
  Best Local Similarity  99.8%;  Pred. No. 3.6e-268;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168

Db       1042 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 1101

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228

Db       1102 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 1161

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288

Db       1162 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 1221

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348

Db       1222 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 1281
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Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1282 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 1341

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1342 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 1401

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1402 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 1461

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1462 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 1521

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1522 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 1581

Qy        649 AGCTATCTGAATGCTTCC 666
              ||||||||||||||||||
Db       1582 AGCTATCTGAATGCTTCC 1599


RESULT 18
AR595957/c
LOCUS       AR595957               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 40 from patent US 6818444.
ACCESSION   AR595957
VERSION     AR595957.1  GI:56646938
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 40 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             76.1%;  Score 507;  DB 2;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 3.6e-268;
  Matches  557;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 499

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 439

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 379

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 319

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 259

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 199

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 139

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        138 AGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATC 79

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 19

Qy        649 AGCTATCTGAATGCTTCC 666
              ||||||||||||||||||
Db         18 AGCTATCTGAATGCTTCC 1


RESULT 19
AX076201
LOCUS       AX076201               669 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 2 from Patent WO0104155.
ACCESSION   AX076201
VERSION     AX076201.1  GI:12710826
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 2 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="feline IL-12 p35"
ORIGIN

  Query Match             45.5%;  Score 303;  DB 2;  Length 669;
  Best Local Similarity   99.2%;  Pred. No. 2.2e-155;
  Matches  503;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              |||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTG 507
              |||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTG 507


RESULT 20
AX076483
LOCUS       AX076483                669 bp    DNA     linear   PAT 07-FEB-2001
DEFINITION  Sequence 9 from Patent WO0104280.
ACCESSION   AX076483
VERSION     AX076483.1  GI:12711035
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 9 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Sequence coding for SEQ ID NO 3, IL-12 p35"
ORIGIN

  Query Match             45.5%;  Score 303;  DB 2;  Length 669;
  Best Local Similarity   99.2%;  Pred. No. 2.2e-155;
  Matches  503;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              |||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCT 360

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATTGATGAGCTG 507
              |||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTG 507


RESULT 21
AX076477
LOCUS       AX076477                4201 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 3 from Patent WO0104280.
ACCESSION   AX076477
VERSION     AX076477.1  GI:12711029
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 3 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .4201
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="IL-12p35 (pMOLfIL-12p35 (e-,_e31-)clone61)"
ORIGIN

  Query Match             45.5%;  Score 303;  DB 2;  Length 4201;
  Best Local Similarity   99.2%;  Pred. No. 1.9e-155;
  Matches  503;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3047 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 3106

Qy         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3107 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 3166

Qy        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3167 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 3226

Qy        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       3227 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 3286

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       3287 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTG 3346

Qy        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360
              |||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db       3347 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCT 3406

Qy        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3407 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 3466

Qy        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3467 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 3526

Qy        481 AACATGCTGACAGCTATTGATGAGCTG 507
              |||||||||||||||||||||||||||
Db       3527 AACATGCTGACAGCTATTGATGAGCTG 3553


RESULT 22
AF054605
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LOCUS       AF054605                285 bp    mRNA    linear   MAM 26-JUL-2000
DEFINITION  Felis catus interleukin 12 p35 subunit mRNA, partial cds.
ACCESSION   AF054605
VERSION     AF054605.1  GI:3126818
KEYWORDS    .
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Harley,R., Helps,C.R., Harbour,D.A., Gruffydd-Jones,T.J. and
            Day,M.J.
  TITLE     Cytokine mRNA expression in lesions in cats with chronic
            gingivostomatitis
  JOURNAL   Clin. Diagn. Lab. Immunol. 6 (4), 471-478 (1999)
   PUBMED   10391845
REFERENCE   2  (bases 1 to 285)
  AUTHORS   Harley,R., Helps,C.R., Gruffydd-Jones,T.J., Day,M.J. and
            Harbour,D.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-1998) Clinical Veterinary Science, University of
            Bristol, Langford House, Langford, Bristol BS40 7DU, U.K.
FEATURES             Location/Qualifiers
     source          1. .285
                     /organism="Felis catus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
                     /cell_line="FL4"
                     /cell_type="T cell"
                     /note="persistant FIV infection"
     CDS             <1. .>285
                     /codon_start=3
                     /product="interleukin 12 p35 subunit"
                     /protein_id="AAC15978.1"
                     /db_xref="GI:3126819"
                     /translation="LLRAISNTLHKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLP
                     LELTMNESCLASREISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVE"
ORIGIN

  Query Match            38.0%;  Score 253;  DB 14;  Length 285;
  Best Local Similarity  100.0%;  Pred. No. 1e-127;
  Matches  253;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 92

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 152

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 212

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 272

Qy        409 TACCAGGTGGAGT 421
              |||||||||||||
Db        273 TACCAGGTGGAGT 285


RESULT 23
AR242451
LOCUS       AR242451                689 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 26 from patent US 6472509.
ACCESSION   AR242451
VERSION     AR242451.1  GI:27288868
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 26 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .689
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match            37.2%;  Score 248;  DB 2;  Length 689;
  Best Local Similarity  98.8%;  Pred. No. 5.5e-125;
  Matches  598;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         49 AACCACCTGGACCACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGA 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         55 AACCACCTGGACCACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGA 114

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 174

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 234

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              |||||||||||||||||||||||||||||||| | ||||||||| | |||||||||
Db        235 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATGAAT 294

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 354

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 414

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              |||||||||||||||||||||||||||||| | ||||||||||||||||||||
Db        415 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATC 474

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 534

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        535 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATC 594

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 654

Qy        649 AGCTA 653
              |||||
Db        655 AGCTA 659


RESULT 24
AR280219
LOCUS       AR280219                689 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 26 from patent US 6518045.
ACCESSION   AR280219
VERSION     AR280219.1  GI:29715609
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
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           Unclassified.
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 26 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .689
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             37.2%;  Score 248;  DB 2;  Length 689;
  Best Local Similarity   98.8%;  Pred. No. 5.5e-125;
  Matches  598;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         49 AACCACCTGGACCACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGA 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         55 AACCACCTGGACCACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGA 114

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 174

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 234

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              |||||||||||||||||||||||||||||||| | ||||||||| | |||||||||
Db        235 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATGAAT 294

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 354

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 414

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              |||||||||||||||||||||||||||||||| | ||||||||||||||||||||||
Db        415 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATC 474

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 534

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        535 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATC 594

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 654

Qy        649 AGCTA 653
              |||||
Db        655 AGCTA 659


RESULT 25
AR322434
LOCUS       AR322434                689 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 26 from patent US 6566097.
ACCESSION   AR322434
VERSION     AR322434.1  GI:33708187
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 26 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .689
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             37.2%;  Score 248;  DB 2;  Length 689;
  Best Local Similarity   98.8%;  Pred. No. 5.5e-125;
  Matches  598;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         49 AACCACCTGGACCACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGA 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         55 AACCACCTGGACCACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGA 114

Qy        109 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 ATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAG 174

Qy        169 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 AAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGAT 234

Qy        229 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAAT 288
              |||||||||||||||||||||||||||||||| | ||||||||| | |||||||||
Db        235 ATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATGAAT 294

Qy        289 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 GAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCC 354

Qy        349 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 AGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATG 414

Qy        409 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATC 468
              |||||||||||||||||||||||||||||||| | ||||||||||||||||||||||
Db        415 TACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATC 474

Qy        469 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 TTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAAC 534

Qy        529 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATC 588
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        535 AGTGTGACTGTGCCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATC 594

Qy        589 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 AAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATG 654

Qy        649 AGCTA 653
              |||||
Db        655 AGCTA 659


RESULT 26
AX154615
LOCUS       AX154615                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 19 from Patent WO0140257.
ACCESSION   AX154615
VERSION     AX154615.1  GI:14536190
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
```

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  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 19 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match           26.7%;  Score 178;  DB 2;  Length 660;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-86;
  Matches  178;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        312 GATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGAC 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 GATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGAC 362

Qy        372 CCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCAT 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 CCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCAT 422

Qy        432 GAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 489
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 GAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480


RESULT 27
AX154616
LOCUS       AX154616                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 20 from Patent WO0140257.
ACCESSION   AX154616
VERSION     AX154616.1  GI:14536191
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 20 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match           18.0%;  Score 120;  DB 2;  Length 660;
  Best Local Similarity  100.0%;  Pred. No. 3.1e-54;
  Matches  120;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        370 ACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCC 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCC 420

Qy        430 ATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 489
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480


RESULT 28
AX154614
LOCUS       AX154614                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 18 from Patent WO0140257.
ACCESSION   AX154614
VERSION     AX154614.1  GI:14536189
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 18 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match           17.3%;  Score 115;  DB 2;  Length 660;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-51;
  Matches  115;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        166 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 225
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 216

Qy        226 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAA 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        217 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAA 271


RESULT 29
AX154621
LOCUS       AX154621                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 25 from Patent WO0140257.
ACCESSION   AX154621
VERSION     AX154621.1  GI:14536196
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 25 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match           17.3%;  Score 115;  DB 2;  Length 660;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-51;
  Matches  115;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        166 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 225
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 216

Qy        226 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAA 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        217 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAA 271


RESULT 30
AX154619
LOCUS       AX154619                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 23 from Patent WO0140257.
ACCESSION   AX154619
VERSION     AX154619.1  GI:14536194
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
```

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           other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 23 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match             15.3%;  Score 102;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-44;
  Matches  102;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        388 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 438

Qy        448 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 489
              |||||||||||||||||||||||||||||||||||||||||
Db        439 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTG 480


RESULT 31
AY191828
LOCUS       AY191828                657 bp    mRNA    linear   SYN 04-FEB-2003
DEFINITION  Synthetic construct evolved IL-12 p35 precursor, mRNA, partial cds.
ACCESSION   AY191828
VERSION     AY191828.1  GI:27729523
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 657)
  AUTHORS   Leong,S.R., Chang,J.C.C., Ong,R., Dawes,G., Stemmer,W.P.C. and
            Punnonen,J.
  TITLE     Optimized expression and specific activity of IL-12 by directed
            molecular evolution
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (3), 1163-1168 (2003)
   PUBMED   12529500
REFERENCE   2  (bases 1 to 657)
  AUTHORS   Leong,S.R., Chang,J.C.C., Ong,R., Dawes,G., Stemmer,W.P.C. and
            Punnonen,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-DEC-2002) Vaccines, Maxygen, Inc., 515 Galveston
            Drive, Redwood City, CA 94063, USA
FEATURES             Location/Qualifiers
     source          1. .657
                     /organism="synthetic construct"
                     /mol_type="mRNA"
                     /db_xref="taxon:32630"
     CDS             1. .>657
                     /codon_start=1
                     /transl_table=11
                     /product="evolved IL-12 p35 precursor"
                     /protein_id="AAO19111.1"
                     /db_xref="GI:27729524"
                     /translation="MCPARSLLLVATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNL
                     LRAVSNMLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELATNESCLASRGI
                     SLITNGSCLASRKTSFMTTLCLGSIYEDLKMYQVEFKTMNAKLLMNPKRQIFLDQNML
                     TAIDELLQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNS
                     S"
     sig_peptide     1. .66
     mat_peptide     67. .657
                     /product="evolved IL-12 p35"
ORIGIN

  Query Match             14.7%;  Score 98;  DB 8;  Length 657;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-42;
  Matches   98;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        166 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 216

Qy        226 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 263
              |||||||||||||||||||||||||||||||||||||
Db        217 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 254


RESULT 32
AX154617
LOCUS       AX154617                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 21 from Patent WO0140257.
ACCESSION   AX154617
VERSION     AX154617.1  GI:14536192
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 21 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match             14.7%;  Score 98;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-42;
  Matches   98;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        166 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 CAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAA 216

Qy        226 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 263
              |||||||||||||||||||||||||||||||||||||
Db        217 GATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTG 254


RESULT 33
AX154620
LOCUS       AX154620                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 24 from Patent WO0140257.
ACCESSION   AX154620
VERSION     AX154620.1  GI:14536195
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 24 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match             12.6%;  Score 84;  DB 2;  Length 660;
  Best Local Similarity   99.3%;  Pred. No. 2.4e-34;
  Matches  134;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy        312 GATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGAC 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 GATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGAC 362

Qy        372 CCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCAT 431
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        363 CCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCAT 422

Qy        432 GAATGCAAAGCTGTT 446
              |||||||||||||||
Db        423 GAATGCAAAGCTGTT 437


RESULT 34
BD171284
LOCUS       BD171284                 591 bp    DNA     linear   PAT 18-FEB-2003
DEFINITION  Novel canine cytokine protein.
ACCESSION   BD171284
VERSION     BD171284.1  GI:28412574
KEYWORDS    JP 2002241398-A/4.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Imamura,T., Maeda,H., Tokiyoshi,Y. and Eda,Y.
  TITLE     Novel canine cytokine protein
  JOURNAL   Patent: JP 2002241398-A 4 28-AUG-2002;
            CHEMO SERO THERAPEUT RES INST
COMMENT     OS   Canine splenocyte
            PN   JP 2002241398-A/4
            PD   28-AUG-2002
            PF   03-JUN-1997 JP 1997161936
            PI   TAKAYUKI IMAMURA,HIROAKI MAEDA,YUKIO TOKIYOSHI,YASUYUKI EDA PC
              C07K14/52,A61K38/00,A61K39/395,C07K16/24,C12N5/10,C12N15/09, PC
            C12P21/02//
            PC   C12P21/08,(C12P21/02,C12R1:91),A61K37/02,C12N5/00,C12N15/00 CC
              Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES            Location/Qualifiers
     source         1. .591
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"
ORIGIN

  Query Match            12.2%;  Score 81;  DB 2;  Length 591;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        223 CTGGCTTCCAGAGAGATCTCT 243


RESULT 35
AR595963
LOCUS       AR595963                 591 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 49 from patent US 6818444.
ACCESSION   AR595963
VERSION     AR595963.1  GI:56646944
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 49 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES            Location/Qualifiers
     source         1. .591
                    /organism="unknown"
                    /mol_type="genomic DNA"
ORIGIN

  Query Match            12.2%;  Score 81;  DB 2;  Length 591;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        223 CTGGCTTCCAGAGAGATCTCT 243


RESULT 36
AR595964/c
LOCUS       AR595964                 591 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 51 from patent US 6818444.
ACCESSION   AR595964
VERSION     AR595964.1  GI:56646945
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 51 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES            Location/Qualifiers
     source         1. .591
                    /organism="unknown"
                    /mol_type="genomic DNA"
ORIGIN

  Query Match            12.2%;  Score 81;  DB 2;  Length 591;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 37
AR595961
LOCUS       AR595961                 666 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 46 from patent US 6818444.
ACCESSION   AR595961
VERSION     AR595961.1  GI:56646942
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 46 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES            Location/Qualifiers
     source         1. .666
                    /organism="unknown"
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                     /mol_type="genomic DNA"
ORIGIN

  Query Match            12.2%;  Score 81;  DB 2;  Length 666;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 38
AR595962/c
LOCUS       AR595962                 666 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 48 from patent US 6818444.
ACCESSION   AR595962
VERSION     AR595962.1  GI:56646943
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 48 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match            12.2%;  Score 81;  DB 2;  Length 666;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 39
AR151062
LOCUS       AR151062                 669 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 2 from patent US 6231850.
ACCESSION   AR151062
VERSION     AR151062.1  GI:15117112
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12
  JOURNAL   Patent: US 6231850-A 2 15-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            12.2%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 40
AR151072
LOCUS       AR151072                 669 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 12 from patent US 6231850.
ACCESSION   AR151072
VERSION     AR151072.1  GI:15117122
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12
  JOURNAL   Patent: US 6231850-A 12 15-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            12.2%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 41
BD014654
LOCUS       BD014654                 669 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy.
ACCESSION   BD014654
VERSION     BD014654.1  GI:22555437
KEYWORDS    JP 2001161378-A/2.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F.
  TITLE     Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy
  JOURNAL   Patent: JP 2001161378-A 2 19-JUN-2001;
            TORAY INDUSTRIES INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 2001161378-A/2
            PD   19-JUN-2001
            PF   26-SEP-2000 JP 2000292946
            PI   FUMIYOSHI OKANO
            PC   C12N15/09,A61K38/00,A61P17/00,A61P17/00,A61P31/04,A61P31/04,
            PC   A61P35/00,
            PC   A61P37/00,C07K1/18,C07K1/22,C07K14/54,C12P21/02//(C12P21/02,
            PC   C12R1:91),
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            PC   (C12P21/02,C12R1:93),C12N15/00,A61K37/02
            CC   Process for producing highly pure protein, interleukin 12,  CC
                 protein
            CC   inhibiting interleukin-12 activity, remedies for mammalian  CC
                 immunopathy and
            CC   method of treating immunopathy
            FH   Key             Location/Qualifiers
            FT   CDS             (1). .(666)
            FT   mat_peptide     (76). .(666).
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Canis sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9616"
ORIGIN

  Query Match             12.2%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 42
BD014664
LOCUS       BD014664                669 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy.
ACCESSION   BD014664
VERSION     BD014664.1  GI:22555447
KEYWORDS    JP 2001161378-A/12.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F.
  TITLE     Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy
  JOURNAL   Patent: JP 2001161378-A 12 19-JUN-2001;
            TORAY INDUSTRIES INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 2001161378-A/12
            PD   19-JUN-2001
            PF   26-SEP-2000 JP 2000292946
            PI   FUMIYOSHI OKANO
            PC   C12N15/09,A61K38/00,A61P17/00,A61P17/00,A61P31/04,A61P31/04,
            PC   A61P35/00,
            PC   A61P37/00,C07K1/18,C07K1/22,C07K14/54,C12P21/02//(C12P21/02,
            PC   C12R1:91),
            PC   (C12P21/02,C12R1:93),C12N15/00,A61K37/02
            CC   Process for producing highly pure protein, interleukin 12,  CC
                 protein
            CC   inhibiting interleukin-12 activity, remedies for mammalian  CC
                 immunopathy and
            CC   method of treating immunopathy
            FH   Key             Location/Qualifiers
            FT   CDS             (1). .(666)
            FT   mat_peptide     (76). .(666).
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Canis sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9616"
ORIGIN

  Query Match             12.2%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 43
E15018
LOCUS       E15018                  669 bp    DNA     linear   PAT 28-JUL-1999
DEFINITION  Canine mRNA for interleukin 12 35kDa subunit,complete cds.
ACCESSION   E15018
VERSION     E15018.1  GI:5709701
KEYWORDS    JP 1998036397-A/2.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F.
  TITLE     CANINE INTERLEUKIN 12 AND ITS PRODUCTION
  JOURNAL   Patent: JP 1998036397-A 2 10-FEB-1998;
            TORAY IND INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 1998036397-A/2
            PD   10-FEB-1998
            PF   08-NOV-1996 JP 1996296789
            PR   08-NOV-1995 JP 95P   289729, 23-MAY-1996 JP 96P   128104 PI
            OKANO FUMIYOSHI
            PC   C07K14/54,C07H21/04,C12N5/10,C12N15/09,C12P21/02,(C12N5/10, PC
              C12R1:91),
            PC   (C12P21/02,C12R1:91);
            CC   strandedness: Double;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .669
            FT                   /organism='Canis sp.'
            FT                   /tissue_type='liver'
            FT   CDS             1. .669
            FT                   /product='interleukin12 35kDa subunit'.
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Canis sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9616"
ORIGIN

  Query Match             12.2%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 44
AR316461
LOCUS       AR316461                669 bp    mRNA    linear   PAT 17-AUG-2003
```

```
DEFINITION  Sequence 2 from patent US 6562334.
ACCESSION   AR316461
VERSION     AR316461.1  GI:33695289
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12 administration as an immune disease treatment
  JOURNAL   Patent: US 6562334-A 2 13-MAY-2003;
            Toray Industries, Inc.;;
            JPX;
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             12.2%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 45
AR316471
LOCUS       AR316471                669 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 12 from patent US 6562334.
ACCESSION   AR316471
VERSION     AR316471.1  GI:33695299
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12 administration as an immune disease treatment
  JOURNAL   Patent: US 6562334-A 12 13-MAY-2003;
            Toray Industries, Inc.;;
            JPX;
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             12.2%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 46
CFU49085
LOCUS       CFU49085                669 bp    mRNA    linear   MAM 13-MAR-1996
DEFINITION  Canis familiaris interleukin-12 p35 subunit mRNA, complete cds.
ACCESSION   U49085
VERSION     U49085.1  GI:1223905
KEYWORDS    .
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Belke-Louis,G.F. and Buettner,M.
  TITLE     Cloning and sequence analysis of the p35 and p40 subunits of canine
            interleukin-12
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Belke-Louis,G.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-FEB-1996) Georg F. Belke-Louis, Institute of Med.
            Microbiology, Veterinaerstr. 13, Muenchen, D-80539, Germany
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Canis familiaris"
                     /mol_type="mRNA"
                     /db_xref="taxon:9615"
     CDS             1. .669
                     /codon_start=1
                     /product="interleukin-12 p35 subunit"
                     /protein_id="AAA92058.1"
                     /db_xref="GI:1223906"
                     /translation="MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHS
                     QNLLRAVSNTLQKARQTLDYIPCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
                     REISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQ
                     NMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSY
                     LNSS"
ORIGIN

  Query Match             12.2%;  Score 81;  DB 14;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 47
BD171283
LOCUS       BD171283                1282 bp    DNA     linear   PAT 18-FEB-2003
DEFINITION  Novel canine cytokine protein.
ACCESSION   BD171283
VERSION     BD171283.1  GI:28412573
KEYWORDS    JP 2002241398-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 1282)
  AUTHORS   Imamura,T., Maeda,H., Tokiyoshi,Y. and Eda,Y.
  TITLE     Novel canine cytokine protein
  JOURNAL   Patent: JP 2002241398-A 3 28-AUG-2002;
            CHEMO SERO THERAPEUT RES INST
COMMENT     OS   Canine splenocyte
            PN   JP 2002241398-A/3
            PD   28-AUG-2002
            PF   03-JUN-1997 JP 1997161936
            PI   TAKAYUKI IMAMURA,HIROAKI MAEDA,YUKIO TOKIYOSHI,YASUYUKI EDA PC
              C07K14/52,A61K38/00,A61K39/395,C07K16/24,C12N5/10,C12N15/09, PC
            C12P21/02//
            PC   C12P21/08,(C12P21/02,C12R1:91),A61K37/02,C12N5/00,C12N15/00 CC
              Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
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     source          1. .1282
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             12.2%;  Score 81;  DB 2;  Length 1282;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 362

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        363 CTGGCTTCCAGAGAGATCTCT 383


RESULT 48
AR596009
LOCUS       AR596009               1455 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 104 from patent US 6818444.
ACCESSION   AR596009
VERSION     AR596009.1  GI:56646990
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1455)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 104 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1455
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             12.2%;  Score 81;  DB 2;  Length 1455;
  Best Local Similarity   100.0%;  Pred. No. 1e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 528

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        529 CTGGCTTCCAGAGAGATCTCT 549


RESULT 49
AR596010/c
LOCUS       AR596010               1455 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 106 from patent US 6818444.
ACCESSION   AR596010
VERSION     AR596010.1  GI:56646991
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1455)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 106 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1455
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             12.2%;  Score 81;  DB 2;  Length 1455;
  Best Local Similarity   100.0%;  Pred. No. 1e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 928

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        927 CTGGCTTCCAGAGAGATCTCT 907


RESULT 50
AR595973
LOCUS       AR595973               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 66 from patent US 6818444.
ACCESSION   AR595973
VERSION     AR595973.1  GI:56646954
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 66 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             12.2%;  Score 81;  DB 2;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 1e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1105 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1164

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db       1165 CTGGCTTCCAGAGAGATCTCT 1185


RESULT 51
AR595974/c
LOCUS       AR595974               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 68 from patent US 6818444.
ACCESSION   AR595974
VERSION     AR595974.1  GI:56646955
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 68 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             12.2%;  Score 81;  DB 2;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 1e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 52
AR595971
LOCUS       AR595971                1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 61 from patent US 6818444.
ACCESSION   AR595971
VERSION     AR595971.1  GI:56646952
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 61 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             12.2%;  Score 81;  DB 2;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 1e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1230

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db       1231 CTGGCTTCCAGAGAGATCTCT 1251


RESULT 53
AR595972/c
LOCUS       AR595972                1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 63 from patent US 6818444.
ACCESSION   AR595972
VERSION     AR595972.1  GI:56646953
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 63 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             12.2%;  Score 81;  DB 2;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 1e-32;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 54
AX076207
LOCUS       AX076207                  71 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 8 from Patent WO0104155.
ACCESSION   AX076207
VERSION     AX076207.1  GI:12710832
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 8 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .71
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer f12p35-1-lang"
ORIGIN

  Query Match             10.7%;  Score 71;  DB 2;  Length 71;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-27;
  Matches   71;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        485 TGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCAC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCAC 60

Qy        545 AGAACTCCTCC 555
              ||||||||||||
Db         61 AGAACTCCTCC 71


RESULT 55
AR008951
LOCUS       AR008951                  660 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 3 from patent US 5756085.
ACCESSION   AR008951
VERSION     AR008951.1  GI:3967756
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Sykes,M. and Wolf,S.F.
  TITLE     Use of interleukin-12 to prevent graft versus host disease
  JOURNAL   Patent: US 5756085-A 3 26-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        619 ATTCG 623
              |||||
Db        610 ATTCG 614
```

```
RESULT 56
BD007071
LOCUS       BD007071                660 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  IL-12 gene expression and delivery systems and uses.
ACCESSION   BD007071
VERSION     BD007071.1  GI:18635442
KEYWORDS    JP 2001503257-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Nodosutoromu,J., Freemark,B. and Dishupande,D.
  TITLE     IL-12 gene expression and delivery systems and uses
  JOURNAL   Patent: JP 2001503257-A 2 13-MAR-2001;
            BARENTISU INC,SYNTEX INC
COMMENT     OS   Unidentified
            PN   JP 2001503257-A/2
            PD   13-MAR-2001
            PF   10-OCT-1997 JP 1998519514
            PR   18-OCT-1996 US    60/028676
            PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
            C12N15/09,A61K31/711,A61K38/00,A61K47/18,A61K47/28,A61K48/00, PC
            A61P11/06,
            PC   C12N15/00,A61K37/02
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .660
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        619 ATTCG 623
              |||||
Db        610 ATTCG 614


RESULT 57
BD007079
LOCUS       BD007079                660 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Gene expression and delivery systems and uses.
ACCESSION   BD007079
VERSION     BD007079.1  GI:18635450
KEYWORDS    JP 2001503258-A/4.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Nodosutoromu,J., Freemark,B. and Dishupande,D.
  TITLE     Gene expression and delivery systems and uses
  JOURNAL   Patent: JP 2001503258-A 4 13-MAR-2001;
            BARENTISU INC
COMMENT     OS   Unidentified
            PN   JP 2001503258-A/4
            PD   13-MAR-2001
            PF   10-OCT-1997 JP 1998519520
            PR   18-OCT-1996 US    60/028687
            PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
            C12N15/09,A61K48/00,A61P11/06,A61P35/00,A61P43/00//C07K14/54, PC
            C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .660
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        619 ATTCG 623
              |||||
Db        610 ATTCG 614


RESULT 58
BD136037
LOCUS       BD136037                660 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Interferon alpha plasmid and delivery system and method of
            preparing and using the same.
ACCESSION   BD136037
VERSION     BD136037.1  GI:23230982
KEYWORDS    JP 2002506647-A/4.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.
  TITLE     Interferon alpha plasmid and delivery system and method of
            preparing and using the same
  JOURNAL   Patent: JP 2002506647-A 4 05-MAR-2002;
            VALENTIS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002506647-A/4
            PD   05-MAR-2002
            PF   12-MAR-1999 JP 2000536861
            PR   19-MAR-1998 US    60/078654
            PI   JEFF NORDSTROM,FEDERICA PERICLE,ALAIN ROLLAND,ROBERT RALSTON
            PC   C12N15/09,A61K38/21,A61K48/00,A61P35/00,C07K14/54,C07K14/56,
            PC   C12N1/15,
            PC   C12N1/19,C12N1/21,C12N5/10//A61K9/127,C12N15/00,A61K37/66, PC
             C12N5/00
            CC   Interferon alpha plasmid and delivery system and method of  CC
                   preparing and
            CC   using the same
            FH   Key             Location/Qualifiers
            FT   source          1. .660
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        619 ATTCG 623
                |||||
Db        610 ATTCG 614


RESULT 59
I28592
LOCUS       I28592                   660 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 3 from patent US 5573764.
ACCESSION   I28592
VERSION     I28592.1  GI:1819368
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Sykes,M. and Wolf,S.F.
  TITLE     Use of interleukin-12 to prevent graft versus host disease
  JOURNAL   Patent: US 5573764-A 3 12-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        619 ATTCG 623
                |||||
Db        610 ATTCG 614


RESULT 60
AX154618
LOCUS       AX154618                 660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 22 from Patent WO0140257.
ACCESSION   AX154618
VERSION     AX154618.1  GI:14536193
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 22 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        216 TGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGA 275
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 TGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGA 266

Qy        276 ATTAA 280
                |||||
Db        267 ATTAA 271


RESULT 61
AX154634
LOCUS       AX154634                 660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 38 from Patent WO0140257.
ACCESSION   AX154634
VERSION     AX154634.1  GI:14536198
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 38 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 609

Qy        619 ATTCG 623
                |||||
Db        610 ATTCG 614


RESULT 62
CQ829447
LOCUS       CQ829447                 702 bp    DNA     linear   PAT 05-JUL-2004
DEFINITION  Sequence 6 from Patent WO2004052929.
ACCESSION   CQ829447
VERSION     CQ829447.1  GI:49732783
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Vandenbroeck,K. and Alloza,I.
  TITLE     Recombinant cell line
  JOURNAL   Patent: WO 2004052929-A 6 24-JUN-2004;
            The Queen's University of Belfast (GB)
FEATURES             Location/Qualifiers
     source          1. .702
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="cDNA for alpha chain of IL-12"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 702;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 624

Qy        619 ATTCG 623
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              |||||
Db        625 ATTCG 629


RESULT 63
AR052862
LOCUS       AR052862                721 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 199 from patent US 5833975.
ACCESSION   AR052862
VERSION     AR052862.1  GI:5977724
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 721)
  AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
  TITLE     Canarypox virus expressing cytokine and/or tumor-associated antigen
            DNA sequence
  JOURNAL   Patent: US 5833975-A 199 10-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .721
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy        619 ATTCG 623
              |||||
Db        671 ATTCG 675


RESULT 64
AR288174
LOCUS       AR288174                721 bp    mRNA    linear   PAT 12-JUN-2003
DEFINITION  Sequence 199 from patent US 6537594.
ACCESSION   AR288174
VERSION     AR288174.1  GI:31675453
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 721)
  AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
  TITLE     Vaccina virus comprising cytokine and/or tumor associated antigen
            genes
  JOURNAL   Patent: US 6537594-A 199 25-MAR-2003;
            Virogenetics Corporation; Troy, NY
FEATURES             Location/Qualifiers
     source          1. .721
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy        619 ATTCG 623
              |||||
Db        671 ATTCG 675


RESULT 65
AR567161
LOCUS       AR567161                721 bp    mRNA    linear   PAT 08-OCT-2004
DEFINITION  Sequence 199 from patent US 6780407.
ACCESSION   AR567161
VERSION     AR567161.1  GI:53984803
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 721)
  AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
  TITLE     Pox virus comprising DNA sequences encoding CEA and B7 antigen
  JOURNAL   Patent: US 6780407-A 199 24-AUG-2004;
            Aventis Pasteur; Swiftwater, PA
FEATURES             Location/Qualifiers
     source          1. .721
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 670

Qy        619 ATTCG 623
              |||||
Db        671 ATTCG 675


RESULT 66
BD105971
LOCUS       BD105971                762 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Animal model for evaluation of vaccines.
ACCESSION   BD105971
VERSION     BD105971.1  GI:23200789
KEYWORDS    JP 2002501375-A/21.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Chang,L.J.
  TITLE     Animal model for evaluation of vaccines
  JOURNAL   Patent: JP 2002501375-A 21 15-JAN-2002;
            LUNG JI CHANG
COMMENT     PN   JP 2002501375-A/21
            PD   15-JAN-2002
            PF   09-APR-1998 JP 1998543062
            PR   09-APR-1997 US    08/838702,01-MAY-1997 US    08/848760 PR
            09-DEC-1997 US    60/069163
            PI   LUNG JI CHANG
            PC   A01K67/027,C12N7/01,C12N1/10,C07K14/16,A61K39/008,C12N1/36, PC
              C12N7/04,
            PC   A61K39/21
            CC   Strandedness: Double;
            CC   Topology: Linear;
            CC   /desc = 'DNA'
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .762
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        619 ATTCG 623
              |||||
Db        712 ATTCG 716


RESULT 67
CQ803343
LOCUS       CQ803343                762 bp    DNA     linear   PAT 10-MAY-2004
DEFINITION  Sequence 3 from Patent WO2004035799.
ACCESSION   CQ803343
VERSION     CQ803343.1  GI:47110209
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Waehler,R. and Schnieders,F.
  TITLE     Viral vectors and the use of the same for gene therapy
  JOURNAL   Patent: WO 2004035799-A 3 29-APR-2004;
            Universitaetsklinikum Hamburg-Eppendorf (DE)
FEATURES             Location/Qualifiers
     source          1. .762
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
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Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        619 ATTCG 623
              |||||
Db        712 ATTCG 716


RESULT 68
AR533401
LOCUS       AR533401                762 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 21 from patent US 6730512.
ACCESSION   AR533401
VERSION     AR533401.1  GI:53923067
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Chang,L.-J.
  TITLE     Combination immunogene therapy
  JOURNAL   Patent: US 6730512-A 21 04-MAY-2004;
            Amdl, Inc.; Tustin, CA
FEATURES             Location/Qualifiers
     source          1. .762
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        619 ATTCG 623
              |||||
Db        712 ATTCG 716


RESULT 69
AF101062
LOCUS       AF101062                762 bp    mRNA    linear   PRI 03-MAR-1999
DEFINITION  Homo sapiens interleukin 12 mRNA, complete cds.
ACCESSION   AF101062
VERSION     AF101062.1  GI:4323578
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Liu,y., Guo,Y. and Wu,M.
  TITLE     Human Interleukin-12 (or Natural Killer Cell Stimulatory Factor, or
            Cytotoxic Lymphocyte Maturation Factor) 35kDa subunit mRNA
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 762)
  AUTHORS   Liu,Y., Guo,Y. and Wu,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-OCT-1998) Molecular Biology Department, Cancer
            Institute of Second Military Medical University, 800 XianYin Road,
            Shanghai 200433, P.R. China
FEATURES             Location/Qualifiers
     source          1. .762
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="3"
                     /map="3p12-q13.2"
                     /cell_line="lymphoblastoid B-cell line NC37"
                     /note="cells induced by phorbol 12-myristate 13 acetate
                     (PMA) and ionophore A23187"
     CDS             1. .762
                     /note="natural killer cell stimulatory factor; cytotoxic
                     lymphocyte maturation factor 35kDa subunit; p35"
                     /codon_start=1
                     /product="interleukin 12"
                     /protein_id="AAD16432.1"
                     /db_xref="GI:4323579"
                     /translation="MWPPGSASQPPPSPAAATGLHPAARPVSLQCRLSMCPARSLLLV
                     ATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEE
                     IDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSS
                     IYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLE
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     variation       132
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ORIGIN

  Query Match             9.8%;  Score 65;  DB 5;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 711

Qy        619 ATTCG 623
              |||||
Db        712 ATTCG 716
```

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RESULT 70
MMU19842
LOCUS       MMU19842                780 bp    mRNA    linear   PRI 03-FEB-1996
DEFINITION  Macaca mulatta interleukin-12 beta p35 subunit (IL-12b) mRNA,
            complete cds.
ACCESSION   U19842
VERSION     U19842.1  GI:644801
KEYWORDS    .
SOURCE      Macaca mulatta (rhesus monkey)
  ORGANISM  Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 780)
  AUTHORS   Villinger,F., Brar,S.S., Mayne,A., Chikkala,N. and Ansari,A.A.
  TITLE     Comparative sequence analysis of cytokine genes from human and
            nonhuman primates
  JOURNAL   J. Immunol. 155 (8), 3946-3954 (1995)
   PUBMED   7561102
REFERENCE   2  (bases 1 to 780)
  AUTHORS   Villinger,F.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JAN-1995) Francois J. Villinger, Emory University,
            Pathology, 1327 Clifton Rd, Atlanta, GA 30322, USA
FEATURES             Location/Qualifiers
     source          1. .780
                     /organism="Macaca mulatta"
                     /mol_type="mRNA"
                     /db_xref="taxon:9544"
                     /clone="RNc IL-12b"
                     /cell_type="peripheral blood mononuclear cells"
                     /tissue_type="blood"
     gene            1. .780
                     /gene="IL-12b"
     CDS             10. .771
                     /gene="IL-12b"
                     /function="NK cell stimulatory factor"
                     /codon_start=1
                     /product="interleukin-12 beta p35 subunit"
                     /protein_id="AAA86707.1"
                     /db_xref="GI:644802"
                     /translation="MWPPGSASQPPPSPATATGLHPAARPEPPQCRLSMCPARSLLLV
                     ATLVLLDYLSLARNLSVATPGPEMFPCLHHSQNLLKAASNTLQKARQILEFYPCTSEE
                     IDHEDITKDKTSTVEACLPLELIKNESCLNSRETSFITNGSCLASRKTSFMMALCLRS
                     IYEDLKMYQVEFKTMNAKLLRDPKRQIFLDQNILGVIDELMQALNFNSETVPQKSSLE
                     EPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 5;  Length 780;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 720

Qy        619 ATTCG 623
              |||||
Db        721 ATTCG 725


RESULT 71
AF180562
LOCUS       AF180562                823 bp    mRNA    linear   PRI 26-SEP-1999
DEFINITION  Homo sapiens interleukin 12, P35 mRNA, complete cds.
ACCESSION   AF180562
VERSION     AF180562.1  GI:5923852
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 823)
  AUTHORS   Hongyuan,J. and Meiyun,Z.
  TITLE     Cloning and sequence analysis of IL-12 cDNA from Chinese
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 823)
  AUTHORS   Hongyuan,J. and Meiyun,Z.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-AUG-1999) Hepatitis, Institute of Virology, CAPM, 100
            Yingxinjie, Xuanwuqu, Beijing 100052, China
FEATURES             Location/Qualifiers
     source          1. .823
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="3"
                     /map="3p12-q13.2"
                     /cell_type="peripheral mononuclear"
     CDS             60. .821
                     /note="NKSF/CLMP; IL12p35; 35kD"
                     /codon_start=1
                     /product="interleukin 12, P35"
                     /protein_id="AAD56385.1"
                     /db_xref="GI:5923853"
                     /translation="MWPPGSASQPPPSPAAATGLHPAARPVSLQCRLSMCPARSLLLV
                     ATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEE
                     IDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSS
                     IYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLE
                     EPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 5;  Length 823;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        711 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 770

Qy        619 ATTCG 623
              |||||
Db        771 ATTCG 775


RESULT 72
BD165801
LOCUS       BD165801                856 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Antibody against cytotoxic lymphocyte maturing factors.
ACCESSION   BD165801
VERSION     BD165801.1  GI:27871613
KEYWORDS    JP 2002167400-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 856)
  AUTHORS   Chizzonite,R.A., Gately,M.K., Gubler,U.A., Hulmes,J.D., Pan,Y.C.E.,
            Podlanski,F.J. and Stern,A.S.
  TITLE     Antibody against cytotoxic lymphocyte maturing factors
  JOURNAL   Patent: JP 2002167400-A 2 11-JUN-2002;
            PROTEIN DESIGN LABS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002167400-A/2
            PD   11-JUN-2002
            PF   14-AUG-2001 JP 2001246031
            PR   22-DEC-1989 US       455708,09-MAY-1990 US       520935 PR
            27-AUG-1990 US       572284
            PI   RICHARD ANTHONY CHIZZONITE,MAURICE KENT GATELY,ULRICH ANDREAS
            PI   GUBLER,
            PI   JEFFREY DAVID HULMES,YU CHING EUGENE PAN,FRANK JOHN PODLANSKI,
            PI   ALVIN SETH STERN
            PC   C07K16/24,C12N15/02,C12N15/02,C12P21/08,C12N15/00,C12N15/00 CC
              Antibody against cytotoxic lymphocyte maturing factors FH   Key
                    Location/Qualifiers
            FT   CDS             (170). .(826).
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FEATURES             Location/Qualifiers
     source          1. .856
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ORIGIN

  Query Match              9.8%;  Score 65;  DB 2;  Length 856;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         719 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 778

Qy         619 ATTCG 623
               |||||
Db         779 ATTCG 783


RESULT 73
CQ716168
LOCUS       CQ716168               1020 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 2102 from Patent WO02068579.
ACCESSION   CQ716168
VERSION     CQ716168.1  GI:42277025
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 2102 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
     source          1. .1020
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match              9.8%;  Score 65;  DB 2;  Length 1020;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         712 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 771

Qy         619 ATTCG 623
               |||||
Db         772 ATTCG 776


RESULT 74
BC104982
LOCUS       BC104982               1021 bp    mRNA    linear   PRI 19-JAN-2006
DEFINITION  Homo sapiens interleukin 12A (natural killer cell stimulatory
            factor 1, cytotoxic lymphocyte maturation factor 1, p35), mRNA
            (cDNA clone MGC:132642 IMAGE:8143985), complete cds.
ACCESSION   BC104982
VERSION     BC104982.1  GI:85397857
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1021)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  PUBMED    12477932
REFERENCE   2  (bases 1 to 1021)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (13-SEP-2005) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Mike Brownstein, NIMH
            cDNA Library Preparation: British Columbia Cancer Research Center
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
            Martin Hirst, Thomas Zeng, Ryan Morin, Michelle Moksa, Johnson
            Pang, Diana Mah, Jing Wang, Kieth Fichter, Eric Chuah, Allen
            Delaney, Rob Kirkpatrick, Agnes Baross, Sarah Barber, Mabel
            Brown-John, Steve S. Chand, William Chow, Ryan Babakaiff, Dave
            Wong, Corey Matsuo, Jaclyn Beland, Susan Gibson, Luis delRio, Ruth
            Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
            Kim MacDonald,  Mike R. Mayo, Josh Moran, Diana Palmquist, JR
            Santos, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang,
            Jacquie Schein, Asim Siddiqui,Steven Jones, Rob Holt, Marco Marra.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRCB Plate: 3 Row: j Column: 15.
FEATURES             Location/Qualifiers
     source          1. .1021
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:132642 IMAGE:8143985"
                     /tissue_type="Brain, cerebral cortex, PCR rescued clones"
                     /clone_lib="NIH_MGC_287"
                     /note="Vector: pCR4-TOPO with reversed insert; Clone
                     identification sequence tag: TCGTTGCT"
     gene            1. .1021
                     /gene="IL12A"
                     /note="synonyms: IL-12A, NFSK, CLMF"
                     /db_xref="GeneID:3592"
                     /db_xref="HGNC:5969"
                     /db_xref="IMGT/GENE-DB:5969"
                     /db_xref="MIM:161560"
     CDS             154. .915
                     /gene="IL12A"
                     /codon_start=1
                     /product="interleukin 12A, precursor"
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                     /db_xref="GeneID:3592"
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                     /db_xref="MIM:161560"
                     /translation="MWPPGSASQPPPSPAAATGLHPAARPVSLQCRLSMCPARSLLLV
                     ATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEE
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                     IYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLE
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ORIGIN

  Query Match             9.8%;  Score 65;  DB 5;  Length 1021;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 864

Qy        619 ATTCG 623
              |||||
Db        865 ATTCG 869


RESULT 75
BC104984
LOCUS       BC104984                1021 bp    mRNA    linear   PRI 19-JAN-2006
DEFINITION  Homo sapiens interleukin 12A (natural killer cell stimulatory
            factor 1, cytotoxic lymphocyte maturation factor 1, p35), mRNA
            (cDNA clone MGC:132644 IMAGE:8143987), complete cds.
ACCESSION   BC104984
VERSION     BC104984.1  GI:85397860
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1021)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1021)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (13-SEP-2005) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Mike Brownstein, NIMH
            cDNA Library Preparation: British Columbia Cancer Research Center
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
            Martin Hirst, Thomas Zeng, Ryan Morin, Michelle Moksa, Johnson
            Pang, Diana Mah, Jing Wang, Kieth Fichter, Eric Chuah, Allen
            Delaney, Rob Kirkpatrick, Agnes Baross, Sarah Barber, Mabel
            Brown-John, Steve S. Chand, William Chow, Ryan Babakaiff, Dave
            Wong, Corey Matsuo, Jaclyn Beland, Susan Gibson, Luis delRio, Ruth
            Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
            Kim MacDonald,  Mike R. Mayo, Josh Moran, Diana Palmquist, JR
            Santos, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang,
            Jacquie Schein, Asim Siddiqui,Steven Jones, Rob Holt, Marco Marra.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRCB Plate: 3 Row: j Column: 17.
FEATURES             Location/Qualifiers
     source          1. .1021
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:132644 IMAGE:8143987"
                     /tissue_type="Brain, cerebral cortex, PCR rescued clones"
                     /clone_lib="NIH_MGC_287"
                     /note="Vector: pCR4-TOPO with reversed insert; Clone
                     identification sequence tag: AAATAGCC"
     gene            1. .1021
                     /gene="IL12A"
                     /note="synonyms: IL-12A, NFSK, CLMF"
                     /db_xref="GeneID:3592"
                     /db_xref="HGNC:5969"
                     /db_xref="IMGT/GENE-DB:5969"
                     /db_xref="MIM:161560"
     CDS             154. .915
                     /gene="IL12A"
                     /codon_start=1
                     /product="interleukin 12A, precursor"
                     /protein_id="AAI04985.1"
                     /db_xref="GI:85397861"
                     /db_xref="GeneID:3592"
                     /db_xref="HGNC:5969"
                     /db_xref="IMGT/GENE-DB:5969"
                     /db_xref="MIM:161560"
                     /translation="MWPPGSASQPPPSPAAATGLHPAARPVSLQCRLSMCPARSLLLV
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                     IYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLE
                     EPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 5;  Length 1021;
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  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
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Db        805 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 864

Qy        619 ATTCG 623
              |||||
Db        865 ATTCG 869


RESULT 76
AR091390
LOCUS       AR091390                1026 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 1 from patent US 5994104.
ACCESSION   AR091390
VERSION     AR091390.1  GI:10018145
KEYWORDS    .
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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1026)
  AUTHORS   Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
  TITLE     Interleukin-12 fusion protein
  JOURNAL   Patent: US 5994104-A 1 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .1026
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 1026;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 778

Qy        619 ATTCG 623
              |||||
Db        779 ATTCG 783


RESULT 77
AR380496
LOCUS       AR380496               1026 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1041 from patent US 6607879.
ACCESSION   AR380496
VERSION     AR380496.1  GI:40088130
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1026)
  AUTHORS   Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.
  TITLE     Compositions for the detection of blood cell and immunological
            response gene expression
  JOURNAL   Patent: US 6607879-A 1041 19-AUG-2003;
            Incyte Corporation; Palo Alto, CA
FEATURES             Location/Qualifiers
     source          1. .1026
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 1026;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 778

Qy        619 ATTCG 623
              |||||
Db        779 ATTCG 783


RESULT 78
HUMCLMF35
LOCUS       HUMCLMF35              1026 bp    mRNA    linear   PRI 27-APR-1993
DEFINITION  Human cytotoxic lymphocyte maturation factor 35 kDa subunit mRNA,
            complete cds.
ACCESSION   M65271 M38443
VERSION     M65271.1  GI:180623
KEYWORDS    cytotoxic lymphocyte maturation factor 35 kDa subunit; interleukin.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1026)
  AUTHORS   Gubler,U., Chua,A.O., Schoenhaut,D.S., Dwyer,C.M., McComas,W.,
            Motyka,R., Nabavi,N., Wolitzky,A.G., Quinn,P.M., Familletti,P.C.
            and Gately,M.K.
  TITLE     Coexpression of two distinct genes is required to generate secreted
            bioactive cytotoxic lymphocyte maturation factor
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 88 (10), 4143-4147 (1991)
  PUBMED    1674604
COMMENT     Original source text: Human, cDNA to mRNA.
FEATURES             Location/Qualifiers
     source          1. .1026
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     CDS             170. .829
                     /codon_start=1
                     /product="cytotoxic lymphocyte maturation factor 35 kDa
                     subunit"
                     /protein_id="AAA35694.1"
                     /db_xref="GI:180624"
                     /translation="MCPARSLLLVATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNL
                     LRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRET
                     SFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNML
                     AVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVTSYLNA
                     S"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 5;  Length 1026;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 778

Qy        619 ATTCG 623
              |||||
Db        779 ATTCG 783


RESULT 79
AR393790
LOCUS       AR393790               1287 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 6 from patent US 6617135.
ACCESSION   AR393790
VERSION     AR393790.1  GI:40120794
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1287)
  AUTHORS   Gillies,S.D. and Lo,K.-M.
  TITLE     Multiple cytokine protein complexes
  JOURNAL   Patent: US 6617135-A 6 09-SEP-2003;
            EMD Lexigen Research Center Corp.; Billerica, MA
FEATURES             Location/Qualifiers
     source          1. .1287
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 1287;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1177 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1236

Qy        619 ATTCG 623
              |||||
Db       1237 ATTCG 1241
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RESULT 80
AX084108
LOCUS       AX084108               1287 bp    DNA     linear   PAT 28-FEB-2001
DEFINITION  Sequence 6 from Patent WO0110912.
ACCESSION   AX084108
VERSION     AX084108.1  GI:13185658
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Gillies,S.D. and Lo,K.M.
  TITLE     Multiple cytokine-antibody complexes
  JOURNAL   Patent: WO 0110912-A 6 15-FEB-2001;
            Lexigen Pharmaceuticals Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .1287
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="human Fc-p35 fusion protein coding sequence"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 1287;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1177 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1236

Qy        619 ATTCG 623
              |||||
Db       1237 ATTCG 1241


RESULT 81
AR050785
LOCUS       AR050785               1316 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 3 from patent US 5830451.
ACCESSION   AR050785
VERSION     AR050785.1  GI:5974149
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1316)
  AUTHORS   Devergne,O. and Kieff,E.D.
  TITLE     Haematopoietic cytokine Epstein Barr virus-induced protein
  JOURNAL   Patent: US 5830451-A 3 03-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .1316
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 1316;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 812

Qy        619 ATTCG 623
              |||||
Db        813 ATTCG 817


RESULT 82
AR212036
LOCUS       AR212036               1316 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 3 from patent US 6399379.
ACCESSION   AR212036
VERSION     AR212036.1  GI:21515515
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1316)
  AUTHORS   Baker,B.F. and Freier,S.M.
  TITLE     Antisense modulation of interleukin 12 p35 subunit expression
  JOURNAL   Patent: US 6399379-A 3 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .1316
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 1316;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 812

Qy        619 ATTCG 623
              |||||
Db        813 ATTCG 817


RESULT 83
HUMNKSFP35
LOCUS       HUMNKSFP35             1316 bp    mRNA    linear   PRI 07-JAN-1995
DEFINITION  Human natural killer cell stimulatory factor (NKSF) mRNA, complete
            cds, clone p35.
ACCESSION   M65291
VERSION     M65291.1  GI:189233
KEYWORDS    cytokine; natural killer cell stimulatory factor.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1316)
  AUTHORS   Wolf,S.F., Temple,P.A., Kobayashi,M., Young,D., Dicig,M., Lowe,L.,
            Dzialo,R., Fitz,L., Ferenz,C., Hewick,R.M., Kelleher,K.,
            Herrmann,S.H., Clark,S.C., Azzoni,L., Chan,S.H., Trinchieri,G. and
            Perussia,B.
  TITLE     Cloning of cDNA for natural killer cell stimulatory factor, a
            heterodimeric cytokine with multiple biologic effects on T and
            natural killer cells
  JOURNAL   J. Immunol. 146 (9), 3074-3081 (1991)
   PUBMED   1673147
COMMENT     Original source text: Human EBV-transformed B cell line RPMI 8866,
            cDNA to mRNA, clone p35.
FEATURES             Location/Qualifiers
     source          1. .1316
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /map="Unassigned"
                     /cell_line="EBV-transformed B cell line RPMI 8866"
     gene            1. .1316
                     /gene="NKSF1"
     CDS             102. .863
                     /gene="NKSF1"
                     /codon_start=1
                     /product="natural killer cell stimulatory factor"
                     /protein_id="AAA59937.1"
                     /db_xref="GI:189234"
                     /db_xref="GDB:G00-127-869"
                     /translation="MWPPGSASQPPPSPAAATGLHPAARPVSLQCRLSMCPARSLLLV
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                     /note="G00-127-869"
     mat_peptide     270. .860
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                     /product="natural killer cell stimulatory factor"
                     /note="G00-127-869"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 5;  Length 1316;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 812

Qy        619 ATTCG 623
              |||||
Db        813 ATTCG 817


RESULT 84
AR082685
LOCUS       AR082685                1364 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 3 from patent US 5976539.
ACCESSION   AR082685
VERSION     AR082685.1  GI:10009475
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1364)
  AUTHORS   Scott,P. and Trinchieri,G.
  TITLE     Compositions and methods for use of IL-12 as an adjuvant
  JOURNAL   Patent: US 5976539-A 3 02-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .1364
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 1364;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 811

Qy        619 ATTCG 623
              |||||
Db        812 ATTCG 816


RESULT 85
AR122961
LOCUS       AR122961                1364 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 3 from patent US 6168923.
ACCESSION   AR122961
VERSION     AR122961.1  GI:14107927
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1364)
  AUTHORS   Scott,P. and Trinchieri,G.
  TITLE     Compositions and methods for use of IL-12 as an adjuvant
  JOURNAL   Patent: US 6168923-A 3 02-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .1364
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 1364;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 811

Qy        619 ATTCG 623
              |||||
Db        812 ATTCG 816


RESULT 86
I28326
LOCUS       I28326                  1364 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 3 from patent US 5571515.
ACCESSION   I28326
VERSION     I28326.1  GI:1819102
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1364)
  AUTHORS   Scott,P. and Trinchieri,G.
  TITLE     Compositions and methods for use of IL-12 as an adjuvant
  JOURNAL   Patent: US 5571515-A 3 05-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .1364
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 1364;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 811

Qy        619 ATTCG 623
              |||||
Db        812 ATTCG 816


RESULT 87
I89771
LOCUS       I89771                  1364 bp    DNA     linear   PAT 10-AUG-1998
DEFINITION  Sequence 3 from patent US 5723127.
ACCESSION   I89771
VERSION     I89771.1  GI:3409711
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1364)
  AUTHORS   Scott,P. and Trinchieri,G.
  TITLE     Compositions and methods for use of IL-12 as an adjuvant
  JOURNAL   Patent: US 5723127-A 3 03-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .1364
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 1364;
```

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  Best Local Similarity   100.0%;  Pred. No. 7.3e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 811

Qy        619 ATTCG 623
              |||||
Db        812 ATTCG 816


RESULT 88
AR309637
LOCUS       AR309637               1395 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 5 from patent US 6555658.
ACCESSION   AR309637
VERSION     AR309637.1  GI:31701688
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1395)
  AUTHORS   Trinchieri,G., Perussia,B., Clark,S.C., Wong,G.G., Hewick,R. and
            Kobayashi,M.
  TITLE     Antibodies to natural killer stimulatory factor
  JOURNAL   Patent: US 6555658-A 5 29-APR-2003;
            Wyeth and The Wistar Institute; Madison, NJ
FEATURES             Location/Qualifiers
     source          1. .1395
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 1395;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
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Db        765 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 824

Qy        619 ATTCG 623
              |||||
Db        825 ATTCG 829


RESULT 89
CS032085
LOCUS       CS032085               1444 bp    DNA     linear   PAT 10-MAR-2005
DEFINITION  Sequence 1591 from Patent WO2005016962.
ACCESSION   CS032085
VERSION     CS032085.1  GI:60731804
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Abbas,A., Clark,H., Ouyang,W., Williams,M.P., Wood,W.I. and Wu,T.D.
  TITLE     Compositions and methods for the treatment of immune related
            diseases
  JOURNAL   Patent: WO 2005016962-A 1591 24-FEB-2005;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1444
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 1444;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
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Db        867 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 926

Qy        619 ATTCG 623
              |||||
Db        927 ATTCG 931


RESULT 90
CS041037
LOCUS       CS041037               1444 bp    DNA     linear   PAT 22-MAR-2005
DEFINITION  Sequence 1591 from Patent WO2005019258.
ACCESSION   CS041037
VERSION     CS041037.1  GI:61848609
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Abbas,A., Clark,H., Ouyang,W., Williams,P.M., Wood,W.I. and Wu,T.D.
  TITLE     Compositions and methods for the treatment of immune related
            diseases
  JOURNAL   Patent: WO 2005019258-A 1591 03-MAR-2005;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1444
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 1444;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 926

Qy        619 ATTCG 623
              |||||
Db        927 ATTCG 931


RESULT 91
CS143811
LOCUS       CS143811               1444 bp    DNA     linear   PAT 19-AUG-2005
DEFINITION  Sequence 53 from Patent WO2005073411.
ACCESSION   CS143811
VERSION     CS143811.1  GI:73658825
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ried,T.
  TITLE     Composition for detecting the response of rectal adenocarcinomas to
            radiochemotherapy
  JOURNAL   Patent: WO 2005073411-A 53 11-AUG-2005;
            DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES             Location/Qualifiers
     source          1. .1444
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
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ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 1444;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
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Db        867 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 926

Qy        619 ATTCG 623
              |||||
Db        927 ATTCG 931


RESULT 92
AR091395
LOCUS       AR091395                1560 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 11 from patent US 5994104.
ACCESSION   AR091395
VERSION     AR091395.1  GI:10018150
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1560)
  AUTHORS   Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
  TITLE     Interleukin-12 fusion protein
  JOURNAL   Patent: US 5994104-A 11 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .1560
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 1560;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1450 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1509

Qy        619 ATTCG 623
              |||||
Db       1510 ATTCG 1514


RESULT 93
AR091394
LOCUS       AR091394                1623 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 9 from patent US 5994104.
ACCESSION   AR091394
VERSION     AR091394.1  GI:10018149
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1623)
  AUTHORS   Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
  TITLE     Interleukin-12 fusion protein
  JOURNAL   Patent: US 5994104-A 9 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .1623
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 1623;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1513 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1572

Qy        619 ATTCG 623
              |||||
Db       1573 ATTCG 1577


RESULT 94
A92078
LOCUS       A92078                  1645 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 2 from Patent WO9821322.
ACCESSION   A92078
VERSION     A92078.1  GI:6740882
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 1645)
  AUTHORS   Junghans,C. and Wittig,B.
  TITLE     DESIGN PRINCIPLE FOR CONSTRUCTING EXPRESSION CONSTRUCTS FOR GENE
            THERAPY
  JOURNAL   Patent: WO 9821322-A 2 22-MAY-1998;
            JUNGHANS CLAAS (DE); SOFT GENE GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .1645
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 1645;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1284 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1343

Qy        619 ATTCG 623
              |||||
Db       1344 ATTCG 1348


RESULT 95
AR230689
LOCUS       AR230689                1645 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 2 from patent US 6451593.
ACCESSION   AR230689
VERSION     AR230689.1  GI:27271470
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1645)
  AUTHORS   Wittig,B. and Junghans,C.
  TITLE     Design principle for construction of expression constructs for gene
            therapy
  JOURNAL   Patent: US 6451593-A 2 17-SEP-2002;
            Soft Gene GmbH; Berlin;
            DEX;
FEATURES             Location/Qualifiers
     source          1. .1645
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 1645;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1284 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 1343

Qy        619 ATTCG 623
              |||||
Db       1344 ATTCG 1348


RESULT 96
CS131489
LOCUS       CS131489               3205 bp    DNA     linear   PAT 02-AUG-2005
DEFINITION  Sequence 8 from Patent WO2005066348.
ACCESSION   CS131489
VERSION     CS131489.1  GI:71794157
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Gillies,S.
  TITLE     Compounds for targeting
  JOURNAL   Patent: WO 2005066348-A 8 21-JUL-2005;
            Antisoma PLC (GB); EMD Lexigen Research Center Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .3205
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HuBC1 heavy chain fused to huIL12 p35 subunit"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 3205;
  Best Local Similarity   100.0%;  Pred. No. 6.8e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3095 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 3154

Qy        619 ATTCG 623
              |||||
Db       3155 ATTCG 3159


RESULT 97
BD136048
LOCUS       BD136048               5686 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Interferon alpha plasmid and delivery system and method of
            preparing and using the same.
ACCESSION   BD136048
VERSION     BD136048.1  GI:23230993
KEYWORDS    JP 2002506647-A/15.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 5686)
  AUTHORS   Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.
  TITLE     Interferon alpha plasmid and delivery system and method of
            preparing and using the same
  JOURNAL   Patent: JP 2002506647-A 15 05-MAR-2002;
            VALENTIS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002506647-A/15
            PD   05-MAR-2002
            PF   12-MAR-1999 JP 2000536861
            PR   19-MAR-1998 US    60/078654
            PI   JEFF NORDSTROM,FEDERICA PERICLE,ALAIN ROLLAND,ROBERT RALSTON
            PC   C12N15/09,A61K38/21,A61K48/00,A61P35/00,C07K14/54,C07K14/56,
            PC   C12N1/15,
            PC   C12N1/19,C12N1/21,C12N5/10//A61K9/127,C12N15/00,A61K37/66, PC
             C12N5/00
            CC   Sequence source: synthetic construct
            FH   Key             Location/Qualifiers
            FT   source          1. .5686
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .5686
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 5686;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2094 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 2153

Qy        619 ATTCG 623
              |||||
Db       2154 ATTCG 2158


RESULT 98
AR091393
LOCUS       AR091393               6139 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 7 from patent US 5994104.
ACCESSION   AR091393
VERSION     AR091393.1  GI:10018148
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 6139)
  AUTHORS   Anderson,R.James., Prentice,H.Grant. and MacDonald,I.Duncan.
  TITLE     Interleukin-12 fusion protein
  JOURNAL   Patent: US 5994104-A 7 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .6139
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             9.8%;  Score 65;  DB 2;  Length 6139;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-24;
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Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4734 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 4793

Qy        619 ATTCG 623
              |||||
Db       4794 ATTCG 4798


RESULT 99
AF404773
LOCUS       AF404773              11792 bp    DNA     linear   PRI 09-AUG-2001
DEFINITION  Homo sapiens interleukin 12A (natural killer cell stimulatory
            factor 1, cytotoxic lymphocyte maturation factor 1, p35) (IL12A)
            gene, complete cds.
ACCESSION   AF404773
VERSION     AF404773.1  GI:15128214
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 11792)
  AUTHORS   Rieder,M.J., Carrington,D.P., Chung,M.-W., Lee,K.L., Poel,C.L.,
            Yi,Q. and Nickerson,D.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2001) Molecular Biotechnology, University of
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            Washington, 1705 NE Pacific, Seattle, WA 98195, USA
COMMENT     To cite this work please use:  SeattleSNPs. NHLBI Program for
            Genomic Applications, UW-FHCRC, Seattle, WA (URL:
            http://pga.mbt.washington.edu).
FEATURES             Location/Qualifiers
     source          1. .11792
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     repeat_region   489. .535
                     /rpt_family="MIR3"
                     /rpt_type=dispersed
     repeat_region   719. .857
                     /rpt_family="L2"
                     /rpt_type=dispersed
     variation       913
                     /frequency="0.01"
                     /replace="c"
     variation       1108
                     /frequency="0.07"
                     /replace="g"
     variation       1250
                     /frequency="0.01"
                     /replace="t"
     variation       1526
                     /frequency="0.04"
                     /replace="g"
     variation       1716. .1721
                     /frequency="0.01"
                     /replace=""
     gene            2030. .8791
                     /gene="IL12A"
     mRNA            join(2030. .2207,3200. .3345,6045. .6158,6484. .6525,
                     6601. .6642,6734. .6877,8439. .8791)
                     /gene="IL12A"
                     /product="interleukin 12A (natural killer cell stimulatory
                     factor 1, cytotoxic lymphocyte maturation factor 1, p35)"
     CDS             join(2192. .2207,3200. .3345,6045. .6158,6484. .6525,
                     6601. .6642,6734. .6877,8439. .8594)
                     /gene="IL12A"
                     /codon_start=1
                     /product="interleukin 12A (natural killer cell stimulatory
                     factor 1, cytotoxic lymphocyte maturation factor 1, p35)"
                     /protein_id="AAK84425.1"
                     /db_xref="GI:15128215"
                     /translation="MCPARSLLLVATLVLLDHLSLARNLPVATPDPGMFPCLHHSQNL
                     LRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRET
                     SFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNML
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                     S"
     repeat_region   2379. .2491
                     /rpt_family="MIR"
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     repeat_region   2533. .2830
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     variation       2651
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     variation       3362
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                     /replace="g"
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                     /rpt_family="Charlie8"
                     /rpt_type=dispersed
     repeat_region   4618. .5111
                     /rpt_family="MLT1D"
                     /rpt_type=dispersed
     variation       4897
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                     /frequency="0.19"
                     /replace="c"
     variation       4909
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                     /frequency="0.01"
                     /replace="t"
     variation       4926
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                     /frequency="0.01"
                     /replace="t"
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                     /frequency="0.03"
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                     /rpt_type=dispersed
     variation       5247
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     variation       5574
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                     /replace="c"
     variation       5636
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                     /frequency="0.32"
                     /replace="g"
     variation       5757
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                     /frequency="0.10"
                     /replace="a"
     variation       6229
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                     /frequency="0.01"
                     /replace="g"
     variation       6238
                     /gene="IL12A"
                     /frequency="0.03"
                     /replace="a"
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                     /rpt_type=dispersed
     repeat_region   7112. .7214
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                     /frequency="0.23"
                     /replace="c"
     variation       7476
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                     /frequency="0.03"
                     /replace="t"
     variation       7519
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                     /frequency="0.02"
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     repeat_region   7749. .7908
                     /rpt_family="MIR"
                     /rpt_type=dispersed
     variation       7824
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                     /frequency="0.02"
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                     /frequency="0.36"
                     /replace="c"
     variation       8335
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                     /frequency="0.04"
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                     /note="Region not scanned for variation"
     variation       9094
                     /frequency="0.22"
                     /replace="c"

  Query Match             9.8%;  Score 65;  DB 5;  Length 11792;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        559 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8484 GAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGA 8543

Qy        619 ATTCG 623
              |||||
Db       8544 ATTCG 8548


RESULT 100
AC010370
LOCUS       AC010370              157079 bp    DNA     linear   PRI 23-JAN-2002
DEFINITION  Homo sapiens chromosome 3 clone CTD-2049J23, complete sequence.
ACCESSION   AC010370
VERSION     AC010370.5  GI:14573679
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 157079)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 157079)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE   3  (bases 1 to 157079)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
REFERENCE   4  (bases 1 to 157079)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JAN-2002) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
COMMENT     On Jun 28, 2001 this sequence version replaced gi:12830118.
            Draft Sequence Produced by DOE Joint Genome Institute
            www.jgi.doe.gov
            Finishing Completed at Stanford Human Genome Center
            www-shgc.stanford.edu
            Quality: Phrap Quality >=40 99.7% of Sequence;
            Estimated Total Number of Errors is 0.4.
FEATURES             Location/Qualifiers
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Job time : 4232.94 secs
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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 10, 2006, 01:16:39 ; Search time 169.912 Seconds
(without alignments)
5434.532 Million cell updates/sec

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Perfect score: 1761
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Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	8	1747	99.2	1599	3	US-09-917-265A-38	Sequence 38, Appl
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ALIGNMENTS

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; Sequence 29, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(987)
US-09-917-265A-29

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RESULT 2
US-09-917-265A-31/c

; Sequence 31, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-31

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Score:                  1761.00         Matches:        329
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Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

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Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

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Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

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Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
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RESULT 3
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; Sequence 55, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(984)
US-09-917-265A-55

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Pred. No.:              1.08e-194      Length:          985
Score:                  1757.00        Matches:         328
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Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984

RESULT 4
US-09-917-265A-57/c
; Sequence 57, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
;   LENGTH: 985
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;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-57

Alignment Scores:
Pred. No.:              1.08e-194       Length:         985
Score:                  1757.00         Matches:        328
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            99.8%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-917-265A-57 (1-985)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGC 2

RESULT 5
US-09-011-143-5
; Sequence 5, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2193 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-5

Alignment Scores:
Pred. No.:              6.32e-194       Length:         2193
Score:                  1755.00         Matches:        328
Percent Similarity:     99.7%           Conservative:   0
Best Local Similarity:  99.7%           Mismatches:     1
Query Match:            99.7%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-011-143-5 (1-2193)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db         64 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTACCTGGTTTTGCTGGCACCTCCTCTC 123
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Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 183

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 243

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 303

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 363

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 423

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 483

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 543

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 603

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 663

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 723

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 783

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 843

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 903

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 963

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 1023

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db       1024 AGCAACTGGGCATCCGTGTCCTGCAGT 1050

RESULT 6
US-09-302-495-5
; Sequence 5, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2193 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-302-495-5

Alignment Scores:
Pred. No.:              6.32e-194      Length:          2193
Score:                  1755.00        Matches:         328
Percent Similarity:     99.7%          Conservative:    0
Best Local Similarity:  99.7%          Mismatches:      1
Query Match:            99.7%          Indels:          0
DB:                     3              Gaps:            0

US-10-821-670A-30 (1-329) x US-09-302-495-5 (1-2193)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db         64 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTACCTGGTTTTGCTGGCACCTCCTCTC 123

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 183

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 243

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 303

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 363
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Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 423

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 483

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 543

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 603

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 663

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 723

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 783

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 843

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 903

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 963

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 1023

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db       1024 AGCAACTGGGCATCCGTGTCCTGCAGT 1050
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RESULT 7
US-10-079-616-5
; Sequence 5, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2193 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-079-616-5

Alignment Scores:
Pred. No.:              6.32e-194      Length:          2193
Score:                  1755.00        Matches:         328
Percent Similarity:     99.7%          Conservative:    0
Best Local Similarity:  99.7%          Mismatches:      1
Query Match:            99.7%          Indels:          0
DB:                     3              Gaps:            0

US-10-821-670A-30 (1-329) x US-10-079-616-5 (1-2193)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db         64 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTACCTGGTTTTGCTGGCACCTCCTCTC 123

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 183

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 243

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 303

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 363

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 423

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 483

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 543

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 603
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Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 663

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 723

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 783

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 843

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 903

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 963

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 1023

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db       1024 AGCAACTGGGCATCCGTGTCCTGCAGT 1050

RESULT 8
US-09-917-265A-38
; Sequence 38, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-09-917-265A-38

Alignment Scores:
Pred. No.:              3.33e-193       Length:         1599
Score:                  1747.00         Matches:        327
Percent Similarity:     99.4%           Conservative:   0
Best Local Similarity:  99.4%           Mismatches:     2
Query Match:            99.2%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-917-265A-38 (1-1599)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||    ||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987

RESULT 9
US-09-917-265A-40/c
; Sequence 40, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
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;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-40

Alignment Scores:
Pred. No.:              3.33e-193      Length:         1599
Score:                  1747.00        Matches:        327
Percent Similarity:     99.4%          Conservative:   0
Best Local Similarity:  99.4%          Mismatches:     2
Query Match:            99.2%          Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-30 (1-329) x US-09-917-265A-40 (1-1599)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db       1599 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 1540

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 1420

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1359 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 1300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1299 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 1240

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1179 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 1120

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db       1119 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 1060

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        999 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 940

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        939 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 880

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        879 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 820

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 760

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        759 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 640

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db        639 AGCAACTGGGCATCCGTGTCCTGCAGT 613

RESULT 10
US-09-917-265A-58
; Sequence 58, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
US-09-917-265A-58

Alignment Scores:
Pred. No.:              4.8e-183       Length:         987
Score:                  1657.00        Matches:        308
Percent Similarity:     96.7%          Conservative:   10
Best Local Similarity:  93.6%          Mismatches:     11
Query Match:            94.1%          Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-30 (1-329) x US-09-917-265A-58 (1-987)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||:::|||||||||||||||||||||||   ||||||
Db          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||:::|||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||   ||||||||||||||||||||||||||||||||||:::|||||||||   |||
Db        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
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Db        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              |||   ||||||||||||||||||||||||||||||   ||||||||||||||:::|||
Db        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              |||:::|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||   :::|||   ||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||:::|||||||||||||||||||||
Db        961 AGCGACTGGGCATCTGTGTCATGCAGT 987

RESULT 11
US-09-917-265A-60/c
; Sequence 60, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-60

Alignment Scores:
Pred. No.:              4.8e-183        Length:         987
Score:                  1657.00         Matches:        308
Percent Similarity:     96.7%           Conservative:   10
Best Local Similarity:  93.6%           Mismatches:     11

Query Match:            94.1%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-917-265A-60 (1-987)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||:::|||||||||||||||||||||||    ||||||
Db        987 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 928

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||:::|||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 808

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||  ||||||||||||||||||||||||||||||||:::|||||||||   |||
Db        747 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 688

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        687 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 628

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db        567 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 508

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              |||   ||||||||||||||||||||||||||||||   ||||||||||||||:::|||
Db        507 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 448

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              |||:::|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 328

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 268

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 208

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||   :::|||   ||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 148

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        147 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 28

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||:::|||||||||||||||||||||
Db         27 AGCGACTGGGCATCTGTGTCATGCAGT 1
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```
RESULT 12
US-09-079-984A-11
; Sequence 11, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,984A
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  990 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 987
;      IDENTIFICATION METHOD:  Similarity
US-09-079-984A-11

Alignment Scores:
Pred. No.:              4.83e-183      Length:         990
Score:                  1657.00        Matches:        308
Percent Similarity:     96.7%          Conservative:   10
Best Local Similarity:  93.6%          Mismatches:     11
Query Match:            94.1%          Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-30 (1-329) x US-09-079-984A-11 (1-990)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              |||||||||||||||||||||||||:::|||||||||||||||||||||||||   ||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              |||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              |||||||||||||||||||||||||||||:::|||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||   ||||||||||||||||||||||||||||||:::|||||||||   |||

Db        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||:::||||||

Db        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||:::|||||||||||||||

Db        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              |||   ||||||||||||||||||||||||||||   ||||||||||||||:::|||

Db        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              |||||||||||||||||||||||||||||||||||||||   :::|||   ||||||

Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||

Db        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||:::|||||||||||||||||||||
Db        961 AGCGACTGGGCATCTGTGTCCTGCAGT 987

RESULT 13
US-09-390-729-11
; Sequence 11, Application US/09390729
; Patent No. 6562334
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
```

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;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy Disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  WordPerfect 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/390,729
;       FILING DATE:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  09/079,984
;       FILING DATE:  15-MAY-1998
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Austin R. Miller
;       REGISTRATION NUMBER:  16,602
;       REFERENCE/DOCKET NUMBER:  1051-98
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (215) 563-1810
;       TELEFAX:  (215) 568-6946
;   INFORMATION FOR SEQ ID NO:  11:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  990 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA to mRNA
;     ORIGINAL SOURCE:
;       ORGANISM:  Canis familiaris
;     FEATURE:
;       NAME/KEY:  Canine IL12
;       LOCATION:  1 to 987
;       IDENTIFICATION METHOD:  Similarity
US-09-390-729-11

Alignment Scores:
Pred. No.:              4.83e-183       Length:         990
Score:                  1657.00         Matches:        308
Percent Similarity:     96.7%           Conservative:   10
Best Local Similarity:  93.6%           Mismatches:     11
Query Match:            94.1%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-390-729-11 (1-990)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||:::|||||||||||||||||||||||||||   ||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              |||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||:::|||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||   ||||||||||||||||||||||||||||||:::|||||||||   |||
Db        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||

Db        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              |||   ||||||||||||||||||||||||||||||   ||||||||||||||:::|||
Db        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||   :::|||   ||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
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Qy        321 SerAsnTrpAlaSerValSerCysSer 329
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Db        961 AGCGACTGGGCATCTGTGTCCTGCAGT 987

RESULT 14
US-09-917-265A-61
; Sequence 61, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-09-917-265A-61

Alignment Scores:
Pred. No.:              1.01e-182       Length:         1599
Score:                  1657.00         Matches:        308
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Best Local Similarity:  93.6%           Mismatches:     11
Query Match:            94.1%           Indels:         0
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US-10-821-670A-30 (1-329) x US-09-917-265A-61 (1-1599)
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Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
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Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
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Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
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Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
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Db        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
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Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
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Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
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Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
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Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
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Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
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Qy        321 SerAsnTrpAlaSerValSerCysSer 329
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RESULT 15
US-09-917-265A-63/c
; Sequence 63, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-63

Alignment Scores:
Pred. No.:              1.01e-182       Length:         1599
Score:                  1657.00         Matches:        308
Percent Similarity:     96.7%           Conservative:   10
Best Local Similarity:  93.6%           Mismatches:     11
Query Match:            94.1%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-917-265A-63 (1-1599)

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Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
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Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
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Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
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Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
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Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
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Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	38	1554	88.2	921	3	US-09-917-265-52	Sequence 52, Appl
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ALIGNMENTS

RESULT 1
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; Sequence 29, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
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; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(987)
; OTHER INFORMATION:
US-09-917-265-29

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Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
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Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987

RESULT 2
US-09-917-265-31/c
; Sequence 31, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-31

Alignment Scores:
Pred. No.:              2.75e-206       Length:         987
Score:                  1761.00         Matches:        329
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-917-265-31 (1-987)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
                 |||||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGCAGT 1

RESULT 3
US-10-821-670-29
; Sequence 29, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
US-10-821-670-29

Alignment Scores:
Pred. No.:              2.75e-206       Length:         987
Score:                  1761.00         Matches:        329
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-30 (1-329) x US-10-821-670-29 (1-987)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
                 |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987

RESULT 4
US-10-821-670-31/c
; Sequence 31, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
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;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-31

Alignment Scores:
Pred. No.:              2.75e-206       Length:         987
Score:                  1761.00         Matches:        329
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-30 (1-329) x US-10-821-670-31 (1-987)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
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Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
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Db         27 AGCAACTGGGCATCCGTGTCCTGCAGT 1

RESULT 5
US-10-041-672C-1
; Sequence 1, Application US/10041672C
; Publication No. US20030157059A1
; GENERAL INFORMATION:
;  APPLICANT: Mologen Forschungs-, Entwicklungs- und Vetriebs GmbH
;  APPLICANT:  Universitat Zurich
;  TITLE OF INVENTION: FELINE INTERLEUKIN-12 AS IMMUNOSTIMULANT
;  FILE REFERENCE: NHL-NP-36
;  CURRENT APPLICATION NUMBER: US/10/041,672C
;  CURRENT FILING DATE:  2002-01-08
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 990
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: feline IL-12 p40
US-10-041-672C-1

Alignment Scores:
Pred. No.:              2.77e-206       Length:         990
Score:                  1761.00         Matches:        329
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     7               Gaps:           0

US-10-821-670A-30 (1-329) x US-10-041-672C-1 (1-990)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987

RESULT 6
US-10-041-672C-10
; Sequence 10, Application US/10041672C
; Publication No. US20030157059A1
; GENERAL INFORMATION:
;  APPLICANT: Mologen Forschungs-, Entwicklungs- und Vetriebs GmbH
;  APPLICANT:  Universitat Zurich
;  TITLE OF INVENTION: FELINE INTERLEUKIN-12 AS IMMUNOSTIMULANT
;  FILE REFERENCE: NHL-NP-36
;  CURRENT APPLICATION NUMBER: US/10/041,672C
;  CURRENT FILING DATE:  2002-01-08
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 4522
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pMol-fil12p40
US-10-041-672C-10

Alignment Scores:
Pred. No.:              2.7e-205      Length:         4522
Score:                  1761.00       Matches:        329
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            100.0%        Indels:         0
DB:                     7             Gaps:           0

US-10-821-670A-30 (1-329) x US-10-041-672C-10 (1-4522)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuAlaProProLeu 20
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db       4007 AGCAACTGGGCATCCGTGTCCTGCAGT 4033

RESULT 7
US-09-917-265-55
; Sequence 55, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
```

```
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(984)
;   OTHER INFORMATION:
US-09-917-265-55

Alignment Scores:
Pred. No.:              8.56e-206      Length:         985
Score:                  1757.00        Matches:        328
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            99.8%          Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-30 (1-329) x US-09-917-265-55 (1-985)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984

RESULT 8
US-09-917-265-57/c
; Sequence 57, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-57

Alignment Scores:
Pred. No.:              8.56e-206      Length:         985
Score:                  1757.00        Matches:        328
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            99.8%          Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-30 (1-329) x US-09-917-265-57 (1-985)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGC 2

RESULT 9
US-10-821-670-55
; Sequence 55, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(984)

US-10-821-670-55

Alignment Scores:
Pred. No.:                8.56e-206      Length:          985
Score:                    1757.00        Matches:         328
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              99.8%          Indels:          0
DB:                       9              Gaps:            0

US-10-821-670A-30 (1-329) x US-10-821-670-55 (1-985)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
                ||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984

RESULT 10
US-10-821-670-57/c
; Sequence 57, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-57

Alignment Scores:
Pred. No.:              8.56e-206      Length:         985
Score:                  1757.00        Matches:        328
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            99.8%          Indels:         0
DB:                     9              Gaps:           0

US-10-821-670A-30 (1-329) x US-10-821-670-57 (1-985)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        321 SerAsnTrpAlaSerValSerCys 328
                ||||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGC 2

RESULT 11
US-10-079-616-5
; Sequence 5, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
```

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;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2193 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-079-616-5

Alignment Scores:
Pred. No.:              5.02e-205      Length:        2193
Score:                  1755.00        Matches:       328
Percent Similarity:     99.7%          Conservative:  0
Best Local Similarity:  99.7%          Mismatches:    1
Query Match:            99.7%          Indels:        0
DB:                     6              Gaps:          0

US-10-821-670A-30 (1-329) x US-10-079-616-5 (1-2193)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db         64 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTACCTGGTTTTGCTGGCACCTCCTCTC 123

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 183

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 243

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 303

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 363

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 423

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 483

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 543

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 603

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 663

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 723

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 783

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        784 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 843

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 903

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 963

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 1023

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db       1024 AGCAACTGGGCATCCGTGTCCTGCAGT 1050

RESULT 12
US-09-917-265-38
; Sequence 38, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
US-09-917-265-38

Alignment Scores:
Pred. No.:              3.04e-204      Length:        1599
Score:                  1747.00        Matches:       327
Percent Similarity:     99.4%          Conservative:  0
Best Local Similarity:  99.4%          Mismatches:    2
Query Match:            99.2%          Indels:        0
DB:                     3              Gaps:          0

US-10-821-670A-30 (1-329) x US-09-917-265-38 (1-1599)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
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Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987

RESULT 13
US-09-917-265-40/c
; Sequence 40, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-40

Alignment Scores:
Pred. No.:              3.04e-204       Length:         1599
Score:                  1747.00         Matches:        327
Percent Similarity:     99.4%           Conservative:   0

Best Local Similarity:  99.4%           Mismatches:     2
Query Match:            99.2%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-30 (1-329) x US-09-917-265-40 (1-1599)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db       1599 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 1540

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 1420

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1359 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 1300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1299 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 1240

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1179 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 1120

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db       1119 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 1060

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        999 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 940

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        939 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 880

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        879 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 820

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 760

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        759 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 640

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
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Db        639 AGCAACTGGGCATCCGTGTCCTGCAGT 613
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RESULT 14
US-10-821-670-38
; Sequence 38, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-10-821-670-38

Alignment Scores:
Pred. No.:              3.04e-204      Length:         1599
Score:                  1747.00        Matches:        327
Percent Similarity:     99.4%          Conservative:   0
Best Local Similarity:  99.4%          Mismatches:     2
Query Match:            99.2%          Indels:         0
DB:                     9              Gaps:           0

US-10-821-670A-30 (1-329) x US-10-821-670-38 (1-1599)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987

RESULT 15
US-10-821-670-40/c
; Sequence 40, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-40

Alignment Scores:
Pred. No.:              3.04e-204      Length:         1599
Score:                  1747.00        Matches:        327
Percent Similarity:     99.4%          Conservative:   0
Best Local Similarity:  99.4%          Mismatches:     2
Query Match:            99.2%          Indels:         0
DB:                     9              Gaps:           0

US-10-821-670A-30 (1-329) x US-10-821-670-40 (1-1599)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db       1599 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 1540

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 1420

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1359 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 1300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1299 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 1240

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1179 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 1120

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              |||||||||||||||||   |||||||||||||||||||||||||||||||||||||||||
Db       1119 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 1060

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        999 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 940

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
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Db        939 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 880

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        879 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 820

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 760

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        759 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
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Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 640

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
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Job time : 1295.3 secs
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Run on: June 10, 2006, 01:18:36 ; Search time 17.1171 Seconds
(without alignments)
3659.318 Million cell updates/sec

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Perfect score: 1761
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Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 253354 seqs, 63461778 residues

Total number of hits satisfying chosen parameters: 506708

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss05h
-USER=US10821670_@CGN_1_1_80_@runat_07062006_110114_26355 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	177	10.1	1363	6	US-10-827-684B-6	Sequence 6, Appli
2	177	10.1	1369	6	US-10-827-684B-5	Sequence 5, Appli
3	176	10.0	1923	7	US-11-145-307A-52	Sequence 52, Appl
4	132.5	7.5	1161	7	US-11-297-134-9	Sequence 9, Appli
5	108	6.1	2341	6	US-10-511-937-349	Sequence 349, App
6	106	6.0	2582	7	US-11-293-697-2331	Sequence 2331, Ap
7	104.5	5.9	2534	7	US-11-293-697-1946	Sequence 1946, Ap
8	99.5	5.7	3597	6	US-10-505-928-651	Sequence 651, App
9	99.5	5.7	3597	6	US-10-511-937-2802	Sequence 2802, Ap
10	99	5.6	5997	7	US-11-313-450-1	Sequence 1, Appli
11	99	5.6	8370	7	US-11-263-326-90	Sequence 90, Appl
12	99	5.6	8377	7	US-11-263-326-95	Sequence 95, Appl
13	99	5.6	8380	7	US-11-263-326-89	Sequence 89, Appl
14	99	5.6	8381	7	US-11-263-326-1	Sequence 1, Appli
15	99	5.6	8381	7	US-11-263-326-3	Sequence 3, Appli
16	99	5.6	8381	7	US-11-263-326-5	Sequence 5, Appli
17	99	5.6	8381	7	US-11-263-326-7	Sequence 7, Appli
18	99	5.6	8381	7	US-11-263-326-8	Sequence 8, Appli
19	99	5.6	8381	7	US-11-263-326-11	Sequence 11, Appl
20	99	5.6	8381	7	US-11-263-326-91	Sequence 91, Appl
21	99	5.6	8381	7	US-11-263-326-92	Sequence 92, Appl
22	99	5.6	8381	7	US-11-263-326-93	Sequence 93, Appl
23	99	5.6	8381	7	US-11-263-326-96	Sequence 96, Appl
24	99	5.6	8381	7	US-11-263-326-97	Sequence 97, Appl
25	99	5.6	8381	7	US-11-263-326-108	Sequence 108, App
26	99	5.6	8381	7	US-11-263-326-136	Sequence 136, App
27	99	5.6	8381	7	US-11-263-326-137	Sequence 137, App
28	99	5.6	8381	7	US-11-263-326-138	Sequence 138, App
29	99	5.6	8381	7	US-11-263-326-139	Sequence 139, App
30	99	5.6	8381	7	US-11-263-326-140	Sequence 140, App
31	99	5.6	8381	7	US-11-263-326-141	Sequence 141, App
32	99	5.6	8381	7	US-11-263-326-142	Sequence 142, App
33	99	5.6	8381	7	US-11-263-326-143	Sequence 143, App
34	99	5.6	8381	7	US-11-263-326-144	Sequence 144, App
35	99	5.6	8388	7	US-11-263-326-94	Sequence 94, Appl
36	97.5	5.5	3646	6	US-10-511-937-358	Sequence 358, App
37	95	5.4	887	6	US-10-511-937-350	Sequence 350, App
38	94	5.3	5193	7	US-11-270-040-5	Sequence 5, Appli
39	94	5.3	8381	7	US-11-263-326-9	Sequence 9, Appli
c 40	93.5	5.3	2208	6	US-10-953-349-3367	Sequence 3367, Ap
41	90.5	5.1	2062	6	US-10-953-349-4146	Sequence 4146, Ap
42	90.5	5.1	3084	6	US-10-511-937-448	Sequence 448, App
43	87.5	5.0	1219	6	US-10-953-349-15072	Sequence 15072, A
44	87.5	5.0	1560	7	US-11-217-529-1952	Sequence 1952, Ap
45	87.5	5.0	2100	7	US-11-217-529-126	Sequence 126, App

ALIGNMENTS

RESULT 1
US-10-827-684B-6
; Sequence 6, Application US/10827684B
; Publication No. US20060115807A1
; GENERAL INFORMATION:
; APPLICANT: Chambers, Ian P
; TITLE OF INVENTION: Improved episomal expression system
; FILE REFERENCE: 78870/00003
; CURRENT APPLICATION NUMBER: US/10/827,684B
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 09/359,672
; PRIOR FILING DATE: 1999-07-23
; PRIOR APPLICATION NUMBER: GB 9701492.2
; PRIOR FILING DATE: 1997-01-24
; PRIOR APPLICATION NUMBER: PCT/GB98/00216
; PRIOR FILING DATE: 1998-01-26
; PRIOR APPLICATION NUMBER: GB 0407043.9
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1363
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-827-684B-6

Alignment Scores:

Pred. No.:	4.73e-10	Length:	1363
Score:	177.00	Matches:	76
Percent Similarity:	40.5%	Conservative:	50
Best Local Similarity:	24.4%	Mismatches:	125

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Query Match:            10.1%          Indels:        61
DB:                     6              Gaps:          13

US-10-821-670A-30 (1-329) x US-10-827-684B-6 (1-1363)

Qy         37 TrpHisProAsp-Ala---ProGlyGluMetValValLeuThrCysAsnThrProGlu-- 54
              ||||||   ||| :::   ||||||      |||   |||   |||          |||
Db         76 TGGCACAGTGACAAGCCTGCCAGGGGCCACCGTTACCCTGATTTGCCCCGGGAAGGAAGC 135

Qy         55 -GluAspAspIleThr------------TrpThrSerAspGlnSerSerGluValLeuGl 70
                  ::::::|||          ::::::      |||:::   |||
Db        136 AGCAGGCAATGTTACCATTCACTGGGTGTACTCTGGCTCACAAAACAGAGAATGGACTAC 195

Qy         70 ySerGlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCy 90
               :::|||   ||||||   ::::::      :::   :::|||   |||   |||   ||
Db        196 CACAGGAAACACACTGGTTCTGAGGGACGTGCAGCTCAGCGACACTGGGGACTATTTATG 255

Qy         90 sHisLysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGl 110
              |               ::::::            ||||||:::
Db        256 CTCCCTGAATGATCACCTGGTGGGGACTGTGCCCTTGCTGGTG----------------- 298

Qy        110 yIleTrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLy 130
                       |||:::      |||:::   :::                    |||
Db        299 ------------GATGTTCCCCCAGAGGAGCCCAAG-----------------CTCTC 327

Qy        130 sCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerTh 150
               |||      ||||||                |||   |||
Db        328 CTGCTTCCGGAAGAACCCCCTTGTCAACGCCATCTGTGAGTGG---------------- 370

Qy        150 rAspLeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCy 170
                                  |||  ||||||   |||         |||
Db        371 --------------------------CGTCCGAGCAGCACCCCCTCTCCAACCACG-- 400

Qy        170 sGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTy 190
                  |||   |||  |||:::|||:::          |||                ::
Db        401 ----AAGGCTGTGCTGTTTGCAAAGAAAATCAACACCACCAAC---GGGAAGAGTGACTT 453

Qy        190 rThrValGluCysGlnGluGlySerAlaCys--------------------------Pr 201
               :   |||   ||||||      ||||||                           ||
Db        454 CCAGGTGCCCTGCCAGTATTC-TCAGCAGCTGAAAAGCTTCTCCTGCCAGGTGGAGATCC 512

Qy        201 oAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTy 221
              |          :::|||:::|||       |||   |||                  |||
Db        513 TGGAGGGTGACAAAGTATACCACATAGTGTCACTGTGCGTTGCAAACAGTGTGGGAAGCA 572

Qy        221 r-GluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysA 241
               ::::::      :::|||           :::::::::||||||||||||    |
Db        573 AGTCCAGCCACAACGAAGCGTTTCACAGCTTAAAAATGGTGCAGCCGGATCCACCTGCCA 632

Qy        241 snLeuGlnLeuLysProLeuLys---AsnSerArgHisValGluValSerTrpGluTyrP 260
              |||||   :::      :::          |||   ::::::||||||||:::::::|
Db        633 ACCTTGTGGTATCAGCCATACCTGGAAGGCCGCGCTGGCTCAAAGTCAGCTGGCAGCACC 692

Qy        260 roAspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnG 280
              ||:::||||||            ||||||:::   |||   |||   ::::::   :::
Db        693 CTGAGACCTGGGACCCG------AGTTACTACTTGCTGCAGTTCCAGCTTCGATACCGAC 746

Qy        280 lyLysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValV 300
                   ::::::|||                |||   :::                ::::   |
Db        747 CTGTATGGTCAAAGGAG---TTCACGGTGTTGCTGCTCCCGGTGGCCCAGTACCAATGCG 803

Qy        300 alCysHisLysAspAlaLys--------------IleArgValGlnAlaArgAspArgT 315
              ||   |||      :::                ::::::|||:::   ::::::
Db        804 TCATCCATGATGCCTTGCGAGGAGTGAAGCACGTGGTCCAGGTCCGTGGGAAGGAGGAGC 863

Qy        315 yrTyrSerSerSerTrpSerAsnTrpAla 324
                         ||||||   |||:::
Db        864 TTGACCTTGGCCAGTGGAGTGAATGGTCC 892

RESULT 2
US-10-827-684B-5
; Sequence 5, Application US/10827684B
; Publication No. US20060115807A1
; GENERAL INFORMATION:
;  APPLICANT: Chambers, Ian P
;  TITLE OF INVENTION: Improved episomal expression system
;  FILE REFERENCE: 78870/00003
;  CURRENT APPLICATION NUMBER: US/10/827,684B
;  CURRENT FILING DATE:  2004-04-19
;  PRIOR APPLICATION NUMBER: US 09/359,672
;  PRIOR FILING DATE: 1999-07-23
;  PRIOR APPLICATION NUMBER: GB 9701492.2
;  PRIOR FILING DATE: 1997-01-24
;  PRIOR APPLICATION NUMBER: PCT/GB98/00216
;  PRIOR FILING DATE: 1998-01-26
;  PRIOR APPLICATION NUMBER: GB 0407043.9
;  PRIOR FILING DATE: 2004-03-29
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 1369
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-827-684B-5

Alignment Scores:
Pred. No.:              4.76e-10        Length:         1369
Score:                  177.00          Matches:        76
Percent Similarity:     40.5%           Conservative:   50
Best Local Similarity:  24.4%           Mismatches:     125
Query Match:            10.1%           Indels:         61
DB:                     6               Gaps:           13

US-10-821-670A-30 (1-329) x US-10-827-684B-5 (1-1369)

Qy         37 TrpHisProAsp-Ala---ProGlyGluMetValValLeuThrCysAsnThrProGlu-- 54
              ||||||   ||| :::   ||||||      |||   |||   |||          |||
Db         82 TGGCACAGTGACAAGCCTGCCAGGGGCCACCGTTACCCTGATTTGCCCCGGGAAGGAAGC 141

Qy         55 -GluAspAspIleThr------------TrpThrSerAspGlnSerSerGluValLeuGl 70
                  ::::::|||          ::::::      |||:::   |||
Db        142 AGCAGGCAATGTTACCATTCACTGGGTGTACTCTGGCTCACAAAACAGAGAATGGACTAC 201

Qy         70 ySerGlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCy 90
               :::|||   ||||||   ::::::      :::   :::|||   |||   |||   ||
Db        202 CACAGGAAACACACTGGTTCTGAGGGACGTGCAGCTCAGCGACACTGGGGACTATTTATG 261

Qy         90 sHisLysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGl 110
              |               ::::::            ||||||:::
Db        262 CTCCCTGAATGATCACCTGGTGGGGACTGTGCCCTTGCTGGTG----------------- 304

Qy        110 yIleTrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLy 130
                       |||:::      |||:::   :::                    |||
Db        305 ------------GATGTTCCCCCAGAGGAGCCCAAG-----------------CTCTC 333

Qy        130 sCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerTh 150
               |||      ||||||                |||   |||
Db        334 CTGCTTCCGGAAGAACCCCCTTGTCAACGCCATCTGTGAGTGG---------------- 376

Qy        150 rAspLeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCy 170
                                  |||  ||||||   |||         |||
Db        377 --------------------------CGTCCGAGCAGCACCCCCTCTCCAACCACG-- 406

Qy        170 sGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTy 190
                  |||   |||  |||:::|||:::          |||                ::
Db        407 ----AAGGCTGTGCTGTTTGCAAAGAAAATCAACACCACCAAC---GGGAAGAGTGACTT 459

Qy        190 rThrValGluCysGlnGluGlySerAlaCys--------------------------Pr 201
               :   |||   ||||||      ||||||                           ||
Db        460 CCAGGTGCCCTGCCAGTATTC-TCAGCAGCTGAAAAGCTTCTCCTGCCAGGTGGAGATCC 518

Qy        201 oAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTy 221
              |          :::|||:::|||       |||   |||                  |||
Db        519 TGGAGGGTGACAAAGTATACCACATAGTGTCACTGTGCGTTGCAAACAGTGTGGGAAGCA 578
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Qy        221 r-GluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysA 241
Db        579 AGTCCAGCCACAACGAAGCGTTTCACAGCTTAAAAATGGTGCAGCCGGATCCACCTGCCA 638

Qy        241 snLeuGlnLeuLysProLeuLys---AsnSerArgHisValGluValSerTrpGluTyrP 260
Db        639 ACCTTGTGGTATCAGCCATACCTGGAAGGCCGCGCTGGCTCAAAGTCAGCTGGCAGCACC 698

Qy        260 roAspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnG 280
Db        699 CTGAGACCTGGGACCCG------AGTTACTACTTGCTGCAGTTCCAGCTTCGATACCGAC 752

Qy        280 lyLysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValV 300
Db        753 CTGTATGGTCAAAGGAG---TTCACGGTGTTGCTGCTCCCGGTGGCCCAGTACCAATGCG 809

Qy        300 alCysHisLysAspAlaLys--------------IleArgValGlnAlaArgAspArgT 315
Db        810 TCATCCATGATGCCTTGCGAGGAGTGAAGCACGTGGTCCAGGTCCGTGGGAAGGAGGAGC 869

Qy        315 yrTyrSerSerSerTrpSerAsnTrpAla 324
Db        870 TTGACCTTGGCCAGTGGAGTGAATGGTCC 898
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RESULT 3
US-11-145-307A-52
; Sequence 52, Application US/11145307A
; Publication No. US20060094035A1
; GENERAL INFORMATION:
; APPLICANT: Arcturus Bioscience, Inc.
; APPLICANT: Erlander, Mark G.
; APPLICANT: Ma, Xiao-Jun
; TITLE OF INVENTION: Identification of Tumors
; FILE REFERENCE: 022041-002020US
; CURRENT APPLICATION NUMBER: US/11/145,307A
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 60/577,084
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 1923
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-145-307A-52

Alignment Scores:

Pred. No.:	1e-09	Length:	1923
Score:	176.00	Matches:	79
Percent Similarity:	37.8%	Conservative:	40
Best Local Similarity:	25.1%	Mismatches:	105
Query Match:	10.0%	Indels:	93
DB:	7	Gaps:	17

US-10-821-670A-30 (1-329) x US-11-145-307A-52 (1-1923)

```
Qy         43 GlyGluMetValValLeuThrCysAsnThrProGluGluAsp---AspIleThrTrpThr 61
Db        264 GGCTCTGACGTGACACTGCCATGTGGGACAGCAAACTGGGATGCTGCGGTGACGTGGCGG 323

Qy         62 ---------SerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGln 78
Db        324 GTAAATGGGACAGACCTGGCCCCTGACCTGCTC---AACGGCTCTCAGCTGGTGCTCCAT 380

Qy         79 ValLysGluPheAlaAspAlaGlyGlnTyrThrCys---HisLysGlyGlyGluValLeu 97
Db        381 GGCCTGGAACTGGGCCACAGTGGCCTCTACGCCTGCTTCCACCGTGACTCCTGGCACCTG 440

Qy         98 SerHisSerPheLeuLeu---------IleHisLysLysGluAspGlyIleTrpSerThr 114
Db        441 CGCCACCAAGTCCTGCTGCATGTGGGCTTGCCGCCGCGGGAGCCT-------------- 485
```

```
Qy        115 AspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLys 134
Db        486 ------------------------------------GTGCTCAGCTGCCGCTCCAAC 506

Qy        135 AsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPhe 154
Db        507 ACTTACCCCAAGGGCTTCTACTGCAGCTGGCATCTGCCCACCCCCACCTACATT------ 560

Qy        155 ThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThr 174
Db        561 ----------------------------CCCAAC------ACCTTCAATGTGACTGTG 584

Qy        175 LeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrValGluCys 194
Db        585 CTGCATGGCTCCAAAATTATGGTC--------------------------------TGT 611

Qy        195 GlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValValValAsp 214
Db        612 GA-GAAGGA---------CCCAGCCCTCAAGAACCGCTGCCACATTCGCTACATGCACCT 661

Qy        215 AlaIleHisLysLeuLysTyrGlu--------------------------------Asn 223
Db        662 GTTCTCCACC--ATCAAGTACAAGGTCTCCATAAGTGTCAGCAATGCCCTGGGCCACAAT 719

Qy        224 TyrThrSerSerPhePheIleArg---AspIleIleLysProAspProProLysAsnLeu 242
Db        720 GCCACAGCTATCACCTTTGACGAGTTCACCATTGTGAAGCCTGATCCTCCAGAAAATGTG 779

Qy        243 GlnLeuLysProLeu---LysAsnSerArgHisValGluValSerTrpGluTyrProAsp 261
Db        780 GTAGCCCGGCCAGTGCCCAGCAACCCTCGCCGGCTGGAGGTGACGTGGCAGACCCCCTCG 839

Qy        262 ThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLys 281
Db        840 ACCTGGCCTGACCCTGAGTCT---TTTCCTCTCAAGTTCTTTCTGCGCTACCGA------ 890

Qy        282 AsnAsnArgGluLysLysAspArgLeuSerValAspLys---------------------- 294
Db        891 ----------------------CCCCTCATCCTGGACCAGTGGCAGCATGTGGAGCTGTCC 929

Qy        295 ---------------ThrSerAlaLysValValCysHisLysAspAlaLysIleArgVal 309
Db        930 GACGGCACAGCACACACCATCACAGATGCCTACGCCGGGAAGGAGTACATTATCCAGGTG 989

Qy        310 GlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAla 324
Db        990 GCAGCCAAGGACAATGAGATT---GGGACATGGAGTGACTGGAGC 1031
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RESULT 4
US-11-297-134-9
; Sequence 9, Application US/11297134
; Publication No. US20060111297A1
; GENERAL INFORMATION:
; APPLICANT: Genzyme Corporation
; APPLICANT: Roberts, Bruce
; TITLE OF INVENTION: BLOOD FACTOR DOMAINS
; FILE REFERENCE: 5270C
; CURRENT APPLICATION NUMBER: US/11/297,134
; CURRENT FILING DATE: 2005-12-08
; PRIOR APPLICATION NUMBER: PCT/US2005/018461
; PRIOR FILING DATE: 2004-06-09
; PRIOR APPLICATION NUMBER: US 60/477,291
; PRIOR FILING DATE: 2003-06-09
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 1161
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-297-134-9

Alignment Scores:

Pred. No.:	2.47e-05	Length:	1161

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Score:                 132.50        Matches:       49
Percent Similarity:    41.1%         Conservative:  41
Best Local Similarity: 22.4%         Mismatches:    86
Query Match:           7.5%          Indels:        43
DB:                    7             Gaps:          9

US-10-821-670A-30 (1-329) x US-11-297-134-9 (1-1161)

Qy       129 LeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIle 148
             ::::::|||   |||      |||                                 |||
Db       110 GTGCAATGCCGAGCCTCTCGGTAC----------------------------CCGATC 139

Qy       149 SerThrAspLeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyVal 168
             :::  |||      :::|||:::     :::      |||:::  |||
Db       140 GCCGTGGATTGCTCCTGGACCCTGCCGCCTGCTCCAAACTCCACCAGCCCC--------- 190

Qy       169 ThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLys 188
                 :::   ::::::     ::::::  :::      |||  :::
Db       191 ---------GTGTCCTTCATTGCCACGTACAGGCTCGGCATGGCTGCCCGGGGCCACAGC 241

Qy       189 ---LysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeu 207
                   :::           ::::::|||         :::      |||
Db       242 TGGCCCTGCCTGCAGCAGACGCCAACGTCCACCAGCTGCACCATCACGGATGTCCAGCTG 301

Qy       208 ------------ProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsn 223
                    |||     :::   |||  |||:::|||          :::
Db       302 TTCTCCATGGCTCCCTACGTGCTCAATGTCACCGCCGTCCACCCCTGGGGCTCCAGCAGC 361

Qy       224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGln 243
                  |||           ||||||||||||||||||||:::   ::::::
Db       362 AGCTTCGTGCCTTTCATAACAGAGCACATCATCAAGCCCGACCCTCCAGAAGGCGTGCGC 421

Qy       244 LeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThrTrp 263
             |||   ::::::         |||||||||:::|||   ::::::   |||   :::|||
Db       422 CTAAGCCCCCTCGCT---GAGCGCCACGTACAGGTGCAGTGGGAGCCTCCCGGGTCCTGG 478

Qy       264 SerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsnAsn 283
                 |||         |||||||||   :::   ::::::   :::   :::
Db       479 CCCTTCCCA---GAGATCTTCTCACTGAAGTACTGGATCCGTTACAAG---CGTCAGGGA 532

Qy       284 ArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHisLys 303
                 :::      |||:::          :::   ::::::   ::::::
Db       533 GCTGCGCGCTTCCACCGGGTGGGGCCCATTGAAGCCACGTCCTTCATCCTC--------- 583

Qy       304 AspAlaLysIleArgValGlnAlaArgAspArgTyrTyr---------------------- 316
                        |||:::   |||   |||||||||
Db       584 ---------AGGGCTGTGCGGCCCCGAGCCAGGTACTACGTCCAAGTGGCGGCTCAGGAC 634

Qy       317 -----------------SerSerSerTrpSerAsnTrpAlaSerValSerCysSer 329
                             |||   ||||||      |||:::   :::   |||
Db       635 CTCACAGACTACGGGGAACTGAGTGACTGGAGTCTCCCCGCCACTGCCACAATGAGC 691

RESULT 5
US-10-511-937-349
; Sequence 349, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
;  APPLICANT: EXPRESSION DIAGNOSTICS, INC.
;  APPLICANT:  Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  APPLICANT:  Prentice, James
;  APPLICANT:  Morris, MacDonald
;  APPLICANT:  Rosenberg, Steven
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
;  TITLE OF INVENTION:  AND MONITORING TRANSPLANT REJECTION
;  FILE REFERENCE: 506612000104
;  CURRENT APPLICATION NUMBER: US/10/511,937
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: PCT/US2003/012946
;  PRIOR FILING DATE: 2003-04-24
;  PRIOR APPLICATION NUMBER: US 10/131,831
;  PRIOR FILING DATE: 2002-04-24
;  PRIOR APPLICATION NUMBER: US 10/325,899
;  PRIOR FILING DATE: 2002-12-20
;  NUMBER OF SEQ ID NOS: 3117
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 349
;   LENGTH: 2341
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-511-937-349

Alignment Scores:
Pred. No.:             0.0309        Length:        2341
Score:                 108.00        Matches:       76
Percent Similarity:    31.9%         Conservative:  39
Best Local Similarity: 21.1%         Mismatches:    102
Query Match:           6.1%          Indels:        144
DB:                    6             Gaps:          15

US-10-821-670A-30 (1-329) x US-10-511-937-349 (1-2341)

Qy         3 ProGlnGlnLeuValIleAlaTrp--------------PheSerLeuValLeuLeuAla 17
             |||   |||      |||   |||                   :::|||:::||||||
Db       275 CCTCTCCAGTGTGGCATCATGTGGCAGCTGCTCCTCCCAACTGCTCTGCTACTTCTAGTT 334

Qy        18 ProProLeuMetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrp 37
                 |||      :::|||   |||   |||      :::|||      |||
Db       335 TCAGCTGGCATGCGGACTGAAGATCTCCCAAAGGCTGTGGTGTTCCTGGAGCCTCAATGG 394

Qy        38 HisProAspAlaProGlyGluMetValValLeuThrCysAsn---------ThrProGlu 54
             :::                 :::   |||   |||   |||           :::||||||
Db       395 TACAGGGTGCTCGAGAAGGACAGTGTGACTCTGAAGTGCCAGGGAGCCTACTCCCCTGAG 454

Qy        55 GluAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGlyLysThr 74
             ::::::          |||      :::::::|||      :::                :::
Db       455 GACAATTCCACACAGTGGTTTCACAATGAGAGCCTC---ATCTCAAGCCAGGCCTCGAGC 511

Qy        75 LeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGly 94
                 |||                  |||:::|||:::|||   |||
Db       512 TACTTCATTGACGCTGCCACAGTCGACGACAGTGGAGAGTACAGGTGCCAGACAAACCTC 571

Qy        95 GluValLeuSerHisSerPheLeuLeu------------------------------- 103
                 ||||||          |||
Db       572 TCCACCCTCAGTGACCCGGTGCAGCTAGAAGTCCATATCGGCTGGCTGTTGCTCCAGGCC 631

Qy       104 ---------IleHisLysLysGluAspGlyIle------------------TrpSerThr 114
                    :::   |||:::||||||   |||                    |||
Db       632 CCTCGGTGGGTGTTCAAGGAGGAAGACCCTATTCACCTGAGGTGTCACAGCTGGAAGAAC 691

Qy       115 AspIleLeu------------------------------------------------- 117
                 |||
Db       692 ACTGCTCTGCATAAGGTCACATATTTACAGAATGGCAAAGGCAGGAAGTATTTTCATCAT 751

Qy       118 ----------------------------------------------------------Arg 118
                                                                        |||
Db       752 AATTCTGACTTCTACATTCCAAAAGCCACACTCAAAGACAGCGGCTCCTACTTCTGCAGG 811

Qy       119 GluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGly 138
                      |||||||||   :::|||      ||||||      :::::|||
Db       812 GGGCTTGTTGGGAGTAAAAATGT-GTCTTCAGAGACTGTGAACATCACCATCACTCA--- 867

Qy       139 ArgPhe--------------------------ThrCysTrp-Trp-------------- 144
             ||||||                         :::   ||| :::
Db       868 AGGTTTGGCAGTGTCAACCATCTCATCATTCTTTCCACCTGGGTACCAAGTCTCTTTCTG 927

Qy       145 ----------------LeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSe 159
                             |||   |||:::   |||   |||   |||:::||||||:::::
Db       928 CTTGGTGATGGTACTCCTTTTTGCAGTGGACACAGGACTATATTTCTCTGTGAAGACAAA 987

Qy       159 rArgGlySerSer-------------------------------------------AspProGl 166
             :     ||||||                                           ||||||||
Db       988 CATTCGAAGCTCAACAAGAGACTGGAAGGACCATAAATTTAAATGGAGAAAGGACCCTCA 1047
```

```
Qy        166 nGlyVal---------------------------------------------------- 168
              |
Db       1048 AGACAAATGACCCCCATCCCATGGGGGTAATAAGAGCAGTAGCAGCAGCATCTCTGAACA 1107

Qy        169 -ThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLy 188
               |||   |||||||||||:::     :::         :::|||  :::::
Db       1108 TTTCTCTGGATTTGCAACCCTATCATCCTCAGGCCTCTCTACAAGCAGCAGGAAACATAG 1167

Qy        188 sLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeu-- 207
              :           |||          |||      :::   ||||||
Db       1168 A---------------ACTCAGAGCCAGATCCCTTATCCAACTCTCGACTTTTCCTTGGT 1212

Qy        208 ----------------------------------------ProIleGluValValVa 213
                                                     |||   |||
Db       1213 CTCCAGTGGAAGGGAAAAGCCCATGATCTTCAAGCAGGGAAGCCCCAGTGAG-------- 1264

Qy        213 lAspAlaIleHis------LysLeuLysTyrGluAsnTyrThrSerSerPhePheIle 230
                  :::|||     |||||||||:::::::::|||||::::::|||   :::
Db       1265 ----TAGCTGCATTCCTAGAAATTGAAGTTTCAGAGCTACACAAACACTTTTTCTGTC 1318

RESULT 6
US-11-293-697-2331
; Sequence 2331, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2331
;   LENGTH: 2582
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-2331

Alignment Scores:
Pred. No.:              0.0587        Length:          2582
Score:                  106.00        Matches:         68
Percent Similarity:     35.3%         Conservative:    44
Best Local Similarity:  21.5%         Mismatches:      136
Query Match:            6.0%          Indels:          69
DB:                     7             Gaps:            14

US-10-821-670A-30 (1-329) x US-11-293-697-2331 (1-2582)

Qy          7 ValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeuMetAlaIleTrpGluLeu 26
              ::::::   |||      |||:::::::|||   |||
Db        223 ATGCTTCTGTGGCTGCTGCTGCTGATCCTGACTCCTGGAAGAGAACAATCAGGGGTGGCC 282

Qy         27 GluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaProGlyGluMetVal 46
               |||   |||   ::::::          |||                 ||||||   |||
Db        283 CCAAAAGCTGTACTTCTCCTCAATCCTCCATGGTCCACAGCCTTCAAAGGAGAAAAAGTG 342

Qy         47 ValLeuThrCysAsnThrProGlu-----------GluAspAspIleThrTrpThrSer 62
               |||   |||::::::                    :::   |||      |||
Db        343 GCTCTCATATGCAGCAGCATATCACATTCCCTAGCCCAGGGAGACACATATTGGTATCAC 402

Qy         63 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 82
              |||:::          :::        |||         ||||||:::   |||
Db        403 GATGAGAAGTTGTTGAAAATAAAACATGACAAG---------ATCCAAATTACAGAG--- 450

Qy         83 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 102
                  |||   |||   |||          |||      ||||||   :::
Db        451 ------CCTGGAAATTACCAATGTAAGACCCGAGGATCCTCCCTCAGTGATGCC------ 498

Qy        103 LeuIleHisLysLysGluAspGlyIleTrp---SerThrAspIleLeuArgGluGlnLys 121
                 :::|||   :::          |||              |||
Db        499 ---GTGCATGTGGAATTTTCACCTGACTGGCTGATCCTGCAGGCTTTACATCCTGTCTTT 555

Qy        122 GluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThr 141
              |||      |||   :::   |||:::|||:::   |||:::
Db        556 GAAGGAGACAAT---GTCATTCTGAGATGTCAGGGGAAAGACAACAAA------------ 600

Qy        142 CysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGly 161
                                  :::|||      |||          |||         |||
Db        601 --------------------AACACTCATCAAAAGGTTTACTACAAGGAT------GGA 633

Qy        162 SerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArg 181
                    |||                              :::   :::   ||||||:::
Db        634 AAACAGCTTCCTAAT--------------------AGTTATAATTTAGAGAAGATCACA 672

Qy        182 ValAsp------AsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAla 199
              |||:::      :::||||||      ||||||
Db        673 GTGAATTCAGTCTCCAGGGATAATAGCAAATAT-----------------------CAT 708

Qy        200 CysProAlaAlaGluGlu------SerLeuProIleGluValValValAspAlaIleHis 217
              |||   |||         :::        |||   |||||||||                ::::::
Db        709 TGTACTGCTTATAGGAAGTTTTACATACTTGACATTGAAGTAACTTCAAAACCCCTAAAT 768

Qy        218 LysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAsp 237
                    |||                  |||:::      :::::::::
Db        769 ATCCAAGTTCAAGAG--------------CTGTTTCTACATCCTGTGCTGAGAGCCAGC 813

Qy        238 ProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrp 257
                        ::::::      |||:::      :::         ::::::|||
Db        814 TCTTCCACGCCCATAGAGGGGAGTCCCATGACCCTGACCTGTGAGACCCAGCTCTCTCCA 873

Qy        258 GluTyrProAspThr---------------------------------------------- 262
              :::   ||||||
Db        874 CAGAGGCCAGATGTCCAGCTGCAATTCTCCCTCTTCAGAGATAGCCAGACCCTCGGATTG 933

Qy        263 ---TrpSerThr-ProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLy 281
                 ||||||    |||   :::      ||||||      |||::::::   ||||||
Db        934 GGCTGGAGCAGGTCCCCCAAACTCCAGATCCCTGCCATGTGGACTGAAGACTCAGGGTCT 993

Qy        281 sAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAla 297
                           :::      |||:::      |||      |||
Db        994 TACTGGTGTGAGGTGGAGACAGTGACTCACAGCATCAAAAAAAGGAGCC 1042

RESULT 7
US-11-293-697-1946
; Sequence 1946, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1946
;   LENGTH: 2534
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1946

Alignment Scores:
Pred. No.:              0.083         Length:          2534
Score:                  104.50        Matches:         62
Percent Similarity:     35.6%         Conservative:    33
Best Local Similarity:  23.2%         Mismatches:      107
Query Match:            5.9%          Indels:          65
DB:                     7             Gaps:            13

US-10-821-670A-30 (1-329) x US-11-293-697-1946 (1-2534)

Qy         46 ValValLeuThrCysAsnThrProGlu---GluAspAspIleThrTrpThrSerAsp--- 63
              :::   |||   |||         :::   |||      :::   |||      |||
```

```
Db        298 CTGGCCCTGCAGTGTGAAGTCTCTGACCCCGAGGCCCATGTGGTGTGGCGCAAAGATGGC 357

Qy         64 ------------------GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIle 77

Db        358 GTGCAGCTGGGCCCCAGTGACAAGTATGACTTCCTGCACACGGCGGGCACGCGGGGGCTC 417

Qy         78 GlnValLysGluPheAla------AspAlaGlyGlnTyrThrCysHisLysGlyGlyGlu 95

Db        418 GTGGTGCATGACGTGAGCCCTGAAGACGCCGGCCTGTACACCTGCCACGTGGGCTCCGAG 477

Qy         96 ValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAsp 115

Db        478 GAG---ACCCGGGCCCGGGTCCGCGTGCACGATCTGCACGTGGGCATC------------ 522

Qy        116 IleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsn 135

Db        523 ------------ACCAAGAGGCTGAAGACAATGGAGGTGCTGGAAGGGGAA--------- 561

Qy        136 TyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThr 155

Db        562 ---AGCTGCAGCTTTGAGTGC------------------------------------- 579

Qy        156 ValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeu 175

Db        580 GTCCTGTCCCACGAGAGTGCCAGCGACCCGGCCATGTGGACAGTCGGTGGGAAGACAGTG 639

Qy        176 SerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGln 195

Db        640 GGCAGCTCCAGCCGCTTCCAGGCCACACGTCAGGGCCGAAAATACATCCTGGTGGTCCGG 699

Qy        196 GluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValValValAspAla 215

Db        700 GAGGCTGCACCAAGTGATGCCGGGGAG--------------------GTGGTCTTCTCT 738

Qy        216 IleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLys 235

Db        739 GTGCGGGGCCTCACCTCCAAG---------GCCTCACTCATTGTCAGA------------ 777

Qy        236 ProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluVal 255

Db        778 ---GAGAGGCCGGCCACCATC---ATCAAGCCCCTGGAA-------------------- 810

Qy        256 SerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGly 275

Db        811 --------------GACCAGTGGGTGGCGCCAGGGGAGGACGTGGAGCTGCGCTGTGAG 855

Qy        276 ValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThr 295

Db        856 CTGTCACGGGCGGGAACGCCCGTGCACTGGCTGAAGGACAGGAAGGCCATCCGCAAGAGC 915

Qy        296 SerAla---LysValValCys 301

Db        916 CAGAAGTATGATGTGGTCTGC 936
```

RESULT 8
US-10-505-928-651
; Sequence 651, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 651
; LENGTH: 3597
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-651

Alignment Scores:

Pred. No.:	0.481	Length:	3597
Score:	99.50	Matches:	56
Percent Similarity:	34.4%	Conservative:	28
Best Local Similarity:	23.0%	Mismatches:	72
Query Match:	5.7%	Indels:	89
DB:	6	Gaps:	11

US-10-821-670A-30 (1-329) x US-10-505-928-651 (1-3597)

```
Qy        135 AsnTyrSerGlyArgPheThrCysTrpTrpLeu-----------ThrAlaIleSerThr 150

Db        284 GACTACATGAGCATCTCTACTTGCGAGTGGAAGATGAATGGTCCCACCAATTGCAGCACC 343

Qy        151 AspLeuLysPheThrValLys--------------SerSerArgGlySerSerAspPro 165

Db        344 GAGCTCCGCCTGTTGTACCAGCTGGTTTTTCTGCTCTCCGAAGCCCACACGTGTATCCCT 403

Qy        166 Gln---------GlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182

Db        404 GAGAACAACGGAGGCGCGGGGTGCGTGTGCCACCTGCTCATGGATGACGTGGTCAGTGCG 463

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGlu-CysGlnGluGlySerAlaCysProAl 202

Db        464 GATAAC---------------TATACACTGGACCTGTGGGCTGGGCAGCAGCTGCTGTGG 508

Qy        202 aAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGl 222

Db        509 AAGGGCTCCTTCAAG-CCCAGCGAG-----------------CAT-------------- 535

Qy        222 uAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLe 242

Db        536 --------------------------------GTGAAACCCAGGGCCCCAGGAAACCT 561

Qy        242 uGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspTh 262

Db        562 GACAGTT--------------------CACACCAATGTCTCCGACACTCTGCTGCTGAC 600

Qy        262 rTrpSerThrProHisSer--------------TyrPheSerLeuThrPheGlyValGl 277

Db        601 CTGGAGCAACCCGTATCCCCCTGACAATTACCTGTATAATCATCTCACCTATGCAGTCAA 660

Qy        277 nValGlnGlyLysAsnAsn--------------------------------ArgGluLy 296

Db        661 CATTTGGAGTGAAAACGACCCGGCAGATTTCAGAATCTATAACGTGACCTACCTAGAACC 720

Qy        286 sLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHisLysAspAlaLy 306

Db        721 CTCCCTCCGCATCGCAGCCAGCACCCTGAAGTCTGGGATT-----------TCCTACAG 768

Qy        306 sIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAla----- 324

Db        769 GGCACGGGTGAGGGCCTGGGCTCAGTGCTATAACACCACCTGGAGTGAGTGGAGCCCCAG 828

Qy        325 ----------------------------------------------------------Se 325

Db        829 CACCAAGTGGCACAACTCCTACAGGGAGCCCTTCGAGCAGCACCTCCTGCTGGGCGTCAG 888

Qy        325 rValSerCys 328

Db        889 CGTTTCCTGC 898
```

RESULT 9
US-10-511-937-2802
; Sequence 2802, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc

```
;  APPLICANT:  Prentice, James
;  APPLICANT:  Morris, MacDonald
;  APPLICANT:  Rosenberg, Steven
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
;  TITLE OF INVENTION:  AND MONITORING TRANSPLANT REJECTION
;  FILE REFERENCE: 506612000104
;  CURRENT APPLICATION NUMBER: US/10/511,937
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: PCT/US2003/012946
;  PRIOR FILING DATE: 2003-04-24
;  PRIOR APPLICATION NUMBER: US 10/131,831
;  PRIOR FILING DATE: 2002-04-24
;  PRIOR APPLICATION NUMBER: US 10/325,899
;  PRIOR FILING DATE: 2002-12-20
;  NUMBER OF SEQ ID NOS: 3117
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2802
;   LENGTH: 3597
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-511-937-2802

Alignment Scores:
Pred. No.:                0.481          Length:          3597
Score:                    99.50          Matches:           56
Percent Similarity:       34.4%          Conservative:      28
Best Local Similarity:    23.0%          Mismatches:        72
Query Match:              5.7%           Indels:            89
DB:                       6              Gaps:              11

US-10-821-670A-30 (1-329) x US-10-511-937-2802 (1-3597)

Qy        135 AsnTyrSerGlyArgPheThrCysTrpTrpLeu------------ThrAlaIleSerThr 150
              :::|||                 ||||||  |||               |||      ||||||
Db        284 GACTACATGAGCATCTCTACTTGCGAGTGGAAGATGAATGGTCCCACCAATTGCAGCACC 343

Qy        151 AspLeuLysPheThrValLys---------------SerSerArgGlySerSerAspPro 165
              :::|||:::       :::                |||         :::      |||
Db        344 GAGCTCCGCCTGTTGTACCAGCTGGTTTTTCTGCTCTCCGAAGCCCACACGTGTATCCCT 403

Qy        166 Gln---------GlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 182
              :::         |||      |||             |||      :::   |||
Db        404 GAGAACAACGGAGGCGCGGGGTGCGTGTGCCACCTGCTCATGGATGACGTGGTCAGTGCG 463

Qy        183 AspAsnArgAspTyrLysLysTyrThrValGlu-CysGlnGluGlySerAlaCysProAl 202
              ||||||               ||||||:::::: |||      ||||||:::|||
Db        464 GATAAC--------------TATACACTGGACCTGTGGGCTGGGCAGCAGCTGCTGTGG 508

Qy        202 aAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGl 222
                  |||   |||   |||                 |||
Db        509 AAGGGCTCCTTCAAG-CCCAGCGAG----------------CAT-------------- 535

Qy        222 uAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLe 242
                                          :::||||||      |||   |||||
Db        536 ---------------------------------GTGAAACCCAGGGCCCCAGGAAACCT 561

Qy        242 uGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspTh 262
              |   :::                 |||      ||||||                ||
Db        562 GACAGTT-----------------CACACCAATGTCTCCGACACTCTGCTGCTGAC 600

Qy        262 rTrpSerThrProHisSer--------------TyrPheSerLeuThrPheGlyValGl 277
              |||||||   |||:::               |||      ||||||:::   |||
Db        601 CTGGAGCAACCCGTATCCCCCTGACAATTACCTGTATAATCATCTCACCTATGCAGTCAA 660

Qy        277 nValGlnGlyLysAsnAsn--------------------------------ArgGluLy 286
               :::      :::|||:::                                  |||
Db        661 CATTTGGAGTGAAAACGACCCGGCAGATTTCAGAATCTATAACGTGACCTACCTAGAACC 720

Qy        286 sLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHisLysAspAlaLy 306
                  |||::::::                :::  :::                    ::
Db        721 CTCCCTCCGCATCGCAGCCAGCACCCTGAAGTCTGGGATT-----------TCCTACAG 768

Qy        306 sIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAla----- 324
```

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              :   ||||||:::|||      :::   |||:::::::::||||||   |||:::
Db        769 GGCACGGGTGAGGGCCTGGGCTCAGTGCTATAACACCACCTGGAGTGAGTGGAGCCCCAG 828

Qy        325 ----------------------------------------------------------Se 325
                                                                         ||
Db        829 CACCAAGTGGCACAACTCCTACAGGGAGCCCTTCGAGCAGCACCTCCTGCTGGGCGTCAG 888

Qy        325 rValSerCys 328
              ||||||||||
Db        889 CGTTTCCTGC 898

RESULT 10
US-11-313-450-1
; Sequence 1, Application US/11313450
; Publication No. US20060110778A1
; GENERAL INFORMATION:
;  APPLICANT: Adorante, Joeseph S.
;  APPLICANT:  Ehring, George R.
;  TITLE OF INVENTION: High-Throughput Screens For Identifying
;  TITLE OF INVENTION:  Selective Persistent Sodium Channels Channel Blockers
;  FILE REFERENCE: 17407 CIP (AP)
;  CURRENT APPLICATION NUMBER: US/11/313,450
;  CURRENT FILING DATE:  2005-12-19
;  PRIOR APPLICATION NUMBER: 09/989797
;  PRIOR FILING DATE: 2001-11-20
;  PRIOR APPLICATION NUMBER: 60/252771
;  PRIOR FILING DATE: 2000-11-22
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 5997
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-313-450-1

Alignment Scores:
Pred. No.:                1.15           Length:          5997
Score:                    99.00          Matches:           46
Percent Similarity:       35.2%          Conservative:      22
Best Local Similarity:    23.8%          Mismatches:        88
Query Match:              5.6%           Indels:            37
DB:                       7              Gaps:              6

US-10-821-670A-30 (1-329) x US-11-313-450-1 (1-5997)

Qy         36 AspTrpHisProAspAlaProGlyGluMet-ValValLeuThrCysAsnThrProGluGl 55
              ||||||  |||      |||      ::: :::  |||      ::::::
Db       2898 GATTGGAAACCTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTCTGAGCTCATTTAGTGC 2957

Qy         55 uAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLe 75
               |||::::::      |||   |||   :::                          ||
Db       2958 AGACAACCTTGCAGCCACTGATGATGATAATGAAATG---------------AATAATCT 3002

Qy         75 uThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGl 95
              |   |||   |||                                |||      |||   ||
Db       3003 CCAAATTGCTGTGGATAGGATGCACAAAGGAGTAGCTTATGTGAAAAGAAAAATATATGA 3062

Qy         95 uValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAs 115
              |   :::      ||||||:::         |||      |||   |||      ||
Db       3063 ATTTATTCAACAGTCCTTCATTAGGAAACAAAAGATTTTAGATGAAATTAAACCACTTGA 3122

Qy        115 pIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAs 135
              |   |||      :::|||:::|||                        |||   :::   ::
Db       3123 TGATCTAAACAACAAGAAAGACAGT--------------------TGTATGTCCAATCA 3161

Qy        135 nTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheTh 155
              :                                |||   |||      ||||||   :::
Db       3162 T-------------------------ACAACAGAAATTGGGAAAGATCTTGACTATCT 3194

Qy        155 rValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThr-- 174
                                         |||      |||   |||   |||      |||
Db       3195 T--------------------AAAGATGTAAATGGAACTACAAGTGGTATAGGAACTGG 3233
```

```
Qy        175 -LeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrValGluCy 194
Db       3234 CAGCAGTGTTGAAAAATACATTATTGATGAAAGTGATTACATGTCATTCATAAACAAC-- 3291

Qy        194 sGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValValValAs 214
Db       3292 ------------------CCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGAGAATC 3332

Qy        214 pAlaIleHisLysLeuLysTyrGluAsnTyrThrSer 226
Db       3333 TGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGT 3369

RESULT 11
US-11-263-326-90
; Sequence 90, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
;  APPLICANT: Wallace, Robyn H
;  APPLICANT:  Mulley, John C
;  APPLICANT:  Berkovic, Samuel F
;  TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
;  FILE REFERENCE: 1386/13/3
;  CURRENT APPLICATION NUMBER: US/11/263,326
;  CURRENT FILING DATE:  2005-10-31
;  PRIOR APPLICATION NUMBER: US 10/482,834
;  PRIOR FILING DATE: 2004-10-12
;  PRIOR APPLICATION NUMBER: PCT/AU2004/001051
;  PRIOR FILING DATE: 2004-08-06
;  PRIOR APPLICATION NUMBER: US 10/451,126
;  PRIOR FILING DATE: 2003-10-08
;  NUMBER OF SEQ ID NOS: 179
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 90
;   LENGTH: 8370
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-263-326-90

Alignment Scores:
Pred. No.:              1.86          Length:         8370
Score:                  99.00         Matches:        46
Percent Similarity:     35.2%         Conservative:   22
Best Local Similarity:  23.8%         Mismatches:     88
Query Match:            5.6%          Indels:         37
DB:                     7             Gaps:           6

US-10-821-670A-30 (1-329) x US-11-263-326-90 (1-8370)

Qy         36 AspTrpHisProAspAlaProGlyGluMet-ValValLeuThrCysAsnThrProGluGl 55
Db       3186 GATTGGAAACCTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTCTGAGCTCATTTAGTGC 3245

Qy         55 uAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLe 75
Db       3246 AGACAACCTTGCAGCCACTGATGATGATAATGAAATG--------------AATAATCT 3290

Qy         75 uThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGl 95
Db       3291 CCAAATTGCTGTGGATAGGATGCACAAAGGAGTAGCTTATGTGAAAAGAAAAATATATGA 3350

Qy         95 uValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAs 115
Db       3351 ATTTATTCAACAGTCCTTCATTAGGAAACAAAAGATTTTAGATGAAATTAAACCACTTGA 3410

Qy        115 pIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAs 135
Db       3411 TGATCTAAACAACAAGAAAGACAGT--------------------TGTATGTCCAATCA 3449

Qy        135 nTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheTh 155
Db       3450 T--------------------------ACAACAGAAATTGGGAAAGATCTTGACTATCT 3482

Qy        155 rValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThr-- 174
Db       3483 T--------------------AAAGATGTAAATGGAACTACAAGTGGTATAGGAACTGG 3521

Qy        175 -LeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrValGluCy 194
Db       3522 CAGCAGTGTTGAAAAATACATTATTGATGAAAGTGATTACATGTCATTCATAAACAAC-- 3579

Qy        194 sGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValValValAs 214
Db       3580 ------------------CCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGAGAATC 3620

Qy        214 pAlaIleHisLysLeuLysTyrGluAsnTyrThrSer 226
Db       3621 TGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGT 3657

RESULT 12
US-11-263-326-95
; Sequence 95, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
;  APPLICANT: Wallace, Robyn H
;  APPLICANT:  Mulley, John C
;  APPLICANT:  Berkovic, Samuel F
;  TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
;  FILE REFERENCE: 1386/13/3
;  CURRENT APPLICATION NUMBER: US/11/263,326
;  CURRENT FILING DATE:  2005-10-31
;  PRIOR APPLICATION NUMBER: US 10/482,834
;  PRIOR FILING DATE: 2004-10-12
;  PRIOR APPLICATION NUMBER: PCT/AU2004/001051
;  PRIOR FILING DATE: 2004-08-06
;  PRIOR APPLICATION NUMBER: US 10/451,126
;  PRIOR FILING DATE: 2003-10-08
;  NUMBER OF SEQ ID NOS: 179
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 95
;   LENGTH: 8377
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-263-326-95

Alignment Scores:
Pred. No.:              1.86          Length:         8377
Score:                  99.00         Matches:        46
Percent Similarity:     35.2%         Conservative:   22
Best Local Similarity:  23.8%         Mismatches:     88
Query Match:            5.6%          Indels:         37
DB:                     7             Gaps:           6

US-10-821-670A-30 (1-329) x US-11-263-326-95 (1-8377)

Qy         36 AspTrpHisProAspAlaProGlyGluMet-ValValLeuThrCysAsnThrProGluGl 55
Db       3197 GATTGGAAACCTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTCTGAGCTCATTTAGTGC 3256

Qy         55 uAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLe 75
Db       3257 AGACAACCTTGCAGCCACTGATGATGATAATGAAATG--------------AATAATCT 3301

Qy         75 uThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGl 95
Db       3302 CCAAATTGCTGTGGATAGGATGCACAAAGGAGTAGCTTATGTGAAAAGAAAAATATATGA 3361

Qy         95 uValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAs 115
Db       3362 ATTTATTCAACAGTCCTTCATTAGGAAACAAAAGATTTTAGATGAAATTAAACCACTTGA 3421

Qy        115 pIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAs 135
Db       3422 TGATCTAAACAACAAGAAAGACAGT--------------------TGTATGTCCAATCA 3460

Qy        135 nTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheTh 155
```

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Db       3461 T-------------------------ACAACAGAAATTGGGAAAGATCTTGACTATCT 3493

Qy        155 rValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThr-- 174

Db       3494 T--------------------AAAGATGTAAATGGAACTACAAGTGGTATAGGAACTGG 3532

Qy        175 -LeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrValGluCy 194

Db       3533 CAGCAGTGTTGAAAAATACATTATTGATGAAAGTGATTACATGTCATTCATAAACAAC-- 3590

Qy        194 sGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValValValAs 214

Db       3591 -------------------CCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGAGAATC 3631

Qy        214 pAlaIleHisLysLeuLysTyrGluAsnTyrThrSer 226

Db       3632 TGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGT 3668

RESULT 13
US-11-263-326-89
; Sequence 89, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
;  APPLICANT: Wallace, Robyn H
;  APPLICANT:  Mulley, John C
;  APPLICANT:  Berkovic, Samuel F
;  TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
;  FILE REFERENCE: 1386/13/3
;  CURRENT APPLICATION NUMBER: US/11/263,326
;  CURRENT FILING DATE:  2005-10-31
;  PRIOR APPLICATION NUMBER: US 10/482,834
;  PRIOR FILING DATE: 2004-10-12
;  PRIOR APPLICATION NUMBER: PCT/AU2004/001051
;  PRIOR FILING DATE: 2004-08-06
;  PRIOR APPLICATION NUMBER: US 10/451,126
;  PRIOR FILING DATE: 2003-10-08
;  NUMBER OF SEQ ID NOS: 179
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 89
;   LENGTH: 8380
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-263-326-89

Alignment Scores:
Pred. No.:              1.87          Length:         8380
Score:                  99.00         Matches:        46
Percent Similarity:     35.2%         Conservative:   22
Best Local Similarity:  23.8%         Mismatches:     88
Query Match:            5.6%          Indels:         37
DB:                     7             Gaps:           6

US-10-821-670A-30 (1-329) x US-11-263-326-89 (1-8380)

Qy          36 AspTrpHisProAspAlaProGlyGluMet-ValValLeuThrCysAsnThrProGluGl 55

Db        3196 GATTGGAAACCTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTCTGAGCTCATTTAGTGC 3255

Qy          55 uAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLe 75

Db        3256 AGACAACCTTGCAGCCACTGATGATGATAATGAAATG--------------AATAATCT 3300

Qy          75 uThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGl 95

Db        3301 CCAAATTGCTGTGGATAGGATGCACAAAGGAGTAGCTTATGTGAAAAGAAAAATATATGA 3360

Qy          95 uValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAs 115

Db        3361 ATTTATTCAACAGTCCTTCATTAGGAAACAAAAGATTTTAGATGAAATTAAACCACTTGA 3420

Qy         115 pIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAs 135

Db        3421 TGATCTAAACAACAAGAAAGACAGT--------------------TGTATGTCCAATCA 3459
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Qy         135 nTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheTh 155

Db        3460 T-------------------------ACAACAGAAATTGGGAAAGATCTTGACTATCT 3492

Qy         155 rValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThr-- 174

Db        3493 T--------------------AAAGATGTAAATGGAACTACAAGTGGTATAGGAACTGG 3531

Qy         175 -LeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrValGluCy 194

Db        3532 CAGCAGTGTTGAAAAATACATTATTGATGAAAGTGATTACATGTCATTCATAAACAAC-- 3589

Qy         194 sGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValValValAs 214

Db        3590 -------------------CCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGAGAATC 3630

Qy         214 pAlaIleHisLysLeuLysTyrGluAsnTyrThrSer 226

Db        3631 TGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGT 3667

RESULT 14
US-11-263-326-1
; Sequence 1, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
;  APPLICANT: Wallace, Robyn H
;  APPLICANT:  Mulley, John C
;  APPLICANT:  Berkovic, Samuel F
;  TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
;  FILE REFERENCE: 1386/13/3
;  CURRENT APPLICATION NUMBER: US/11/263,326
;  CURRENT FILING DATE:  2005-10-31
;  PRIOR APPLICATION NUMBER: US 10/482,834
;  PRIOR FILING DATE: 2004-10-12
;  PRIOR APPLICATION NUMBER: PCT/AU2004/001051
;  PRIOR FILING DATE: 2004-08-06
;  PRIOR APPLICATION NUMBER: US 10/451,126
;  PRIOR FILING DATE: 2003-10-08
;  NUMBER OF SEQ ID NOS: 179
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
;   LENGTH: 8381
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-263-326-1

Alignment Scores:
Pred. No.:              1.87          Length:         8381
Score:                  99.00         Matches:        46
Percent Similarity:     35.2%         Conservative:   22
Best Local Similarity:  23.8%         Mismatches:     88
Query Match:            5.6%          Indels:         37
DB:                     7             Gaps:           6

US-10-821-670A-30 (1-329) x US-11-263-326-1 (1-8381)

Qy          36 AspTrpHisProAspAlaProGlyGluMet-ValValLeuThrCysAsnThrProGluGl 55

Db        3197 GATTGGAAACCTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTCTGAGCTCATTTAGTGC 3256

Qy          55 uAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLe 75

Db        3257 AGACAACCTTGCAGCCACTGATGATGATAATGAAATG--------------AATAATCT 3301

Qy          75 uThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGl 95

Db        3302 CCAAATTGCTGTGGATAGGATGCACAAAGGAGTAGCTTATGTGAAAAGAAAAATATATGA 3361

Qy          95 uValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAs 115

Db        3362 ATTTATTCAACAGTCCTTCATTAGGAAACAAAAGATTTTAGATGAAATTAAACCACTTGA 3421
```

```
Qy        115 pIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAs 135
              |   |||      :::|||:::|||                   |||   :::   ::
Db       3422 TGATCTAAACAACAAGAAAGACAGT-------------------TGTATGTCCAATCA 3460

Qy        135 nTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheTh 155
              :                                 |||   |||     ||||||   :::
Db       3461 T-------------------------ACAACAGAAATTGGGAAAGATCTTGACTATCT 3493

Qy        155 rValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThr-- 174
                                       |||     |||   |||   |||     |||
Db       3494 T--------------------AAAGATGTAAATGGAACTACAAGTGGTATAGGAACTGG 3532

Qy        175 -LeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrValGluCy 194
               |||   ||||||     :::|||     ||||||     :::
Db       3533 CAGCAGTGTTGAAAAATACATTATTGATGAAAGTGATTACATGTCATTCATAAACAAC-- 3590

Qy        194 sGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValValValAs 214
                                 |||:::       ::::::||||||   |||
Db       3591 -------------------CCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGAGAATC 3631

Qy        214 pAlaIleHisLysLeuLysTyrGluAsnTyrThrSer 226
                        |||     |||:::::::::|||
Db       3632 TGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGT 3668
```

RESULT 15
US-11-263-326-3
; Sequence 3, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulley, John C
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT APPLICATION NUMBER: US/11/263,326
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US 10/482,834
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 8381
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-263-326-3

Alignment Scores:

Pred. No.:	1.87	Length:	8381
Score:	99.00	Matches:	46
Percent Similarity:	35.2%	Conservative:	22
Best Local Similarity:	23.8%	Mismatches:	88
Query Match:	5.6%	Indels:	37
DB:	7	Gaps:	6

US-10-821-670A-30 (1-329) x US-11-263-326-3 (1-8381)

```
Qy         36 AspTrpHisProAspAlaProGlyGluMet-ValValLeuThrCysAsnThrProGluGl 55
              ||||||   |||      |||      ::: :::   |||      ::::::
Db       3197 GATTGGAAACCTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTCTGAGCTCATTTAGTGC 3256

Qy         55 uAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLe 75
               |||::::::      |||   |||   :::                          ||
Db       3257 AGACAACCTTGCAGCCACTGATGATGATAATGAAATG--------------AATAATCT 3301

Qy         75 uThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGl 95
              |   |||   |||                        |||         |||      ||
Db       3302 CCAAATTGCTGTGGATAGGATGCACAAAGGAGTAGCTTATGTGAAAAGAAAAATATATGA 3361

Qy         95 uValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAs 115
```

```
              |   :::      ||||||:::         |||      |||   |||         ||
Db       3362 ATTTATTCAACAGTCCTTCATTAGGAAACAAAAGATTTTAGATGAAATTAAACCACTTGA 3421

Qy         115 pIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAs 135
               |   |||      :::|||:::|||                   |||   :::   ::
Db       3422 TGATCTAAACAACAAGAAAGACAGT-------------------TGTATGTCCAATCA 3460

Qy         135 nTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheTh 155
               :                                 |||   |||     ||||||   :::
Db       3461 T-------------------------ACAACAGAAATTGGGAAAGATCTTGACTATCT 3493

Qy         155 rValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThr-- 174
                                        |||     |||   |||   |||     |||
Db       3494 T--------------------AAAGATGTAAATGGAACTACAAGTGGTATAGGAACTGG 3532

Qy         175 -LeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrValGluCy 194
                |||   ||||||     :::|||     ||||||     :::
Db       3533 CAGCAGTGTTGAAAAATACATTATTGATGAAAGTGATTACATGTCATTCATAAACAAC-- 3590

Qy         194 sGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValValValAs 214
                                  |||:::       ::::::||||||   |||
Db       3591 -------------------CCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGAGAATC 3631

Qy         214 pAlaIleHisLysLeuLysTyrGluAsnTyrThrSer 226
                         |||     |||:::::::::|||
Db       3632 TGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGT 3668
```

Search completed: June 10, 2006, 01:22:35
Job time : 34.1171 secs

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OM nucleic - nucleic search, using sw model

Run on: June 10, 2006, 03:13:25 ; Search time 3793.55 Seconds
(without alignments)
15525.205 Million cell updates/sec

Title: US-10-821-670A-26
Perfect score: 921
Sequence: 1 atatgggaactggagaaaaa.....gggcatccgtgtcctgcagt 921

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
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8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	921	100.0	921	2	AR595948	AR595948 Sequence
c 2	921	100.0	921	2	AR595949	AR595949 Sequence
3	921	100.0	1006	14	FCIL12P40	Y07762 Felis catus
4	921	100.0	1533	2	AR595959	AR595959 Sequence
c 5	921	100.0	1533	2	AR595960	AR595960 Sequence
6	921	100.0	1599	2	AR595956	AR595956 Sequence
c 7	921	100.0	1599	2	AR595957	AR595957 Sequence
8	919.4	99.8	921	2	AR242436	AR242436 Sequence
9	919.4	99.8	921	2	AR280204	AR280204 Sequence
10	919.4	99.8	921	2	AR322419	AR322419 Sequence
11	919.4	99.8	987	2	AR595950	AR595950 Sequence
c 12	919.4	99.8	987	2	AR595951	AR595951 Sequence
13	919.4	99.8	2193	2	AR242435	AR242435 Sequence
14	919.4	99.8	2193	2	AR280203	AR280203 Sequence
15	919.4	99.8	2193	2	AR322418	AR322418 Sequence
16	917.8	99.7	921	2	AR242437	AR242437 Sequence
17	917.8	99.7	921	2	AR280205	AR280205 Sequence
18	917.8	99.7	921	2	AR322420	AR322420 Sequence
19	917.4	99.6	985	2	AR595967	AR595967 Sequence
c 20	917.4	99.6	985	2	AR595968	AR595968 Sequence
21	916.2	99.5	990	2	AX076200	AX076200 Sequence
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23	916.2	99.5	4522	2	AX076209	AX076209 Sequence
24	916.2	99.5	4522	2	AX076476	AX076476 Sequence
25	913	99.1	990	14	FCU83184	U83184 Felis catus
26	825	89.6	921	2	AR595965	AR595965 Sequence
c 27	825	89.6	921	2	AR595966	AR595966 Sequence
28	825	89.6	990	2	AR151071	AR151071 Sequence
29	825	89.6	990	2	BD014663	BD014663 Process f
30	825	89.6	990	2	E15017	E15017 Canine mRNA
31	825	89.6	990	2	AR316470	AR316470 Sequence
32	825	89.6	1015	14	CFU49100	U49100 Canis famil
33	825	89.6	2267	2	AR596011	AR596011 Sequence
c 34	825	89.6	2267	2	AR596012	AR596012 Sequence
35	823.4	89.4	987	2	AR595969	AR595969 Sequence
c 36	823.4	89.4	987	2	AR595970	AR595970 Sequence
37	823.4	89.4	1533	2	AR595973	AR595973 Sequence
c 38	823.4	89.4	1533	2	AR595974	AR595974 Sequence
39	823.4	89.4	1599	2	AR595971	AR595971 Sequence
c 40	823.4	89.4	1599	2	AR595972	AR595972 Sequence
41	821.8	89.2	990	2	BD014653	BD014653 Process f
42	818.6	88.9	990	2	AR151061	AR151061 Sequence
43	818.6	88.9	990	2	AR316460	AR316460 Sequence
44	804	87.3	924	2	BD171282	BD171282 Novel can
45	804	87.3	2154	2	BD171281	BD171281 Novel can

ALIGNMENTS

RESULT 1
AR595948
LOCUS AR595948 921 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 26 from patent US 6818444.
ACCESSION AR595948
VERSION AR595948.1 GI:56646929
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 921)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 26 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .921
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 100.0%; Score 921; DB 2; Length 921;
Best Local Similarity 100.0%; Pred. No. 3.1e-265;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
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Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
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Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
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Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Qy        661 CAACTGAAGCCATTAAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
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Db        661 CAACTGAAGCCATTAAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
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Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
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Db        901 TGGGCATCCGTGTCCTGCAGT 921
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RESULT 2
AR595949/c
LOCUS       AR595949                921 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 28 from patent US 6818444.
ACCESSION   AR595949
VERSION     AR595949.1  GI:56646930
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS.  Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 28 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
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ORIGIN

  Query Match           100.0%;  Score 921;  DB 2;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-265;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
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Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
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Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
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Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

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Qy        661 CAACTGAAGCCATTAAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
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Db        261 CAACTGAAGCCATTAAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
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Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
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Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
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Db         21 TGGGCATCCGTGTCCTGCAGT 1
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RESULT 3
FCIL12P40
LOCUS       FCIL12P40               1006 bp    mRNA    linear   MAM 18-APR-2005
DEFINITION  Felis catus mRNA for interleukin-12 p40 chain.
ACCESSION   Y07762
VERSION     Y07762.1  GI:2102664
KEYWORDS    interleukin-12 p40.
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SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1
  AUTHORS   Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
  TITLE     Molecular cloning of cat interleukin-12
  JOURNAL   Immunogenetics 45 (6), 462-463 (1997)
   PUBMED   9089110
REFERENCE   2  (bases 1 to 1006)
  AUTHORS   Schijns,V.E.C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
            Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
            Utrecht, NETHERLANDS
FEATURES             Location/Qualifiers
     source          1. .1006
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                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
                     /cell_type="lymphocyte"
                     /tissue_type="peripheral blood"
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ORIGIN

  Query Match           100.0%;  Score 921;  DB 14;  Length 1006;
  Best Local Similarity  100.0%;  Pred. No. 3.1e-265;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

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Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
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Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
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Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
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Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
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Qy        901 TGGGCATCCGTGTCCTGCAGT 921
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Db        967 TGGGCATCCGTGTCCTGCAGT 987


RESULT 4
AR595959
LOCUS       AR595959               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 43 from patent US 6818444.
ACCESSION   AR595959
VERSION     AR595959.1  GI:56646940
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 43 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
ORIGIN

  Query Match           100.0%;  Score 921;  DB 2;  Length 1533;
  Best Local Similarity  100.0%;  Pred. No. 3.5e-265;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Db         121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Qy         361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
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Db         361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy         421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Db         601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy         661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
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Qy         781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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Db         781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy         841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy         901 TGGGCATCCGTGTCCTGCAGT 921
                |||||||||||||||||||||
Db         901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 5
AR595960/c
LOCUS       AR595960               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 45 from patent US 6818444.
ACCESSION   AR595960
VERSION     AR595960.1  GI:56646941
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 45 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           100.0%;  Score 921;  DB 2;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-265;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy          61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy         301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy         361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy         421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy         481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy         541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy         601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy         661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy         721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy         781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy         841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy         901 TGGGCATCCGTGTCCTGCAGT 921
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Db        633 TGGGCATCCGTGTCCTGCAGT 613


RESULT 6
AR595956
LOCUS       AR595956               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 38 from patent US 6818444.
ACCESSION   AR595956
VERSION     AR595956.1  GI:56646937
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 38 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           100.0%;  Score 921;  DB 2;  Length 1599;
  Best Local Similarity  100.0%;  Pred. No. 3.5e-265;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              ||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987


RESULT 7
AR595957/c
LOCUS       AR595957               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 40 from patent US 6818444.
ACCESSION   AR595957
VERSION     AR595957.1  GI:56646938
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 40 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           100.0%;  Score 921;  DB 2;  Length 1599;
  Best Local Similarity  100.0%;  Pred. No. 3.5e-265;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114
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Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
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Db        633 TGGGCATCCGTGTCCTGCAGT 613
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RESULT 8
AR242436
LOCUS       AR242436                921 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 6 from patent US 6472509.
ACCESSION   AR242436
VERSION     AR242436.1  GI:27288853
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 6 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
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ORIGIN

  Query Match           99.8%;  Score 919.4;  DB 2;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 9.3e-265;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
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Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
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Db        901 TGGGCATCCGTGTCCTGCAGT 921
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RESULT 9
AR280204
LOCUS       AR280204                921 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 6 from patent US 6518045.
ACCESSION   AR280204
VERSION     AR280204.1  GI:29715594
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 6 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
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            EPX;
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
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ORIGIN

  Query Match           99.8%;  Score 919.4;  DB 2;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 9.3e-265;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 10
AR322419
LOCUS       AR322419                921 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 6 from patent US 6566097.
ACCESSION   AR322419
VERSION     AR322419.1  GI:33708172
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 6 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match           99.8%;  Score 919.4;  DB 2;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 9.3e-265;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 11
AR595950
LOCUS       AR595950                 987 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 29 from patent US 6818444.
ACCESSION   AR595950
VERSION     AR595950.1  GI:56646931
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 29 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           99.8%;  Score 919.4;  DB 2;  Length 987;
  Best Local Similarity   99.9%;  Pred. No. 9.4e-265;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987


RESULT 12
AR595951/c
LOCUS       AR595951                 987 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 31 from patent US 6818444.
ACCESSION   AR595951
VERSION     AR595951.1  GI:56646932
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 31 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           99.8%;  Score 919.4;  DB 2;  Length 987;
  Best Local Similarity   99.9%;  Pred. No. 9.4e-265;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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RESULT 14
AR280203
LOCUS       AR280203               2193 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 5 from patent US 6518045.
ACCESSION   AR280203
VERSION     AR280203.1  GI:29715593
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2193)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 5 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .2193
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match           99.8%;  Score 919.4;  DB 2;  Length 2193;
  Best Local Similarity   99.9%;  Pred. No. 1.1e-264;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 189

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 249

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 309

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 369

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 429

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 489

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 549

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 609

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 669

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 729

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 789

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 849

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 909

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 969

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 1029

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db       1030 TGGGCATCCGTGTCCTGCAGT 1050


RESULT 15
AR322418
LOCUS       AR322418               2193 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 5 from patent US 6566097.
ACCESSION   AR322418
VERSION     AR322418.1  GI:33708171
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2193)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 5 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .2193
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match           99.8%;  Score 919.4;  DB 2;  Length 2193;
  Best Local Similarity   99.9%;  Pred. No. 1.1e-264;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 189

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 249

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 309

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 369

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 429

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 489

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          490 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 549

Qy          421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
                |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db          550 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 609

Qy          481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          610 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 669

Qy          541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          670 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 729

Qy          601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          730 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 789

Qy          661 CAACTGAAGCCATTAAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          790 CAACTGAAGCCATTAAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 849

Qy          721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          850 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 909

Qy          781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          910 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 969

Qy          841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          970 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 1029

Qy          901 TGGGCATCCGTGTCCTGCAGT 921
                |||||||||||||||||||||
Db         1030 TGGGCATCCGTGTCCTGCAGT 1050
```

Search completed: June 10, 2006, 15:46:21
Job time : 3795.55 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 10, 2006, 03:13:22 ; Search time 680.349 Seconds
(without alignments)
9438.451 Million cell updates/sec

Title: US-10-821-670A-26
Perfect score: 921
Sequence: 1 atatgggaactggagaaaaa.....gggcatccgtgtcctgcagt 921

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	921	100.0	921	6	ABK98942	Abk98942 Feline in
c 2	921	100.0	921	6	ABK98943	Abk98943 Feline in
c 3	921	100.0	921	14	ADV34681	Adv34681 Feline si
4	921	100.0	921	14	ADV34679	Adv34679 Feline si
c 5	921	100.0	1533	6	ABK98954	Abk98954 Feline in
6	921	100.0	1533	6	ABK98953	Abk98953 Feline in
c 7	921	100.0	1533	14	ADV34697	Adv34697 Feline si
8	921	100.0	1533	14	ADV34695	Adv34695 Feline si
9	921	100.0	1599	6	ABK98950	Abk98950 Feline in
c 10	921	100.0	1599	6	ABK98951	Abk98951 Feline in
11	921	100.0	1599	14	ADV34691	Adv34691 Feline si
c 12	921	100.0	1599	14	ADV34693	Adv34693 Feline si
13	919.4	99.8	921	2	AAV56626	Aav56626 Feline FL
14	919.4	99.8	987	6	ABK98944	Abk98944 Feline in
c 15	919.4	99.8	987	6	ABK98945	Abk98945 Feline in
16	919.4	99.8	987	14	ADV34682	Adv34682 Feline si
c 17	919.4	99.8	987	14	ADV34684	Adv34684 Feline si
18	919.4	99.8	2193	2	AAV56625	Aav56625 Feline FL
19	917.8	99.7	921	2	AAV56627	Aav56627 Feline FL
c 20	917.4	99.6	985	6	ABK98962	Abk98962 Feline in
21	917.4	99.6	985	6	ABK98961	Abk98961 Feline in
22	917.4	99.6	985	14	ADV34707	Adv34707 Feline N-
c 23	917.4	99.6	985	14	ADV34709	Adv34709 Feline N-
24	916.2	99.5	990	4	AAF26082	Aaf26082 Feline IL
25	916.2	99.5	990	4	AAF26085	Aaf26085 Feline IL
26	916.2	99.5	4522	4	AAF26076	Aaf26076 Feline IL
27	916.2	99.5	4522	4	AAF26094	Aaf26094 Plasmid p
28	825	89.6	921	6	ABK98959	Abk98959 Canine in
c 29	825	89.6	921	6	ABK98960	Abk98960 Canine in
c 30	825	89.6	921	14	ADV34706	Adv34706 Canine si
31	825	89.6	921	14	ADV34704	Adv34704 Canine si
32	825	89.6	990	2	AAV13817	Aav13817 Canine IL
33	825	89.6	990	2	AAX03162	Aax03162 Nucleic a
34	825	89.6	990	2	AAX35625	Aax35625 Nucleic a
35	825	89.6	990	4	AAI64388	Aai64388 Canine co
36	825	89.6	1015	13	ADT04849	Adt04849 Canine in
c 37	825	89.6	2267	6	ABK99006	Abk99006 Canine in
38	825	89.6	2267	6	ABK99005	Abk99005 Canine in
39	825	89.6	2267	14	ADV34757	Adv34757 Canine si
c 40	825	89.6	2267	14	ADV34759	Adv34759 Canine si
41	823.4	89.4	987	6	ABK98963	Abk98963 Canine in
c 42	823.4	89.4	987	6	ABK98964	Abk98964 Canine in
c 43	823.4	89.4	987	14	ADV34712	Adv34712 Canine si
44	823.4	89.4	987	14	ADV34710	Adv34710 Canine si
45	823.4	89.4	1533	6	ABK98967	Abk98967 Canine in

ALIGNMENTS

RESULT 1
ABK98942
ID ABK98942 standard; cDNA; 921 BP.
XX
AC ABK98942;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p40-921 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69302.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 1; Page 49-50; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain

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CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 921 BP; 277 A; 227 C; 230 G; 187 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 921;  DB 6;  Length 921;
  Best Local Similarity  100.0%;  Pred. No. 9.6e-275;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 2
ABK98943/c
ID   ABK98943 standard; cDNA; 921 BP.
XX
AC   ABK98943;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p40-921 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Disclosure; Page 51; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 921 BP; 187 A; 230 C; 227 G; 277 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 921;  DB 6;  Length 921;
  Best Local Similarity  100.0%;  Pred. No. 9.6e-275;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802
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Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCAGT 1
```

RESULT 3
ADV34681/c
ID ADV34681 standard; DNA; 921 BP.
XX
AC ADV34681;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain mature IL-12p40 complementary DNA, nFeIL-12p40 921.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Felis catus.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 3; SEQ ID NO 28; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain mature IL-12p40 subunit
CC complementary DNA.
XX
SQ Sequence 921 BP; 187 A; 230 C; 227 G; 277 T; 0 U; 0 Other;

Query Match 100.0%; Score 921; DB 14; Length 921;
Best Local Similarity 100.0%; Pred. No. 9.6e-275;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382
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Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCAGT 1
```

RESULT 4
ADV34679
ID ADV34679 standard; cDNA; 921 BP.
XX
AC ADV34679;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain mature IL-12p40 protein cDNA, nFeIL-12p40 921.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; gene; ss.
XX
OS Felis catus.
XX
FH Key   Location/Qualifiers
FT CDS   1. .921
FT   /*tag= a
FT   /product= "PFeIL-12p40 307 protein"
FT   /partial
FT   /note= "No start and stop codon"
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
DR P-PSDB; ADV34680.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Claim 23; SEQ ID NO 26; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain mature IL-12p40 subunit
CC protein encoding cDNA.
XX
SQ Sequence 921 BP; 277 A; 227 C; 230 G; 187 T; 0 U; 0 Other;

Query Match 100.0%; Score 921; DB 14; Length 921;
Best Local Similarity 100.0%; Pred. No. 9.6e-275;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 5
ABK98954/c
ID   ABK98954 standard; cDNA; 1533 BP.
XX
AC   ABK98954;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1533 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 66-67; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 921;  DB 6;  Length 1533;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-274;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613


RESULT 6
ABK98953
ID   ABK98953 standard; cDNA; 1533 BP.
XX
AC   ABK98953;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1533 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
```

PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69307.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 63-64; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

Query Match 100.0%; Score 921; DB 6; Length 1533;
Best Local Similarity 100.0%; Pred. No. 1.3e-274;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921
```

RESULT 7
ADV34697/c
ID ADV34697 standard; DNA; 1533 BP.
XX
AC ADV34697;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain IL-12 complementary DNA, nFeIL-12 1533.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Felis catus.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 3; SEQ ID NO 45; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic

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CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 complementary DNA.
XX
SQ   Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 921;  DB 14;  Length 1533;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-274;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613


RESULT 8
ADV34695
ID   ADV34695 standard; cDNA; 1533 BP.
XX
AC   ADV34695;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1533
FT                   /*tag=  a
FT                   /product= "PFeIL-12 511 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34696.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 43; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 921;  DB 14;  Length 1533;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-274;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 9
ABK98950
ID   ABK98950 standard; cDNA; 1599 BP.
XX
AC   ABK98950;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1599 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69306.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 58-60; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 921;  DB 6;  Length 1599;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-274;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
                |||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987


RESULT 10
ABK98951/c
ID   ABK98951 standard; cDNA; 1599 BP.
XX
AC   ABK98951;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1599 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 61-62; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 921;  DB 6;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-274;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
                ||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613


RESULT 11
ADV34691
ID   ADV34691 standard; cDNA; 1599 BP.
XX
AC   ADV34691;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1599
FT                   /*tag=  a
FT                   /product= "PFeIL-12p533 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34692.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 38; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 921;  DB 14;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-274;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              ||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987


RESULT 12
ADV34693/c
ID   ADV34693 standard; DNA; 1599 BP.
XX
AC   ADV34693;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 complementary DNA, nFeIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
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XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 3; SEQ ID NO 40; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain IL-12 complementary DNA.
XX
SQ Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

Query Match 100.0%; Score 921; DB 14; Length 1599;
Best Local Similarity 100.0%; Pred. No. 1.3e-274;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994
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Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613
```

RESULT 13
AAV56626
ID AAV56626 standard; cDNA; 921 BP.
XX
AC AAV56626;
XX
DT 23-NOV-1998 (first entry)
XX
DE Feline FLAFp40 cDNA mature transcript #1.
XX
KW Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW T lymphocyte cell; autoimmune disease; ds.
XX
OS Felis catus.
XX
PN WO9746583-A1.
XX
PD 11-DEC-1997.
XX
PF 29-MAY-1997; 97WO-JP001824.
XX
PR 04-JUN-1996; 96JP-00165249.
XX
PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI Imamura T, Maeda H, Fujiyasu T, Imagawa Y, Tokiyoshi S;
XX
DR WPI; 1998-042118/04.
DR P-PSDB; AAW76174.
XX
PT Novel feline cytokine protein - useful for treating feline auto:immune
PT diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS Claim 20; Page 55; 94pp; Japanese.
XX
CC This sequence encodes a novel feline cytokine mature protein, FLAFp40.
CC This protein can be used in the production of a FLAFp35/FLAFp40
CC heterodimer which can potentiate the cytotoxic activity of feline
CC cytotoxic T lymphocyte cells. Such proteins are used for treatment of
CC feline autoimmune diseases e.g. as caused by feline herpes virus or
CC feline calcivirus
XX
SQ Sequence 921 BP; 276 A; 227 C; 231 G; 187 T; 0 U; 0 Other;

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  Query Match             99.8%;  Score 919.4;  DB 2;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 3e-274;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 14
ABK98944
ID   ABK98944 standard; cDNA; 987 BP.
XX
AC   ABK98944;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p40-987 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69303.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 51-53; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 987 BP; 283 A; 250 C; 246 G; 208 T; 0 U; 0 Other;

  Query Match             99.8%;  Score 919.4;  DB 6;  Length 987;
  Best Local Similarity   99.9%;  Pred. No. 3.1e-274;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
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```
Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
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Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987
```

```
RESULT 15
ABK98945/c
ID   ABK98945 standard; cDNA; 987 BP.
XX
AC   ABK98945;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p40-987 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 3; Page 54; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 987 BP; 208 A; 246 C; 250 G; 283 T; 0 U; 0 Other;
```

```
  Query Match             99.8%;  Score 919.4;  DB 6;  Length 987;
  Best Local Similarity   99.9%;  Pred. No. 3.1e-274;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262
```

```
Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCAGT 1
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Search completed: June 10, 2006, 04:50:57
Job time : 681.349 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 10, 2006, 03:16:38 ; Search time 5378.58 Seconds
(without alignments)
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Title: US-10-821-670A-26
Perfect score: 921
Sequence: 1 atatgggaactggagaaaaa.....gggcatccgtgtcctgcagt 921

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est3:*
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5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
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12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	6	506.4	55.0	772	5	CD559450	CD559450 AGENCOURT
c	7	501.4	54.4	736	5	CD559453	CD559453 AGENCOURT
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	11	467.6	50.8	1839	6	AK162981	AK162981 Mus muscu
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	27	168	18.2	375	4	BY222535	BY222535 BY222535
	28	163.8	17.8	346	4	BY164658	BY164658 BY164658
	29	160.8	17.5	355	4	BY221814	BY221814 BY221814
	30	106.2	11.5	666	4	BY749553	BY749553 BY749553
c	31	95.2	10.3	668	14	AG079702	AG079702 Pan trogl
	32	73.4	8.0	704	13	CZ422673	CZ422673 1018376 R
	33	65.8	7.1	850	3	BU291084	BU291084 603603708
c	34	63.6	6.9	324	11	AQ981401	AQ981401 RPCI-23-3
	35	53.8	5.8	645	13	CL344654	CL344654 RPCI44_27
	36	47.8	5.2	657	13	CL344592	CL344592 RPCI44_27
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c	39	42.2	4.6	801	2	BI661062	BI661062 603304362
c	40	41.2	4.5	772	11	BZ070797	BZ070797 ljr96a09.
c	41	40.4	4.4	919	12	CG071974	CG071974 PUFYL33TB
	42	40.2	4.4	642	4	CA351258	CA351258 622276 NC
	43	40.2	4.4	862	12	CG277764	CG277764 OG5BA27TC
	44	39.8	4.3	401	4	BW814962	BW814962 BW814962
	45	39.8	4.3	807	13	CW996377	CW996377 OA_BBa007

ALIGNMENTS

RESULT 1
CK130264
LOCUS CK130264 756 bp mRNA linear EST 02-DEC-2003
DEFINITION AGENCOURT_14496566 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971871 5', mRNA sequence.
ACCESSION CK130264
VERSION CK130264.1 GI:38622200
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 756)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: h column: 02
High quality sequence start: 5
High quality sequence stop: 731.
FEATURES Location/Qualifiers
source 1. .756
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971871"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:

loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 57.4%; Score 528.4; DB 5; Length 756;
Best Local Similarity 88.6%; Pred. No. 3.5e-141;
Matches 584; Conservative 0; Mismatches 72; Indels 3; Gaps 1;

```
Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              |||||||||||| ||||| | |||||||| ||||| ||||| ||| | || ||||||||
Db        100 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 159

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||  | || ||||||||||||  ||||||||||||
Db        160 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 219

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              |||||||||||||| ||| |||||||||| ||||| ||||||||||||||||||| |||
Db        220 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 279

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              | ||||||||||||||| |||||||| |||||||||||||||||| ||||||||| ||||
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Db        400 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 459

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Db        520 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 579

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||| ||| |||    ||||| |||||||||| ||||||| |||||||||||| |||
Db        580 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 636

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              || |||||||| || |||||||| ||| ||||||| ||  |||||||||||||||| |||
Db        637 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAA 696

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCT 659
              |||||||||||||||||||||||||||||||||||| |||| ||||||||||||||| |
Db        697 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCNAACCTGACCCACCCAAGAACTT 755
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RESULT 2
CD559605
LOCUS CD559605 735 bp mRNA linear EST 26-NOV-2003
DEFINITION AGENCOURT_14496534 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971870 5', mRNA sequence.
ACCESSION CD559605
VERSION CD559605.2 GI:38558937
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 735)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585673.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: IRBK2 row: h column: 01
High quality sequence stop: 709.
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source 1. .735
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971870"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 57.2%; Score 526.4; DB 5; Length 735;
Best Local Similarity 88.7%; Pred. No. 1.3e-140;
Matches 582; Conservative 0; Mismatches 71; Indels 3; Gaps 1;

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Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db         83 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 142

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||  | || ||||||||||||  ||||||||||||
Db        143 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 202

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              |||||||||||||| ||| |||||||||| ||||| ||||||||||||||||||| |||
Db        203 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 262

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              | ||||||||||||||| |||||||| |||||||||||||||||| ||||||||| ||||
Db        263 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 322
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Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||| | |||||||||||||||||||||||||||||||||||||| |||| ||| |||||||||
Db        323 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 382

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              |||||||||||| |||||||| ||| ||||| ||||||||||||||||||||||||||||
Db        383 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 442

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              |||||||||||| |||||||||| ||||||| ||||| |||||| ||||||||||||||
Db        443 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAGAGCAGCAGAGGCTCT 502

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||||| |||||| || ||||| || |||||||| |||||||  ||||||| |
Db        503 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 562

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||| ||| |||    ||||| |||||||||| ||||||| |||||||||||| |||
Db        563 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 619

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              || |||||||| || |||||||| ||| ||||||| ||  ||||||||||||||| |||
Db        620 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAA 679

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAA 656
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        680 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAA 735
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RESULT 3
CD559607
LOCUS CD559607 747 bp mRNA linear EST 26-NOV-2003
DEFINITION AGENCOURT_14497061 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971868 5', mRNA sequence.
ACCESSION CD559607
VERSION CD559607.2 GI:38558941
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 747)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585675.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: g column: 11
High quality sequence start: 14
High quality sequence stop: 671.

FEATURES Location/Qualifiers
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/clone="IMAGE:6971868"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 56.4%; Score 519; DB 5; Length 747;
Best Local Similarity 88.1%; Pred. No. 1.8e-138;
Matches 577; Conservative 0; Mismatches 75; Indels 3; Gaps 1;

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Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db         95 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 154

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||  | || ||||||||||||  ||||||||||||
Db        155 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 214

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              |||||||||||||| ||| |||||||||| ||||| |||||||||||||||||||| |||
Db        215 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 274

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              | |||||||||||||| |||||||| |||||||||||||||| ||||||||| ||||
Db        275 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 334

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Db        335 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 394

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              |||||||||||| |||||||| ||| ||||| ||||||||||||||||||||||||||||
Db        395 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 454

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              |||||||||||| |||||||||| ||||||| ||||| ||||||||||||||||||||||
Db        455 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 514

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| |||||| || ||||| || |||||||| |||||||  ||||||| |
Db        515 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 574

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||| ||| |||    ||||| |||||||||| ||||||| |||||||||||| |||
Db        575 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 631

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              || |||||||| || |||||||| ||| |||||||     |||||||||| |||| |||
Db        632 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATTGCGTTCACAAGCTCCAGTATGAA 691

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGA 655
              ||||||||| ||||||||||||||||||||||||||||||| |||||||||| |
Db        692 AACTACACCCGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAAA 746
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RESULT 4
CD559604
LOCUS CD559604 772 bp mRNA linear EST 26-NOV-2003
DEFINITION AGENCOURT_14496598 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971872 5', mRNA sequence.
ACCESSION CD559604

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VERSION     CD559604.2  GI:38558934
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 772)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585672.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 03
            High quality sequence start: 13
            High quality sequence stop: 750.
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                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN
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Query Match 56.0%; Score 515.4; DB 5; Length 772;
Best Local Similarity 87.9%; Pred. No. 2.1e-137;
Matches 574; Conservative 0; Mismatches 76; Indels 3; Gaps 1;

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Db        104 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 163

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              |||||||||||||||||||||  | || ||||||||||||  ||||||||||||
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Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Db        224 GACCAGAGCAGTGAGGTCCTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 283

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              | |||||||||||||| |||||||| |||||||||||||||| ||||||||| ||||
Db        284 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 343

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||| | |||||||||||||||||||||||||||||||||||||||| |||| ||| |||||||||
Db        344 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 403

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              |||||||||||| |||||||| ||| ||||| |||||||||||||||||||||||||||||
Db        404 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 463

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
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Db        464 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 523

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Db        641 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAA 700

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAA 653
              |||||||||||||||||||||||||||||||||||| | |  |   || ||
Db        701 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAACCTGACCAACCCAAA 753
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RESULT 5
CD559448/c
LOCUS       CD559448                785 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496712 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971874 5', mRNA sequence.
ACCESSION   CD559448
VERSION     CD559448.2  GI:38453466
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 785)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585516.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 05
            High quality sequence stop: 696.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971874"
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                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
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loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 55.1%; Score 507.6; DB 5; Length 785;
Best Local Similarity 85.7%; Pred. No. 3.8e-135;
Matches 588; Conservative 0; Mismatches 94; Indels 4; Gaps 2;

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Qy      236 TCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGA 295
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Db      774 TCGCTCTGCTGCTCACAAAAGGAAGATGGAATTGGTCCACTGATAT-TTAAAGGACCAGA 716

Qy      296 AAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCA 355
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Db      715 AAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCA 656

Qy      356 CCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAG 415
            ||||||||||||||||| |||||||||| ||||||| ||||| ||||||||||||||||
Db      655 CCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAG 596

Qy      416 GCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCA 475
            ||||  |||||||||||||| |||||| || ||||| || |||||||| |||||||  ||||
Db      595 GCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCA 536

Qy      476 GAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCC 535
            ||| |||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||||
Db      535 GAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCC 479

Qy      536 CGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGT 595
            | ||||| |||||||| || |||||||| ||| ||||||| ||  ||||||||||||||||
Db      478 CAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGT 419

Qy      596 ACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGA 655
            | |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db      418 ATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGA 359

Qy      656 ACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTG 715
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Db      358 ACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTG 299

Qy      716 ACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCA 775
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Qy      776 AGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGT 835
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Qy      836 GCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGA 895
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Qy      896 GCAACTGGGCATCCGTGTCCTGCAGT 921
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Db      118 GCGAATGGGCATCTGTGCCCTGCAGT 93
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RESULT 6
CD559450/c

LOCUS CD559450 772 bp mRNA linear EST 19-NOV-2003
DEFINITION AGENCOURT_14496612 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971872 5', mRNA sequence.
ACCESSION CD559450
VERSION CD559450.2 GI:38453469
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 772)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585518.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: h column: 03
High quality sequence start: 2
High quality sequence stop: 753.
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/clone="IMAGE:6971872"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 55.0%; Score 506.4; DB 5; Length 772;
Best Local Similarity 86.5%; Pred. No. 8.3e-135;
Matches 582; Conservative 0; Mismatches 87; Indels 4; Gaps 2;

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Qy      309 TAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCT 368
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Db      711 TAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCT 652

Qy      369 GACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCC 428
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Db        651 GACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCTGACCC 592

Qy        429 CCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAG 488

Db        591 CCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAACAA 532

Qy        489 GGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGA 548

Db        531 GGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCTGAGGA 475

Qy        549 GAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACAC 608

Db        474 GAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACAC 415

Qy        609 CAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAA 668

Db        414 CAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAA 355

Qy        669 GCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCAC 728

Db        354 GCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTAC 295

Qy        729 CCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGA 788

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Qy        789 AAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGC 848

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Qy        849 CAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATC 908

Db        174 CAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAATGGGCATC 115

Qy        909 CGTGTCCTGCAGT 921

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RESULT 7
CD559453/c
LOCUS       CD559453                736 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14497154 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971869 5', mRNA sequence.
ACCESSION   CD559453
VERSION     CD559453.2  GI:38453475
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 736)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585521.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: g  column: 12
            High quality sequence stop: 683.
FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match           54.4%;  Score 501.4;  DB 5;  Length 736;
  Best Local Similarity 87.1%;  Pred. No. 2.3e-133;
  Matches  574;  Conservative    0;  Mismatches   81;  Indels    4;  Gaps    2;

Qy        263 GAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAA 322

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Qy        323 AATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTA 382

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Qy        383 CCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTT 442

Db        613 CTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGT 554

Qy        443 GTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGT 502

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Qy        623 TCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATT 682

Db        376 TCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATT 317

Qy        683 CTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACT 742

Db        316 CTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACATTCCTACT 257

Qy        743 TCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGAC 802

Db        256 TCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGCAAGAGAGAAAAGAAAGATAGAG 197

Qy        803 TCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGC 862

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Db        136 GGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAATGGGCATCTGTGCCCTGCAGT 78
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RESULT 8
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LOCUS       CD559451                762 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496580 NIH_MGC_195 Homo sapiens cDNA clone
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ACCESSION   CD559451
VERSION     CD559451.2  GI:38453471
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585519.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 02
            High quality sequence start: 38
            High quality sequence stop: 761.
FEATURES             Location/Qualifiers
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                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             54.3%;  Score 499.8;  DB 5;  Length 762;
  Best Local Similarity   86.9%;  Pred. No. 6.8e-133;
  Matches  573;  Conservative    0;  Mismatches   82;  Indels    4;  Gaps    2;

Qy        263 GAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAA 322
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Db        634 CTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGT 575

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Db        574 GCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAACAAGGAGTAT---GAGT 518

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Db        457 AGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCA 398

Qy        623 TCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATT 682
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Db        337 CTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACATTCCTACT 278

Qy        743 TCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGAC 802
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RESULT 9
CD559452/c
LOCUS       CD559452                754 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496548 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971870 5', mRNA sequence.
ACCESSION   CD559452
VERSION     CD559452.2  GI:38453473
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 754)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585520.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 01
            High quality sequence start: 130
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FEATURES             Location/Qualifiers
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                    /lab_host="DH5A (T1 phage-resistant)"
                    /clone_lib="NIH_MGC_195"
                    /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                    loxP-HindIII; Clones from this library have been
                    PCR-amplified using gene-specific primers to contain the
                    complete open reading frame (based on known gene sequences
                    available from NCBI's RefSeq). Template for PCR is cDNA
                    derived from either pooled cytoplasmic polyA RNA from 30
                    cells lines or pooled total RNA from 10 different tissues
                    (from BD Biosciences/Clontech and Washington University).
                    PCR products are directionally cloned into the loxP sites
                    of the pDNR-Dual vector. Library constructed by Dr.
                    Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                    Expression Laboratory, Research Technology Program, SAIC
                    Frederick, NCI-Frederick, Frederick, MD 21702). For
                    information on which gene each clone represents, please
                    visit our anonymous ftp site at
                    ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                    a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match           51.8%;  Score 477.4;  DB 5;  Length 754;
  Best Local Similarity   84.8%;  Pred. No. 2.1e-126;
  Matches  559;  Conservative    0;  Mismatches   96;  Indels    4;  Gaps    2;

Qy        263 GAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAA 322
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Db        752 GAATTTGGTCCAATGATAT-TTAAAGGACCAGAAAGAACCCAAAAATAAGACCTTTCTAA 694

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Qy        383 CCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTT 442
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Qy        443 GTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGT 502
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Qy        503 ACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTG 562
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Qy        563 AAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCA 622
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Db        456 AGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACCAGCAGGTTTTTCA 397

Qy        623 TCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATT 682
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Db        276 TTTCCCTGACATTTTGCGTTCAGGTTCAGGGCAAGAGCAAGAGAGAAAAGAAAGATAGAG 217

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Qy        863 AAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 921
              |||   ||||| |||||||||||||  |||||| | |||||||  ||| |||||||
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RESULT 10
CD559449/c
LOCUS       CD559449                766 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496649 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971873 5', mRNA sequence.
ACCESSION   CD559449
VERSION     CD559449.2  GI:38453467
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 766)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585517.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 04
            High quality sequence stop: 641.
FEATURES             Location/Qualifiers
     source          1. .766
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971873"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match           51.2%;  Score 471.8;  DB 5;  Length 766;
  Best Local Similarity   85.6%;  Pred. No. 8.7e-125;
  Matches  537;  Conservative    0;  Mismatches   87;  Indels    3;  Gaps    1;

Qy        295 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 354
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Db        714 AGAAGAACCCAGAAATAGTACTTTCTAAGATGCGAGGCCAAGAAGTATTCTGGACGTTTC 655

Qy        355 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 414
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Db        654 ACCTGGTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 595

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Db        594 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 535

Qy        475 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 534
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Db        534 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 478

Qy        535 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 594
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Qy        595 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 654
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Qy        655 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 714
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Qy        715 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 774
              |||||||||| || |||||||||||||||||| | |||||  |||| ||||||||||||
Db        297 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 238

Qy        775 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 834
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Db        237 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 178

Qy        835 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 894
              |||| |||  |||||  ||  |||||  |||  ||||||||||||||||||||  |||
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Db        117 AGCGAATGGGCATCTGTGCCCTGCAGT 91
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RESULT 11
AK162981
LOCUS AK162981 1839 bp mRNA linear HTC 21-SEP-2005
DEFINITION Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430014H12 product:interleukin 12b, full insert sequence.
ACCESSION AK162981
VERSION AK162981.1 GI:74188061
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
CONSRTM RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
PUBMED 11217851
REFERENCE 5
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
CONSRTM FANTOM Consortium
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420 (6915), 563-573 (2002)
PUBMED 12466851
REFERENCE 6
AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M.,

Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.

CONSRTM FANTOM Consortium
TITLE The transcriptional landscape of the mammalian genome
JOURNAL Science 309 (5740), 1559-1563 (2005)
PUBMED 16141072

REFERENCE 7
AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.
CONSRTM RIKEN Genome Exploration Research Group
TITLE Antisense transcription in the mammalian transcriptome
JOURNAL Science 309 (5740), 1564-1566 (2005)
PUBMED 16141073

REFERENCE 8 (bases 1 to 1839)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers
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ORIGIN

Query Match 50.8%; Score 467.6; DB 6; Length 1839;
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Matches 681; Conservative 0; Mismatches 224; Indels 39; Gaps 4;

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RESULT 12
CD559602

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LOCUS       CD559602                745 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496684 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971874 5', mRNA sequence.
ACCESSION   CD559602
VERSION     CD559602.2  GI:38558930
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 745)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585670.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 05
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                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN
```

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  Query Match           50.1%;  Score 461.8;  DB 5;  Length 745;
  Best Local Similarity  86.2%;  Pred. No. 6.8e-122;
  Matches  535;  Conservative    0;  Mismatches   82;  Indels    4;  Gaps    2;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              |||||||||||| ||||| | |||||||| ||||| ||||| ||| | || ||||||||
Db         72 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 131

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||  | || ||||||||||||  ||||||||||||
Db        132 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 191

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              |||||||||||||| ||| |||||||||| ||||| ||||||||||||||||||| |||
Db        192 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 251

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              | ||||||||||||||| |||||||| |||||||||||||||||| ||||||||| ||||
Db        252 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 311

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Db        312 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 371

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              |||||||||||| |||||||| ||| ||||| ||||||||||||||||||||||||||||
Db        372 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 431

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
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Db        432 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 491

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| |||||| || ||||| || |||||||| |||||||  ||||||| |
Db        492 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 551

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||| |||
Db        552 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 608

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              || |||||||| || |||||||| ||| ||||||| ||   ||||||||||| ||   ||
Db        609 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGC-CGTCACAAGCTCATGTTGAAA 667

Qy        601 AACTACACCAGCAGCTTCTTC 621
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Db        668 ATACACCACGGCTTCTTTCTC 688
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RESULT 13
AK155593

```
LOCUS       AK155593                2908 bp    mRNA    linear   HTC 21-SEP-2005
DEFINITION  Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN
            full-length enriched library, clone:F730005O03 product:interleukin
            12b, full insert sequence.
ACCESSION   AK155593
VERSION     AK155593.1  GI:74212721
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   PUBMED   10349636
```

REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
CONSRTM RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
PUBMED 11217851
REFERENCE 5
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
CONSRTM FANTOM Consortium
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420 (6915), 563-573 (2002)
PUBMED 12466851
REFERENCE 6
AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.
CONSRTM FANTOM Consortium
TITLE The transcriptional landscape of the mammalian genome
JOURNAL Science 309 (5740), 1559-1563 (2005)
PUBMED 16141072
REFERENCE 7
AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.
CONSRTM RIKEN Genome Exploration Research Group
TITLE Antisense transcription in the mammalian transcriptome
JOURNAL Science 309 (5740), 1564-1566 (2005)
PUBMED 16141073
REFERENCE 8 (bases 1 to 2908)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

```
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
            Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
            Trust/MRC building Addenbrookes Hospital Cambridge) whose
            assistance we gratefully acknowledge.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES              Location/Qualifiers
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                      /clone="F730005O03"
                      /cell_type="B6-derived CD11 +ve dendritic cells"
                      /clone_lib="RIKEN full-length enriched mouse cDNA library"
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                      putative"
ORIGIN

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  Best Local Similarity   72.1%;  Pred. No. 3.6e-120;
  Matches  681;  Conservative    0;  Mismatches  224;  Indels   40;  Gaps    5;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db        527 ATGTGGGAGCTGGAGAAAGACGTTTATGTTGTAGAGGTGGACTGGACTCCCGATGCCCCT 586

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Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Db        647 GACCAGAGACATGGAGTCATAGGCTCTGGAAAGACCCTGACCATCACTGTCAAAGAGTTT 706

Qy        181 GCAGATGCTGGCCAG-TATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCT 239
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Qy        300 ATCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTG 359
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Qy        360 CTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTC 419
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Db        938 CCCTGACTCTCGGGCAGTGACATGTGGAATGGCGTCTCTGTCTGCAGAGAAGGTCACACT 997

Qy        480 GGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGC 539
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Qy        540 TGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGA 599
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Qy        600 AAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCT 659
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Db       1118 GAACTACAGCACCAGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTT 1177

Qy        660 GCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACAC 719
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Db       1295 AGAAAAGATGAAGGAGACAGAGGAGGGGTGTAACCAGAAAGGTGCGTTCCTCGTAGAGAA 1354

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RESULT 14
CD559454/c
LOCUS       CD559454                725 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14497089 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971868 5', mRNA sequence.
ACCESSION   CD559454
VERSION     CD559454.2  GI:38453478
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 725)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585522.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: g  column: 11
            High quality sequence start: 13
            High quality sequence stop: 573.
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                      PCR-amplified using gene-specific primers to contain the
                      complete open reading frame (based on known gene sequences
                      available from NCBI's RefSeq). Template for PCR is cDNA
                      derived from either pooled cytoplasmic polyA RNA from 30
                      cells lines or pooled total RNA from 10 different tissues
```

(from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 47.3%; Score 436; DB 5; Length 725;
Best Local Similarity 83.9%; Pred. No. 2e-114;
Matches 517; Conservative 0; Mismatches 95; Indels 4; Gaps 2;

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Qy        486 CAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGA 545
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Qy        906 ATCCGTGTCCTGCAGT 921
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RESULT 15
CD559603
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DEFINITION AGENCOURT_14496630 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971873 5', mRNA sequence.
ACCESSION CD559603
VERSION CD559603.2 GI:38558932
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 724)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585671.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: IRBK2 row: h column: 04
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FEATURES Location/Qualifiers
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/lab_host="DH5A (T1 phage-resistant)"
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/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 39.7%; Score 365.6; DB 5; Length 724;
Best Local Similarity 89.9%; Pred. No. 4.9e-94;
Matches 392; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

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Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
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Db        200 GACCAGAGCAGTGAGGTCCTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 259

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              | |||||||||||||| |||||||| |||||||||||||||||| ||||||||| ||||
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Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
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Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
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Qy        421 TCTGACCCCCAAGAGG 436
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Job time : 5379.58 secs
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 10, 2006, 04:51:14 ; Search time 198.814 Seconds
(without alignments)
8667.862 Million cell updates/sec

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Perfect score: 921
Sequence: 1 atatgggaactggagaaaaa.....gggcatccgtgtcctgcagt 921

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	921	100.0	921	3	US-09-917-265A-26	Sequence 26, Appl
c 2	921	100.0	921	3	US-09-917-265A-28	Sequence 28, Appl
3	921	100.0	1533	3	US-09-917-265A-43	Sequence 43, Appl
c 4	921	100.0	1533	3	US-09-917-265A-45	Sequence 45, Appl
5	921	100.0	1599	3	US-09-917-265A-38	Sequence 38, Appl
c 6	921	100.0	1599	3	US-09-917-265A-40	Sequence 40, Appl
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8	919.4	99.8	921	3	US-09-302-495-6	Sequence 6, Appli
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10	919.4	99.8	987	3	US-09-917-265A-29	Sequence 29, Appl
c 11	919.4	99.8	987	3	US-09-917-265A-31	Sequence 31, Appl
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44	727.4	79.0	1623	2	US-08-751-767A-9	Sequence 9, Appli
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ALIGNMENTS

RESULT 1
US-09-917-265A-26
; Sequence 26, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(921)
US-09-917-265A-26

Query Match 100.0%; Score 921; DB 3; Length 921;
Best Local Similarity 100.0%; Pred. No. 4.9e-290;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

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Db        901 TGGGCATCCGTGTCCTGCAGT 921
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RESULT 2
US-09-917-265A-28/c
; Sequence 28, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265A-28

Query Match 100.0%; Score 921; DB 3; Length 921;
Best Local Similarity 100.0%; Pred. No. 4.9e-290;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCAGT 1
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RESULT 3
US-09-917-265A-43
; Sequence 43, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.

```
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-09-917-265A-43

  Query Match            100.0%;  Score 921;  DB 3;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 6.9e-290;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 4
US-09-917-265A-45/c
; Sequence 45, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-45

  Query Match            100.0%;  Score 921;  DB 3;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 6.9e-290;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
                 ||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613


RESULT 5
US-09-917-265A-38
; Sequence 38, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-09-917-265A-38

  Query Match           100.0%;  Score 921;  DB 3;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-290;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
                 ||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987


RESULT 6
US-09-917-265A-40/c
; Sequence 40, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
```

US-09-917-265A-40

Query Match 100.0%; Score 921; DB 3; Length 1599;
Best Local Similarity 100.0%; Pred. No. 7.1e-290;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
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Db        633 TGGGCATCCGTGTCCTGCAGT 613
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RESULT 7
US-09-011-143-6

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; Sequence 6, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  921 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-6
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Query Match 99.8%; Score 919.4; DB 3; Length 921;
Best Local Similarity 99.9%; Pred. No. 1.6e-289;
Matches 920; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
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Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
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Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
                |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
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Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
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Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
                |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 8
US-09-302-495-6
; Sequence 6, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-302-495-6

  Query Match             99.8%;  Score 919.4;  DB 3;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 1.6e-289;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
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Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
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Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
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Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

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Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
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Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
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Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 9
US-10-079-616-6
; Sequence 6, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-079-616-6

  Query Match           99.8%;  Score 919.4;  DB 3;  Length 921;
  Best Local Similarity 99.9%;  Pred. No. 1.6e-289;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
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Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

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Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
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Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
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Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
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Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
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Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
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Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 10
US-09-917-265A-29
; Sequence 29, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
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;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
US-09-917-265A-29

  Query Match            99.8%;  Score 919.4;  DB 3;  Length 987;
  Best Local Similarity  99.9%;  Pred. No. 1.7e-289;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
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Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987


RESULT 11
US-09-917-265A-31/c
; Sequence 31, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-31

  Query Match            99.8%;  Score 919.4;  DB 3;  Length 987;
  Best Local Similarity  99.9%;  Pred. No. 1.7e-289;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442
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Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
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Db         21 TGGGCATCCGTGTCCTGCAGT 1
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```
RESULT 12
US-09-011-143-5
; Sequence 5, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2193 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-5

  Query Match            99.8%;  Score 919.4;  DB 3;  Length 2193;
  Best Local Similarity  99.9%;  Pred. No. 2.9e-289;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 189

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 249

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 309

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 369

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 429

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 489

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 549

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 TCTGACCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 609

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 669

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 729

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 789

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 849

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 909

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 969

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 1029
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Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db       1030 TGGGCATCCGTGTCCTGCAGT 1050


RESULT 13
US-09-302-495-5
; Sequence 5, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2193 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-302-495-5

  Query Match             99.8%;  Score 919.4;  DB 3;  Length 2193;
  Best Local Similarity   99.9%;  Pred. No. 2.9e-289;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 189

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 249

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 309

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 369

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 429

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 489

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 549

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 609

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 669

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 729

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 789

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 849

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 909

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 969

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 1029

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db       1030 TGGGCATCCGTGTCCTGCAGT 1050


RESULT 14
US-10-079-616-5
; Sequence 5, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
```

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;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 5:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 2193 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-079-616-5

  Query Match             99.8%;  Score 919.4;  DB 3;  Length 2193;
  Best Local Similarity   99.9%;  Pred. No. 2.9e-289;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db        730 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 789

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RESULT 15
US-09-011-143-7
; Sequence 7, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  921 base pairs
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;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-7

  Query Match             99.7%;  Score 917.8;  DB 3;  Length 921;
  Best Local Similarity   99.8%;  Pred. No. 5.5e-289;
  Matches  919;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Search completed: June 10, 2006, 18:08:46
Job time : 198.814 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 10, 2006, 07:19:28 ; Search time 1050.01 Seconds
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Title: US-10-821-670A-26
Perfect score: 921
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	2	921	100.0	921	3	US-09-917-265-28	Sequence 28, Appl
	3	921	100.0	921	9	US-10-821-670-26	Sequence 26, Appl
c	4	921	100.0	921	9	US-10-821-670-28	Sequence 28, Appl
	5	921	100.0	1533	3	US-09-917-265-43	Sequence 43, Appl
c	6	921	100.0	1533	3	US-09-917-265-45	Sequence 45, Appl
	7	921	100.0	1533	9	US-10-821-670-43	Sequence 43, Appl
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ALIGNMENTS

RESULT 1
US-09-917-265-26
; Sequence 26, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(921)
; OTHER INFORMATION:
US-09-917-265-26

Query Match 100.0%; Score 921; DB 3; Length 921;
Best Local Similarity 100.0%; Pred. No. 1.3e-285;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921
```

RESULT 2
US-09-917-265-28/c
; Sequence 28, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Felis catus

US-09-917-265-28

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  Query Match             100.0%;  Score 921;  DB 3;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-285;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCAGT 1
```

RESULT 3
US-10-821-670-26

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; Sequence 26, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(921)
US-10-821-670-26

  Query Match            100.0%;  Score 921;  DB 9;  Length 921;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-285;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 4
US-10-821-670-28/c
; Sequence 28, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-28

  Query Match            100.0%;  Score 921;  DB 9;  Length 921;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-285;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502
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Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCAGT 1
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RESULT 5
US-09-917-265-43
; Sequence 43, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)
; OTHER INFORMATION:
US-09-917-265-43

Query Match 100.0%; Score 921; DB 3; Length 1533;
Best Local Similarity 100.0%; Pred. No. 1.7e-285;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921
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RESULT 6
US-09-917-265-45/c
; Sequence 45, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-45

  Query Match            100.0%;  Score 921;  DB 3;  Length 1533;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-285;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613
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RESULT 7
US-10-821-670-43
; Sequence 43, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-10-821-670-43

  Query Match            100.0%;  Score 921;  DB 9;  Length 1533;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-285;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
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Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 8
US-10-821-670-45/c
; Sequence 45, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-45

  Query Match             100.0%;  Score 921;  DB 9;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-285;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
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Db       1233 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
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Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
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Db        633 TGGGCATCCGTGTCCTGCAGT 613


RESULT 9
US-09-917-265-38
; Sequence 38, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
US-09-917-265-38

  Query Match             100.0%;  Score 921;  DB 3;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-285;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
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Qy          61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
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Db         127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy         121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Db         247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Db         307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy         301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy         361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy         421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy         481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Db         547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy         541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy         601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Db         667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy         661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy         721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
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Db         787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy         781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy         841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy         901 TGGGCATCCGTGTCCTGCAGT 921
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Db         967 TGGGCATCCGTGTCCTGCAGT 987


RESULT 10
US-09-917-265-40/c
; Sequence 40, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-40

  Query Match             100.0%;  Score 921;  DB 3;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-285;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db        1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy          61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy         301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy         361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy         421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy         481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy         541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy         601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy         661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy         721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
pb         813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy         781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy         841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634
```

```
Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613


RESULT 11
US-10-821-670-38
; Sequence 38, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-10-821-670-38

  Query Match            100.0%;  Score 921;  DB 9;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-285;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              ||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987


RESULT 12
US-10-821-670-40/c
; Sequence 40, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-40

  Query Match            100.0%;  Score 921;  DB 9;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-285;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234
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Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613


RESULT 13
US-10-079-616-6
; Sequence 6, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-079-616-6

  Query Match           99.8%;  Score 919.4;  DB 6;  Length 921;
  Best Local Similarity  99.9%;  Pred. No. 4.3e-285;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 14
US-09-917-265-29
; Sequence 29, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
;   OTHER INFORMATION:
US-09-917-265-29

  Query Match             99.8%;  Score 919.4;  DB 3;  Length 987;
  Best Local Similarity   99.9%;  Pred. No. 4.5e-285;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
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Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
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Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
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Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
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Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
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Db        967 TGGGCATCCGTGTCCTGCAGT 987


RESULT 15
US-09-917-265-31/c
; Sequence 31, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-31

  Query Match             99.8%;  Score 919.4;  DB 3;  Length 987;
  Best Local Similarity   99.9%;  Pred. No. 4.5e-285;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
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Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Db        501 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
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Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
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Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
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OM nucleic - nucleic search, using sw model

Run on: June 10, 2006, 15:46:40 ; Search time 15.9657 Seconds
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Perfect score: 921
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 253354 seqs, 63461778 residues

Total number of hits satisfying chosen parameters: 506708

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	36.8	4.0	3401	6	US-10-196-749-411	Sequence 411, App
	2	34.8	3.8	3166	7	US-11-293-697-739	Sequence 739, App
c	3	34.4	3.7	1438	6	US-10-953-349-20792	Sequence 20792, A
	4	34.4	3.7	2268	7	US-11-217-529-1612	Sequence 1612, Ap
	5	33.8	3.7	1948	6	US-10-508-063A-4	Sequence 4, Appli
	6	33.2	3.6	2513	7	US-11-293-697-145	Sequence 145, App
	7	32.4	3.5	2152	6	US-10-953-349-38921	Sequence 38921, A
	8	32	3.5	620	6	US-10-953-349-32903	Sequence 32903, A
	9	32	3.5	2024	7	US-11-293-697-1253	Sequence 1253, Ap
	10	31.8	3.5	1404	6	US-10-471-571A-5411	Sequence 5411, Ap
c	11	31.8	3.5	1906	6	US-10-953-349-22720	Sequence 22720, A
c	12	31.4	3.4	1636	6	US-10-953-349-22635	Sequence 22635, A
c	13	31.4	3.4	6051	7	US-11-313-450-9	Sequence 9, Appli
	14	31.2	3.4	1286	7	US-11-145-307A-72	Sequence 72, Appl
	15	31	3.4	2843	7	US-11-293-697-1498	Sequence 1498, Ap
c	16	30.8	3.3	992	6	US-10-953-349-31065	Sequence 31065, A
	17	30.8	3.3	2630	7	US-11-293-697-1769	Sequence 1769, Ap
	18	30.8	3.3	2640	6	US-10-527-411-29	Sequence 29, Appl
	19	30.8	3.3	3930	7	US-11-217-529-76026	Sequence 76026, A
	20	30.6	3.3	1210	6	US-10-953-349-23356	Sequence 23356, A
	21	30.6	3.3	1761	6	US-10-953-349-22246	Sequence 22246, A
	22	30.6	3.3	2619	7	US-11-302-678-18	Sequence 18, Appl
	23	30.6	3.3	3232	7	US-11-302-678-16	Sequence 16, Appl
c	24	30.4	3.3	296	7	US-11-301-554-517	Sequence 517, App
	25	30.4	3.3	444	7	US-11-217-529-79558	Sequence 79558, A
c	26	30.4	3.3	1467	7	US-11-217-529-79610	Sequence 79610, A
c	27	30.4	3.3	2249	7	US-11-293-697-442	Sequence 442, App
c	28	30.4	3.3	3294	7	US-11-293-697-1397	Sequence 1397, Ap
c	29	30.2	3.3	924	7	US-11-217-529-1898	Sequence 1898, Ap
	30	30.2	3.3	1848	6	US-10-519-335-5	Sequence 5, Appli
	31	30.2	3.3	1878	6	US-10-519-335-3	Sequence 3, Appli
	32	30.2	3.3	1932	6	US-10-519-335-1	Sequence 1, Appli
	33	30	3.3	1376	6	US-10-527-411-71	Sequence 71, Appl
	34	30	3.3	1376	6	US-10-527-411-73	Sequence 73, Appl
	35	30	3.3	1376	6	US-10-527-411-75	Sequence 75, Appl
	36	30	3.3	1376	6	US-10-527-411-77	Sequence 77, Appl
	37	30	3.3	1385	6	US-10-527-411-69	Sequence 69, Appl
	38	30	3.3	2600	6	US-10-527-411-33	Sequence 33, Appl
	39	30	3.3	2600	6	US-10-527-411-35	Sequence 35, Appl
	40	30	3.3	2600	6	US-10-527-411-37	Sequence 37, Appl
	41	30	3.3	2609	6	US-10-527-411-31	Sequence 31, Appl
	42	30	3.3	2625	6	US-10-527-411-150	Sequence 150, App
	43	30	3.3	2625	6	US-10-527-411-164	Sequence 164, App
	44	30	3.3	2625	6	US-10-527-411-166	Sequence 166, App
	45	30	3.3	2625	6	US-10-527-411-168	Sequence 168, App

ALIGNMENTS

RESULT 1
US-10-196-749-411
; Sequence 411, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 411
; LENGTH: 3401
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-196-749-411

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  Query Match             4.0%;  Score 36.8;  DB 6;  Length 3401;
  Best Local Similarity   46.5%;  Pred. No. 0.096;
  Matches  119;  Conservative    0;  Mismatches  137;  Indels    0;  Gaps    0;

Qy        474 CAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTG 533
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Db        130 CACCGTCTACTACGTGCACAACATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAG 189

Qy        534 CCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAA 593
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Db        190 CCTGACGGGCTACCGCACCTACCGCTGTGCCCACCCCCTGGCCACACTCTTCAAGATCCT 249

Qy        594 GTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAA 653
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Db        250 GGCGTCCTTCTACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCATGTACACACTGTG 309

Qy        654 GAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCC 713
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Db        310 GTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTTGAGTCGATCCGTGAGGAGAGCAG 369

Qy        714 TGACACCTGGAGCACC 729
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Db        370 CTACAGCGACATCCCC 385


RESULT 2
US-11-293-697-739
; Sequence 739, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 739
;   LENGTH: 3166
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-739

  Query Match             3.8%;  Score 34.8;  DB 7;  Length 3166;
  Best Local Similarity   49.5%;  Pred. No. 0.4;
  Matches   90;  Conservative    0;  Mismatches   92;  Indels    0;  Gaps    0;

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Qy        531 CTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCT 590
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Db       1478 CAGGCTGAAAACCGAGCACAACATAACCGTGCTGGTCTCCGACGTCAATGACAACGCCCC 1537

Qy        591 CAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACC 650
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Db       1538 CATCTTCACCCAAACCTCCTACACCCTGTTCGTCCGCGAGAACAACAGCCCCGCCCTGCA 1597

Qy        651 CA 652
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Db       1598 CA 1599


RESULT 3
US-10-953-349-20792/c
; Sequence 20792, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20792
;   LENGTH: 1438
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-20792

  Query Match             3.7%;  Score 34.4;  DB 6;  Length 1438;
  Best Local Similarity   50.0%;  Pred. No. 0.32;
  Matches   86;  Conservative    0;  Mismatches   86;  Indels    0;  Gaps    0;

Qy        177 ATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTT 236
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Db       1331 ATAGGCACATGGAAGCAATTACTCCTTCACCATATGAGAACAACACTGGAGTCAAGCATG 1272

Qy        237 CCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAA 296
              ||||  || ||| |    |||  ||   |   ||| || | || || | | ||   ||
Db       1271 GATCCTAATCCACTAGTTCGAAACTGTGTTAAACTCCTCTCAAATTTTCATGCAATCTAA 1212

Qy        297 AGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGA 348
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Db       1211 CTGTAACACTGATAACATCTTTTTTACCCCTTATGTAATACTTTACTGCTGA 1160


RESULT 4
US-11-217-529-1612
; Sequence 1612, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1612
;   LENGTH: 2268
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-1612

  Query Match             3.7%;  Score 34.4;  DB 7;  Length 2268;
  Best Local Similarity   59.0%;  Pred. No. 0.43;
  Matches   59;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy         84 CAATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGG 143
              ||||||  |||||||||  ||||||      |||  | | |     | ||   ||  |   |
Db       1869 CAATACCCCTGAAGAAAATGACACTGAGGGGAAGTATAATACAATCAAGAAAAGCTCGGA 1928

Qy        144 CTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCA 183
                | || | ||  |||  | ||    |  ||||||||||  ||
Db       1929 TTATGATGAATCTCATATCACGAATATCAAAGAATTACCA 1968


RESULT 5
US-10-508-063A-4
; Sequence 4, Application US/10508063A
; Publication No. US20060088832A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: Deutsches Krebsforschungszentrum
;  APPLICANT:  ANGEL, Peter
;  APPLICANT:  FURSTENBERGER, Gerhard
;  APPLICANT:  BREITENBACH, Ute
;  APPLICANT:  RICHTER, Harmut
;  APPLICANT:  HESS, Jochen
;  APPLICANT:  TUCKERMAN, Jan
;  TITLE OF INVENTION: TAP-70, A NOVEL MARKER FOR EPITHELIAL TUMORS
;  FILE REFERENCE: 31304-701.831
;  CURRENT APPLICATION NUMBER: US/10/508,063A
;  CURRENT FILING DATE:  2004-09-16
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 1948
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-508-063A-4

  Query Match           3.7%;  Score 33.8;  DB 6;  Length 1948;
  Best Local Similarity  52.4%;  Pred. No. 0.61;
  Matches   99;  Conservative    0;  Mismatches   87;  Indels    3;  Gaps    1;

Qy        429 CCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAG 488
              | ||| ||  | | | | ||    ||   |||  |  | |  || || ||     | |
Db       1111 CAAAGTGGCCAATGGGGCAGAGATGAAGATCTTGGGTGTGTGGGACACAGAAATTAGCCT 1170

Qy        489 GGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGA 548
              ||   | |  |||   |  |  |||| || || || ||  ||| ||   || |  ||||
Db       1171 GGGCAAGACAAAGCTGAAGGCCGAGTTTCTGGTGGCCAACGCCAGC---GCAGAAGAGGC 1227

Qy        549 GAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACAC 608
               |   |   ||  || ||| ||  ||||   | |  |  |||  | | |||| ||  |||
Db       1228 TATTATTGGCACAGACGTCTTGCAGGACCACAATGCCGTGCTGGACTTCGAACACCGCAC 1287

Qy        609 CAGCAGCTT 617
              | ||| | |
Db       1288 CTGCACCCT 1296


RESULT 6
US-11-293-697-145
; Sequence 145, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 145
;   LENGTH: 2513
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-145

  Query Match           3.6%;  Score 33.2;  DB 7;  Length 2513;
  Best Local Similarity  52.1%;  Pred. No. 1.1;
  Matches   74;  Conservative    0;  Mismatches   68;  Indels    0;  Gaps    0;

Qy        561 TGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTT 620
              |||| | |   |||| |||      |  |  |  |||| | |||| || | |     || |
Db        973 TGAAATGGCCCTGGATGCTGAGTTCCTGGACGTGTACAAGAACTGCAACGGGGTGGTCAT 1032

Qy        621 CATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAA 680
               ||    ||||| | ||| | |     |   |||  || | |  | | |||   ||||
Db       1033 GATGTTCGACATTACCAAGCAGTGGACCTTCAATTACATTCTCCGGGAGCTTCCAAAAGT 1092

Qy        681 TTCTCGGCATGTGGAAGTGAGC 702
                |    || |||  |||| ||
Db       1093 GCCCACCCACGTGCCAGTGTGC 1114


RESULT 7
US-10-953-349-38921
; Sequence 38921, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38921
;   LENGTH: 2152
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-38921

  Query Match           3.5%;  Score 32.4;  DB 6;  Length 2152;
  Best Local Similarity  47.9%;  Pred. No. 1.8;
  Matches   93;  Conservative    0;  Mismatches  101;  Indels    0;  Gaps    0;

Qy        458 TCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTC 517
              |||| || ||| || ||||       | |  | |  | | |||| | || |  ||| |
Db        475 TCTCGGCCGAGGAGATCAGCTCCATGATCCTGAACAAGATGAAGGAGACGGCCGAGGCTT 534

Qy        518 AGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACG 577
              |    ||||   ||  | |  || | |  | | | ||      |  ||   |    |
Db        535 ACCTCGGCACCACCATCAAGAACGCTGTCGTCACCGTCCCGGCCTACTTCAACGACTCCC 594

Qy        578 CTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCA 637
                    ||      |||| |||    |  || |  | || ||  | ||| |  ||||||||
Db        595 AGCGCCAGGCCACCAAGGACGCCGGCGTCATCTCCGGCCTCAACGTCATGCGCATCATCA 654

Qy        638 AACCGGACCCACCC 651
              |   |  | |  ||
Db        655 ACGAGCCCACCGCC 668


RESULT 8
US-10-953-349-32903
; Sequence 32903, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32903
;   LENGTH: 620
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-32903

  Query Match           3.5%;  Score 32;  DB 6;  Length 620;
  Best Local Similarity  47.1%;  Pred. No. 1.1;
  Matches   98;  Conservative    0;  Mismatches  110;  Indels    0;  Gaps    0;

Qy        508 GTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTC 567
              |||||||       | |    ||    || |||||| | |  |   |  ||   |   ||
Db         90 GTGGAGTTGGCAAAAGCTCATGAGATCCAGGCTGCTGTGCTGTTGCACCCTTCTTTTGTT 149

Qy        568 GTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGG 627
                 || |||| |||  |  || |||||| || ||  |  | |  | |        ||
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Db        150 ACCGTTGACGATATCAAAGAGGTCAAGTGCGCAATTTCTATCCTCGGAGCTGAGATTGAC 209

Qy        628 GACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGG 687

Db        210 AAAATGTCCCCACCGGAGCTAATCAAGCAGTTCGAGCAGGTCCTTTCTTTGAACTCAGGG 269

Qy        688 CATGTGGAAGTGAGCTGGGAATACCCTG 715

Db        270 GTTGGCCACTTCGTCAAGATCTTCCCTG 297


RESULT 9
US-11-293-697-1253
; Sequence 1253, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1253
;   LENGTH: 2024
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1253

  Query Match             3.5%;  Score 32;  DB 7;  Length 2024;
  Best Local Similarity   50.7%;  Pred. No. 2.4;
  Matches   77;  Conservative    0;  Mismatches   75;  Indels    0;  Gaps    0;

Qy        144 CTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTG 203

Db        496 CTCTGTTGAAAGTTTGTTTCACCAGCAAATACTTTCTTCTTGTGCCAAAAGCTATAACTT 555

Qy        204 TCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGG 263

Db        556 TGATCAATATAGGAAGGTCTTTACTCATTCATCATTGCTTAATCAACAAGAGGAAATAGA 615

Qy        264 AATTTGGTCCACTGATATCTTAAGGGAACAGA 295

Db        616 TATTTGGGGAAAACATCACATATATGATAAAA 647


RESULT 10
US-10-471-571A-5411
; Sequence 5411, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 5411
;   LENGTH: 1404
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-5411

  Query Match             3.5%;  Score 31.8;  DB 6;  Length 1404;
  Best Local Similarity   57.6%;  Pred. No. 2.2;
  Matches   57;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy        262 GGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTA 321

Db         11 GTAATTTTTTAAATGTAGAGTTAATAGGTACTAAAATAATAACAATGGAAGACTTTTATA 70

Qy        322 AAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Db         71 AAATGAAGGAAGAAGAATTTTTCTTAAAATCTAAGCTAC 109


RESULT 11
US-10-953-349-22720/c
; Sequence 22720, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22720
;   LENGTH: 1906
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-22720

  Query Match             3.5%;  Score 31.8;  DB 6;  Length 1906;
  Best Local Similarity   61.4%;  Pred. No. 2.6;
  Matches   51;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy        160 ACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAG 219

Db        918 ACTATCCAAGTCACTGACATTGCAGTTCCCATTATTTAACGCAGTCATATCTATAGAGGA 859

Qy        220 GTTCTGAGCCATTCGTTCCTCCT 242

Db        858 ATTTTGAGCCAATGCTTCCTCCT 836


RESULT 12
US-10-953-349-22635/c
; Sequence 22635, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22635
;   LENGTH: 1636
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-22635

  Query Match             3.4%;  Score 31.4;  DB 6;  Length 1636;
  Best Local Similarity   46.9%;  Pred. No. 3.2;
  Matches   98;  Conservative    0;  Mismatches  111;  Indels    0;  Gaps    0;

Qy        584 ACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGG 643

Db       1479 ACACAGTCATGGACTTTTCATATCCATCTCACTCTTGCATGCGGATGATACACCTAATGG 1420

Qy        644 ACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCT 703

Db       1419 ACTGTCCCTTCAGCATTAAATCAAAAGCTTTGTTGATCTCTGAGAATGGAACTGTGTGAG 1360

Qy        704 GGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTAC 763
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Db       1359 TGATGAATTTGTCCACTTCTAGCTCCCCACTCATGTACTTCTCGACAACAGATGGAAGAT 1300

Qy        764 AGGTCCAGGGCAAGAACAACAGAGAAAAG 792
              ||| |  ||   | |      | |||||
Db       1299 CGGTGCGTGGTTTGTAGTTGCCATAAAAG 1271


RESULT 13
US-11-313-450-9/c
; Sequence 9, Application US/11313450
; Publication No. US20060110778A1
; GENERAL INFORMATION:
;  APPLICANT: Adorante, Joeseph S.
;  APPLICANT:  Ehring, George R.
;  TITLE OF INVENTION: High-Throughput Screens For Identifying
;  TITLE OF INVENTION:  Selective Persistent Sodium Channels Channel Blockers
;  FILE REFERENCE: 17407 CIP (AP)
;  CURRENT APPLICATION NUMBER: US/11/313,450
;  CURRENT FILING DATE:  2005-12-19
;  PRIOR APPLICATION NUMBER: 09/989797
;  PRIOR FILING DATE: 2001-11-20
;  PRIOR APPLICATION NUMBER: 60/252771
;  PRIOR FILING DATE: 2000-11-22
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 6051
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-313-450-9

  Query Match             3.4%;  Score 31.4;  DB 7;  Length 6051;
  Best Local Similarity   59.6%;  Pred. No. 7.5;
  Matches   53;  Conservative    0;  Mismatches   36;  Indels    0;  Gaps    0;

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              |||| | ||  || ||   || ||||||    ||||   || ||| | |||| || |||
Db       5636 AACTTCTCCTCCATCTGGATCTTCAGGGCGTCCATCTCCCCAGACTCCCCCAGGACCCTT 5577

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCA 689
              |||||  ||   | ||  ||   |||
Db       5576 TTGGTGAAGGCAAAGAGAATGTCCATGCA 5548


RESULT 14
US-11-145-307A-72
; Sequence 72, Application US/11145307A
; Publication No. US20060094035A1
; GENERAL INFORMATION:
;  APPLICANT: Arcturus Bioscience, Inc.
;  APPLICANT:  Erlander, Mark G.
;  APPLICANT:  Ma, Xiao-Jun
;  TITLE OF INVENTION: Identification of Tumors
;  FILE REFERENCE: 022041-002020US
;  CURRENT APPLICATION NUMBER: US/11/145,307A
;  CURRENT FILING DATE:  2005-06-03
;  PRIOR APPLICATION NUMBER: US 60/577,084
;  PRIOR FILING DATE: 2004-06-04
;  NUMBER OF SEQ ID NOS: 268
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72
;   LENGTH: 1286
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-145-307A-72

  Query Match             3.4%;  Score 31.2;  DB 7;  Length 1286;
  Best Local Similarity   50.7%;  Pred. No. 3.2;
  Matches   75;  Conservative    0;  Mismatches   73;  Indels    0;  Gaps    0;

Qy        468 GAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAG 527
              | ||||    |||||  |   ||| |   || ||| ||   ||||    | ||    | |
Db        632 GCAGGTGGAGGTGGAGGAGGAGGAGTTCCAGGAGTTCATCCTGGACACACTGGTCCTCTG 691

Qy        528 TGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAA 587
              || ||||   |||  |||   ||   | || ||| | | |   |  || ||
Db        692 CCTGCAGGAGGATGCCACCGAGGCCCTGGGCAGCAATGTGGTGCTTGTCCTGAAGCAGAA 751

Qy        588 GCTCAAGTACGAAAACTACACCAGCAGC 615
              ||||     ||  ||| | | || | ||
Db        752 GCTCCTCAGCGCCAACCAGAACATCCGC 779


RESULT 15
US-11-293-697-1498
; Sequence 1498, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1498
;   LENGTH: 2843
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1498

  Query Match             3.4%;  Score 31;  DB 7;  Length 2843;
  Best Local Similarity   48.6%;  Pred. No. 6.2;
  Matches   85;  Conservative    0;  Mismatches   90;  Indels    0;  Gaps    0;

Qy        497 AGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTAC 556
              ||  |||| ||| | ||    || |        |||  ||||||  ||  | ||||| |
Db       1858 AGGTGTACGCAGAGAAGAAGGAGAATTCACCAGCCCCCCCGGCACCCATGCAGAGCATCT 1917

Qy        557 CCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCT 616
              |||  |   ||  || |   | |  | | ||  ||       |  ||  || |  || ||
Db       1918 CCAGCGGCATCAGGGAGACAGTGAGCCCCCAGGACATCGTGCAGGACGCCATCCACAACT 1977

Qy        617 TCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCC 671
              ||| |  |    ||     | |  || | |   ||| | ||  |   |  | |||
Db       1978 TCTCCCCCGCCTACCAGCACTACACGCAGCAGGCCACGCACGAGGCGCCCAGGCC 2032


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Job time : 15.9657 secs
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2006, 22:33:03 ; Search time 5834.3 Seconds
(without alignments)
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Title: US-10-821-670A-26
Perfect score: 921
Sequence: 1 atatgggaactggagaaaaa.....gggcatccgtgtcctgcagt 921

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 6366136 seqs, 31973710525 residues

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Database : GenEmbl:*
1: gb_env:*
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10: gb_vi:*
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12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	921	100.0	921	2	AR595948	AR595948 Sequence
c	2	921	100.0	921	2	AR595949	AR595949 Sequence
	3	921	100.0	1006	14	FCIL12P40	Y07762 Felis catus
	4	921	100.0	1533	2	AR595959	AR595959 Sequence
c	5	921	100.0	1533	2	AR595960	AR595960 Sequence
	6	921	100.0	1599	2	AR595956	AR595956 Sequence
c	7	921	100.0	1599	2	AR595957	AR595957 Sequence
	8	870	94.5	921	2	AR242436	AR242436 Sequence
	9	870	94.5	921	2	AR280204	AR280204 Sequence
	10	870	94.5	921	2	AR322419	AR322419 Sequence
	11	870	94.5	987	2	AR595950	AR595950 Sequence
c	12	870	94.5	987	2	AR595951	AR595951 Sequence
	13	870	94.5	2193	2	AR242435	AR242435 Sequence
	14	870	94.5	2193	2	AR280203	AR280203 Sequence
	15	870	94.5	2193	2	AR322418	AR322418 Sequence
	16	868	94.2	985	2	AR595967	AR595967 Sequence
c	17	868	94.2	985	2	AR595968	AR595968 Sequence
	18	819	88.9	921	2	AR242437	AR242437 Sequence
	19	819	88.9	921	2	AR280205	AR280205 Sequence
	20	819	88.9	921	2	AR322420	AR322420 Sequence
	21	780	84.7	990	14	FCU83184	U83184 Felis catus
	22	768	83.4	990	2	AX076200	AX076200 Sequence
	23	768	83.4	990	2	AX076482	AX076482 Sequence
	24	768	83.4	4522	2	AX076209	AX076209 Sequence
	25	768	83.4	4522	2	AX076476	AX076476 Sequence
	26	331	35.9	431	14	AF054607	AF054607 Felis cat
	27	83	9.0	990	2	AX154603	AX154603 Sequence
	28	66	7.2	921	2	AR595965	AR595965 Sequence
c	29	66	7.2	921	2	AR595966	AR595966 Sequence
	30	66	7.2	924	2	BD171282	BD171282 Novel can
	31	66	7.2	987	2	AR595969	AR595969 Sequence
c	32	66	7.2	987	2	AR595970	AR595970 Sequence
	33	66	7.2	990	2	AR151061	AR151061 Sequence
	34	66	7.2	990	2	AR151071	AR151071 Sequence
	35	66	7.2	990	2	BD014653	BD014653 Process f
	36	66	7.2	990	2	BD014663	BD014663 Process f
	37	66	7.2	990	2	E15017	E15017 Canine mRNA
	38	66	7.2	990	2	AR316460	AR316460 Sequence
	39	66	7.2	990	2	AR316470	AR316470 Sequence
	40	66	7.2	1533	2	AR595973	AR595973 Sequence
c	41	66	7.2	1533	2	AR595974	AR595974 Sequence
	42	66	7.2	1599	2	AR595971	AR595971 Sequence
c	43	66	7.2	1599	2	AR595972	AR595972 Sequence
	44	66	7.2	2154	2	BD171281	BD171281 Novel can
	45	66	7.2	2267	2	AR596011	AR596011 Sequence
c	46	66	7.2	2267	2	AR596012	AR596012 Sequence
	47	63	6.8	588	14	AF349536	AF349536 Canis fam
	48	63	6.8	1015	14	CFU49100	U49100 Canis famil
	49	61	6.6	621	7	BV242752	BV242752 S234P6134
	50	61	6.6	984	2	AX154598	AX154598 Sequence
	51	60	6.5	984	2	AX154599	AX154599 Sequence
	52	53	5.8	975	2	AX154602	AX154602 Sequence
	53	51	5.5	452	14	AF333121	AF333121 Canis fam
	54	51	5.5	821	6	RNU16674	U16674 Rattus norv
	55	51	5.5	1008	6	AF133197	AF133197 Rattus no
	56	49	5.3	984	2	AX154600	AX154600 Sequence
	57	49	5.3	1425	6	AF421395	AF421395 Sigmodon
	58	44	4.8	224	14	DQ152965	DQ152965 Ovis arie
	59	44	4.8	525	14	CEU10160	U10160 Cervus elap
	60	44	4.8	906	2	BD021808	BD021808 Natural k
	61	44	4.8	906	2	BD021809	BD021809 Natural k
	62	44	4.8	969	2	AX154601	AX154601 Sequence
	63	44	4.8	984	14	AF004024	AF004024 Ovis arie
	64	44	4.8	984	14	AF209435	AF209435 Ovis arie
	65	44	4.8	987	2	AR008950	AR008950 Sequence
	66	44	4.8	987	2	BD007070	BD007070 IL-12 gen
	67	44	4.8	987	2	BD007076	BD007076 Gene expr
	68	44	4.8	987	2	BD105974	BD105974 Animal mo
	69	44	4.8	987	2	BD136034	BD136034 Interfero
	70	44	4.8	987	2	CQ803342	CQ803342 Sequence
	71	44	4.8	987	2	CS131491	CS131491 Sequence
	72	44	4.8	987	2	I28591	I28591 Sequence 1
	73	44	4.8	987	2	AR533404	AR533404 Sequence
	74	44	4.8	987	2	AX154633	AX154633 Sequence
	75	44	4.8	993	14	AY603406	AY603406 Capra hir
	76	44	4.8	993	14	CEU57752	U57752 Cervus elap
	77	44	4.8	1005	5	AY234218	AY234218 Papio anu
	78	44	4.8	1005	5	CTU19834	U19834 Cercocebus
	79	44	4.8	1007	5	AF180563	AF180563 Homo sapi
	80	44	4.8	1008	14	AB246273	AB246273 Bubalus c
	81	44	4.8	1008	14	AB246353	AB246353 Bubalus b
	82	44	4.8	1008	14	AB246358	AB246358 Bubalus b
	83	44	4.8	1012	14	AF007576	AF007576 Capra hir
	84	44	4.8	1012	14	AY198121	AY198121 Bubalus b
	85	44	4.8	1012	14	BTU11815	U11815 Bos taurus
	86	44	4.8	1018	2	AR052857	AR052857 Sequence
	87	44	4.8	1018	2	AR288169	AR288169 Sequence
	88	44	4.8	1018	2	AR567156	AR567156 Sequence
	89	44	4.8	1019	2	E35794	E35794 Process for
	90	44	4.8	1029	2	CQ829448	CQ829448 Sequence
	91	44	4.8	1046	5	BC074723	BC074723 Homo sapi

92	44	4.8	1073	5	BC067498	BC067498 Homo sapi
93	44	4.8	1073	5	BC067499	BC067499 Homo sapi
94	44	4.8	1073	5	BC067500	BC067500 Homo sapi
95	44	4.8	1073	5	BC067501	BC067501 Homo sapi
96	44	4.8	1073	5	BC067502	BC067502 Homo sapi
97	44	4.8	1080	5	MMU19841	U19841 Macaca mula
98	44	4.8	1389	2	AR393788	AR393788 Sequence
99	44	4.8	1389	2	AX084106	AX084106 Sequence
100	44	4.8	1397	2	BD165800	BD165800 Antibody
101	44	4.8	1399	2	AR091391	AR091391 Sequence
102	44	4.8	1399	5	HUMCLMF40	M65272 Human cytot
103	44	4.8	1560	2	AR091395	AR091395 Sequence
104	44	4.8	1623	2	AR091394	AR091394 Sequence
105	44	4.8	1870	2	A92079	A92079 Sequence 3
106	44	4.8	1870	2	AR230691	AR230691 Sequence
107	44	4.8	2307	2	CQ715179	CQ715179 Sequence
108	44	4.8	2318	2	AR228993	AR228993 Sequence
109	44	4.8	2318	5	HUMNKSFP40	M65290 Human natur
110	44	4.8	2362	2	AR082684	AR082684 Sequence
111	44	4.8	2362	2	AR122960	AR122960 Sequence
112	44	4.8	2362	2	I28325	I28325 Sequence 1
113	44	4.8	2362	2	AR309636	AR309636 Sequence
114	44	4.8	2362	2	I89770	I89770 Sequence 1
115	44	4.8	5686	2	BD136048	BD136048 Interfero
116	44	4.8	6139	2	AR091393	AR091393 Sequence
117	39	4.2	993	14	AB107654	AB107654 Lama glam
118	39	4.2	15648	5	AF512686	AF512686 Homo sapi
119	39	4.2	18340	5	AY008847	AY008847 Homo sapi
120	39	4.2	108511	5	AC011418	AC011418 Homo sapi
121	38	4.1	446	14	AF091134	AF091134 Canis fam
122	37	4.0	508	6	AF097507	AF097507 Cavia por
123	37	4.0	999	6	AB025724	AB025724 Cavia por
c 124	35	3.8	681	7	BV440664	BV440664 S237P6324
125	35	3.8	972	8	AY191829	AY191829 Synthetic
126	35	3.8	975	2	AX154597	AX154597 Sequence
127	35	3.8	2090	14	SSU08317	U08317 Sus scrofa
128	32	3.5	1058	14	ECIL12P40	Y11129 Equus cabal
129	32	3.5	1626	8	AF401989	AF401989 Synthetic
c 130	30	3.3	30	2	AX027245	AX027245 Sequence
131	30	3.3	73	2	AR439759	AR439759 Sequence
132	30	3.3	73	2	AX268996	AX268996 Sequence
133	30	3.3	200	5	AY591921	AY591921 Macaca fa
134	30	3.3	600	2	E26663	E26663 Improved me
135	30	3.3	932	14	AY686641S1	AY686641 Equus cab
136	30	3.3	1061	2	AR069654	AR069654 Sequence
137	30	3.3	1143	6	AF128214	AF128214 Mus muscu
138	30	3.3	1143	6	AF128215	AF128215 Mus muscu
139	30	3.3	1381	6	BC103608	BC103608 Mus muscu
140	30	3.3	1381	6	BC103609	BC103609 Mus muscu
141	30	3.3	1381	6	BC103610	BC103610 Mus muscu
142	30	3.3	1381	6	BC103614	BC103614 Mus muscu
143	30	3.3	1409	2	AR393787	AR393787 Sequence
144	30	3.3	1409	2	AX084105	AX084105 Sequence
145	30	3.3	1472	2	AR393786	AR393786 Sequence
146	30	3.3	1472	2	AX084104	AX084104 Sequence
147	30	3.3	1569	2	AR393796	AR393796 Sequence
148	30	3.3	1569	2	AX084114	AX084114 Sequence
149	30	3.3	1582	14	AY686641S2	AY686644 Equus cab
150	30	3.3	1669	8	AF411293	AF411293 Synthetic
151	30	3.3	1840	6	MUSIL40A	M86671 Mus musculu
152	30	3.3	2013	2	AR393795	AR393795 Sequence
153	30	3.3	2013	2	AX084113	AX084113 Sequence
154	30	3.3	2438	2	CQ812173	CQ812173 Sequence
155	30	3.3	2709	2	AR393797	AR393797 Sequence
156	30	3.3	2709	2	AX084115	AX084115 Sequence
157	30	3.3	5252	2	CQ803341	CQ803341 Sequence
158	30	3.3	5966	2	BD136050	BD136050 Interfero
159	30	3.3	9049	2	CQ803350	CQ803350 Sequence
160	30	3.3	10633	2	CQ803349	CQ803349 Sequence
161	30	3.3	11746	2	CQ803348	CQ803348 Sequence
162	30	3.3	38246	2	CQ803351	CQ803351 Sequence
163	30	3.3	285389	12	AC096348	AC096348 Rattus no
164	29	3.1	528	6	AF082494	AF082494 Marmota m
165	29	3.1	984	6	AF288519	AF288519 Marmota m
166	29	3.1	984	6	MMIL12P40	X97019 M.monax mRN
167	29	3.1	1000	6	S82420S3	S82422 interleukin
168	29	3.1	76047	6	AL669944	AL669944 Mouse DNA
169	29	3.1	110000	12	AC073744_2	Continuation (3 of
170	29	3.1	110000	12	AC073744_3	Continuation (4 of
171	29	3.1	189236	6	AL607030	AL607030 Mouse DNA
c 172	29	3.1	268294	12	AC020885	AC020885 Mus muscu
173	29	3.1	287927	12	AC079530	AC079530 Mus muscu
174	28	3.0	2276	6	AB085792	AB085792 Mesocrice
c 175	25	2.7	25	2	AR595992	AR595992 Sequence
c 176	24	2.6	26	2	E26678	E26678 Improved me
177	24	2.6	987	2	BD007077	BD007077 Gene expr
178	24	2.6	987	2	BD007078	BD007078 Gene expr
179	24	2.6	987	2	BD136035	BD136035 Interfero
180	24	2.6	987	2	BD136036	BD136036 Interfero
181	23	2.5	500	6	S82420S4	S82423 interleukin
c 182	23	2.5	110000	12	AC073744_3	Continuation (4 of
183	23	2.5	142974	12	AC152028	AC152028 Dasypus n
184	23	2.5	268294	12	AC020885	AC020885 Mus muscu
c 185	22	2.4	25	2	AR595994	AR595994 Sequence
186	22	2.4	399	2	CS211342	CS211342 Sequence
187	22	2.4	399	2	CS214984	CS214984 Sequence
188	22	2.4	399	6	AF046211	AF046211 Mesocrice
189	22	2.4	37305	5	HS344F5	AL031712 Human DNA
c 190	22	2.4	87350	2	AR345191	AR345191 Sequence
c 191	22	2.4	87543	2	AR228903	AR228903 Sequence
c 192	22	2.4	87543	5	HSWRNG2	AF181897 Homo sapi
193	22	2.4	189944	5	AC009563	AC009563 Homo sapi
194	22	2.4	195680	5	AC120498	AC120498 Homo sapi
c 195	22	2.4	222263	12	AC156871	AC156871 Bos tauru
196	22	2.4	265786	5	AE006466	AE006466 Homo sapi
197	21	2.3	21	2	AX962589	AX962589 Sequence
c 198	21	2.3	21	2	AX027243	AX027243 Sequence
199	21	2.3	21	2	AX027244	AX027244 Sequence
200	21	2.3	23	2	E26688	E26688 Improved me

ALIGNMENTS

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RESULT 1
AR595948
LOCUS       AR595948                 921 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 26 from patent US 6818444.
ACCESSION   AR595948
VERSION     AR595948.1  GI:56646929
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 26 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 921;  DB 2;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
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Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
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Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
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Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
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Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
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Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
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Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
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Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 2
AR595949/c
LOCUS       AR595949                921 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 28 from patent US 6818444.
ACCESSION   AR595949
VERSION     AR595949.1  GI:56646930
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 28 16-NOV-2004;
            Heska Corporation; Fort Collins, CO

FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           100.0%;  Score 921;  DB 2;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
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Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
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Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
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Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
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Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
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Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
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Db         21 TGGGCATCCGTGTCCTGCAGT 1
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RESULT 3
FCIL12P40
LOCUS       FCIL12P40               1006 bp    mRNA    linear   MAM 18-APR-2005
DEFINITION  Felis catus mRNA for interleukin-12 p40 chain.
ACCESSION   Y07762
VERSION     Y07762.1  GI:2102664
KEYWORDS    interleukin-12 p40.
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1
  AUTHORS   Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
  TITLE     Molecular cloning of cat interleukin-12
  JOURNAL   Immunogenetics 45 (6), 462-463 (1997)
   PUBMED   9089110
REFERENCE   2  (bases 1 to 1006)
  AUTHORS   Schijns,V.E.C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
            Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
            Utrecht, NETHERLANDS
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /cell_type="lymphocyte"
                     /tissue_type="peripheral blood"
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     CDS             1. .990
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                     /db_xref="InterPro:IPR003961"
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ORIGIN

  Query Match           100.0%;  Score 921;  DB 14;  Length 1006;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
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Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
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Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
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Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
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Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
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Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
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Db        967 TGGGCATCCGTGTCCTGCAGT 987


RESULT 4
AR595959
LOCUS       AR595959                1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 43 from patent US 6818444.
ACCESSION   AR595959
VERSION     AR595959.1  GI:56646940
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 43 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
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  Query Match           100.0%;  Score 921;  DB 2;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
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Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
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Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
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Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
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Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
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Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
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RESULT 5
AR595960/c
LOCUS       AR595960               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 45 from patent US 6818444.
ACCESSION   AR595960
VERSION     AR595960.1  GI:56646941
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 45 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
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ORIGIN

  Query Match           100.0%;  Score 921;  DB 2;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

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Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
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Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
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Db        633 TGGGCATCCGTGTCCTGCAGT 613


RESULT 6
AR595956
LOCUS       AR595956               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 38 from patent US 6818444.
ACCESSION   AR595956
VERSION     AR595956.1  GI:56646937
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 38 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
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ORIGIN

  Query Match             100.0%;  Score 921;  DB 2;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

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Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
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Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

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Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
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Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
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Db        967 TGGGCATCCGTGTCCTGCAGT 987


RESULT 7
AR595957/c
LOCUS       AR595957               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 40 from patent US 6818444.
ACCESSION   AR595957
VERSION     AR595957.1  GI:56646938
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 40 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 921;  DB 2;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
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Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
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Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
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Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
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Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
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Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
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Db        633 TGGGCATCCGTGTCCTGCAGT 613


RESULT 8
AR242436
LOCUS       AR242436                 921 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 6 from patent US 6472509.
ACCESSION   AR242436
VERSION     AR242436.1  GI:27288853
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 6 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .921
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ORIGIN

  Query Match           94.5%;  Score 870;  DB 2;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Db           1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
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Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
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Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
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Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
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Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
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Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
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Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 9
AR280204
LOCUS       AR280204                 921 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 6 from patent US 6518045.
ACCESSION   AR280204
VERSION     AR280204.1  GI:29715594
KEYWORDS    .
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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 6 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .921
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ORIGIN

  Query Match             94.5%;  Score 870;  DB 2;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
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Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
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Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
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Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
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Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
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Qy        901 TGGGCATCCGTGTCCTGCAGT 921
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Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 10
AR322419
LOCUS       AR322419                 921 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 6 from patent US 6566097.
ACCESSION   AR322419
VERSION     AR322419.1  GI:33708172
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 6 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .921
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  Query Match             94.5%;  Score 870;  DB 2;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
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Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
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Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
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Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
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Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
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Qy        901 TGGGCATCCGTGTCCTGCAGT 921
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Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 11
AR595950
LOCUS       AR595950                 987 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 29 from patent US 6818444.
ACCESSION   AR595950
VERSION     AR595950.1  GI:56646931
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 29 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .987
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ORIGIN

  Query Match             94.5%;  Score 870;  DB 2;  Length 987;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
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Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
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Db        967 TGGGCATCCGTGTCCTGCAGT 987


RESULT 12
AR595951/c
LOCUS       AR595951                 987 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 31 from patent US 6818444.
ACCESSION   AR595951
VERSION     AR595951.1  GI:56646932
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 31 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             94.5%;  Score 870;  DB 2;  Length 987;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCAGT 1


RESULT 13
AR242435
LOCUS       AR242435               2193 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 5 from patent US 6472509.
ACCESSION   AR242435
VERSION     AR242435.1  GI:27288852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2193)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 5 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .2193
                     /organism="unknown"
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ORIGIN

  Query Match             94.5%;  Score 870;  DB 2;  Length 2193;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 189

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 249

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 309

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 369

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 429

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 489

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 549

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 609

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 669

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 729

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 789

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
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Db        790 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 849

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
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Db        850 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 909

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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Db        910 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 969

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 1029

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
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Db       1030 TGGGCATCCGTGTCCTGCAGT 1050


RESULT 14
AR280203
LOCUS       AR280203                2193 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 5 from patent US 6518045.
ACCESSION   AR280203
VERSION     AR280203.1  GI:29715593
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2193)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 5 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
ORIGIN

  Query Match             94.5%;  Score 870;  DB 2;  Length 2193;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db        130 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 189

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 249

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 309

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 369

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 429

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 489

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 549

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        550 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 609

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Db        610 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 669

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 729

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 789

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 849

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 909

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 1029

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db       1030 TGGGCATCCGTGTCCTGCAGT 1050


RESULT 15
AR322418
LOCUS       AR322418                2193 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 5 from patent US 6566097.
ACCESSION   AR322418
VERSION     AR322418.1  GI:33708171
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2193)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 5 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
ORIGIN

  Query Match             94.5%;  Score 870;  DB 2;  Length 2193;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 189

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 249

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 309

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 369
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Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 429

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 489

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 549

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 609

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 669

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 729

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 789

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 849

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 909

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 969

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 1029

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              .|||||||||||||||||||
Db       1030 TGGGCATCCGTGTCCTGCAGT 1050


RESULT 16
AR595967
LOCUS       AR595967                985 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 55 from patent US 6818444.
ACCESSION   AR595967
VERSION     AR595967.1  GI:56646948
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 985)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 55 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .985
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             94.2%;  Score 868;  DB 2;  Length 985;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCA 919
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Db        967 TGGGCATCCGTGTCCTGCA 985


RESULT 17
AR595968/c
LOCUS       AR595968                985 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 57 from patent US 6818444.
ACCESSION   AR595968
VERSION     AR595968.1  GI:56646949
KEYWORDS    .
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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 985)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 57 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .985
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             94.2%;  Score 868;  DB 2;  Length 985;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 860

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 800

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 740

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 680

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 620

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 560

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 500

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 440

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 380

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 320

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 260

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 200

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 140

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 80

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 20

Qy        901 TGGGCATCCGTGTCCTGCA 919
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Db         19 TGGGCATCCGTGTCCTGCA 1


RESULT 18
AR242437
LOCUS       AR242437                921 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 7 from patent US 6472509.
ACCESSION   AR242437
VERSION     AR242437.1  GI:27288854
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 7 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             88.9%;  Score 819;  DB 2;  Length 921;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches  919;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
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Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 19
AR280205
LOCUS       AR280205                 921 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 7 from patent US 6518045.
ACCESSION   AR280205
VERSION     AR280205.1  GI:29715595
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 7 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             88.9%;  Score 819;  DB 2;  Length 921;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches  919;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 20
AR322420
LOCUS       AR322420                 921 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 7 from patent US 6566097.
ACCESSION   AR322420
VERSION     AR322420.1  GI:33708173
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 7 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             88.9%;  Score 819;  DB 2;  Length 921;
  Best Local Similarity   99.8%;  Pred. No. 0;
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  Matches  919;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 21
FCU83184
LOCUS       FCU83184                990 bp    mRNA    linear   MAM 16-JUL-1999
DEFINITION  Felis catus interleukin-12 p40 subunit (IL-12) mRNA, complete cds.
ACCESSION   U83184
VERSION     U83184.1  GI:2735050
KEYWORDS    .
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Nucleotide and predicted peptide sequence of feline interleukin-12
            (IL-12)
  JOURNAL   DNA Seq. 8 (1-2), 77-82 (1997)
   PUBMED   9522125
REFERENCE   2  (bases 1 to 990)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal
            Veterinary Medicine, University of Zurich, Winterthurerstrasse 260,
            Zurich, ZH 8057, Switzerland
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="Felis catus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
     CDS             1. .990
                     /note="cytokine"
                     /codon_start=1
                     /product="interleukin-12 p40 subunit"
                     /protein_id="AAB93835.1"
                     /db_xref="GI:2735051"
                     /translation="MHPQQLVIAWFSLVLLAPPLMAIWELEKNVYVVELDWHPDAPGE
                     MVVLTCDTPEEDDITWTSDQSSEVLGSGKTLTIQVKEFADAGQYTCHKGGEVLSHSFL
                     LIHKKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFTVKSSR
                     GSSDPQGVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPAAEESLPIEVVVDAIHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFGV
                     QVQGKNNREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSNWASVSCS"
ORIGIN

  Query Match           84.7%;  Score 780;  DB 14;  Length 990;
  Best Local Similarity 99.9%;  Pred. No. 0;
  Matches  830;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         91 CCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGT 150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 CCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGT 216

Qy        151 AAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAA 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        217 AAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAA 276

Qy        211 GGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGG 270
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        277 GGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGG 336

Qy        271 TCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAG 330
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        337 TCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAG 396

Qy        331 GCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTG 390
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        397 GCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTG 456

Qy        391 AAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCA 450
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        457 AAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCA 516

Qy        451 GCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTG 510
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Db        517 GCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTG 576

Qy        511 GAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTG 570
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Db        577 GAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTG 636

Qy        571 GTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGAC 630
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        637 GTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGAC 696

Qy        631 ATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCAT 690
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        697 ATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCAT 756

Qy        691 GTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTA 750
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        757 GTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTA 816

Qy        751 ACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTG 810
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        817 ACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTG 876

Qy        811 GACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGA 870
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        877 GACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGA 936

Qy        871 GACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        937 GACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987


RESULT 22
AX076200
LOCUS       AX076200                990 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 1 from Patent WO0104155.
ACCESSION   AX076200
VERSION     AX076200.1  GI:12710825
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 1 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .990
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
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ORIGIN

  Query Match            83.4%;  Score 768;  DB 2;  Length 990;
  Best Local Similarity  99.7%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
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Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
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Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              ||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987


RESULT 23
AX076482
LOCUS       AX076482                990 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 8 from Patent WO0104280.
ACCESSION   AX076482
VERSION     AX076482.1  GI:12711034
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 8 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Sequence coding for SEQ ID NO 2, IL-12 p40"
ORIGIN
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  Query Match             83.4%;  Score 768;  DB 2;  Length 990;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
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Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987


RESULT 24
AX076209
LOCUS       AX076209               4522 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 10 from Patent WO0104155.
ACCESSION   AX076209
VERSION     AX076209.1  GI:12710834
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 10 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .4522
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Plasmid pMol-fil12p40"
ORIGIN

  Query Match             83.4%;  Score 768;  DB 2;  Length 4522;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3113 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 3172

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       3173 GGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 3232

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3233 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 3292

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3293 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 3352

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3353 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 3412

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3413 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 3472

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3473 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 3532

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       3533 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 3592

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3593 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 3652

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3653 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 3712

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3713 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 3772

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3773 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 3832
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Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3833 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 3892

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3893 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 3952

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       3953 AAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGGAGCAAC 4012

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db       4013 TGGGCATCCGTGTCCTGCAGT 4033


RESULT 25
AX076476
LOCUS       AX076476                4522 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 2 from Patent WO0104280.
ACCESSION   AX076476
VERSION     AX076476.1  GI:12711028
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 2 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .4522
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="IL-12p40"
ORIGIN

  Query Match           83.4%;  Score 768;  DB 2;  Length 4522;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3113 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 3172

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       3173 GGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 3232

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3233 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 3292

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3293 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 3352

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3353 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 3412

Qy        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3413 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 3472

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3473 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 3532

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       3533 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 3592

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3593 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 3652

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3653 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 3712

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3713 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 3772

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3773 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 3832

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3833 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 3892

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3893 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 3952

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       3953 AAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGGAGCAAC 4012

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db       4013 TGGGCATCCGTGTCCTGCAGT 4033


RESULT 26
AF054607
LOCUS       AF054607                431 bp    mRNA    linear   MAM 26-JUL-2000
DEFINITION  Felis catus interleukin 12 p40 subunit mRNA, partial cds.
ACCESSION   AF054607
VERSION     AF054607.1  GI:3126822
KEYWORDS    .
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1  (bases 1 to 431)
  AUTHORS   Harley,R., Helps,C.R., Harbour,D.A., Gruffydd-Jones,T.J. and
            Day,M.J.
  TITLE     Cytokine mRNA expression in lesions in cats with chronic
            gingivostomatitis
  JOURNAL   Clin. Diagn. Lab. Immunol. 6 (4), 471-478 (1999)
   PUBMED   10391845
REFERENCE   2  (bases 1 to 431)
  AUTHORS   Harley,R., Helps,C.R., Gruffydd-Jones,T.J., Day,M.J. and
            Harbour,D.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-1998) Clinical Veterinary Science, University of
            Bristol, Langford House, Langford, Bristol BS40 7DU, U.K.
FEATURES             Location/Qualifiers
     source          1. .431
                     /organism="Felis catus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
                     /cell_line="FL4"
                     /cell_type="T cell"
                     /note="persistant FIV infection"
     CDS             <1. .>431
                     /codon_start=1
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                     /product="interleukin 12 p40 subunit"
                     /protein_id="AAC15980.1"
                     /db_xref="GI:3126823"
                     /translation="CHKGXEVLSHSXVLIXEKEDGIWSTDILREQKESKNKIFLKCEA
                     KNYSGRFTCWWLTAISTDLKFTVKSSRGSSDPQGVTCGAATLSAEKVRVDNRDYKKYT
                     VECQEGSACPAAEESLPIEVVVDAIHKLKYENYTSSFFIRD"
ORIGIN

  Query Match            35.9%;  Score 331;  DB 14;  Length 431;
  Best Local Similarity  99.7%;  Pred. No. 3e-165;
  Matches  381;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        251 AAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAAATA 310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         50 AAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAAATA 109

Qy        311 AGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGA 370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        110 AGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGA 169

Qy        371 CGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCC 430
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 CGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCC 229

Qy        431 AAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGG 490
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 AAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGG 289

Qy        491 ATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGA 550
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 ATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGA 349

Qy        551 GCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCA 610
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 GCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCA 409

Qy        611 GCAGCTTCTTCATCAGGGACAT 632
              |||||||||||||||||||||
Db        410 GCAGCTTCTTCATCAGGGACAT 431


RESULT 27
AX154603
LOCUS       AX154603                990 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 7 from Patent WO0140257.
ACCESSION   AX154603
VERSION     AX154603.1  GI:14536186
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 7 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match             9.0%;  Score 83;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-32;
  Matches   83;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        799 AGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGC 858
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 AGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGC 924

Qy        859 GTGCAAGCCAGAGACCGCTACTA 881
              |||||||||||||||||||||||
Db        925 GTGCAAGCCAGAGACCGCTACTA 947


RESULT 28
AR595965
LOCUS       AR595965                921 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 52 from patent US 6818444.
ACCESSION   AR595965
VERSION     AR595965.1  GI:56646946
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 52 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             7.2%;  Score 66;  DB 2;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 2e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy        531 CTGCCC 536
              ||||||
Db        531 CTGCCC 536


RESULT 29
AR595966/c
LOCUS       AR595966                921 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 54 from patent US 6818444.
ACCESSION   AR595966
VERSION     AR595966.1  GI:56646947
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 54 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             7.2%;  Score 66;  DB 2;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 2e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy        531 CTGCCC 536
              ||||||
Db        391 CTGCCC 386


RESULT 30
```

```
BD171282
LOCUS       BD171282                924 bp    DNA     linear   PAT 18-FEB-2003
DEFINITION  Novel canine cytokine protein.
ACCESSION   BD171282
VERSION     BD171282.1  GI:28412572
KEYWORDS    JP 2002241398-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 924)
  AUTHORS   Imamura,T., Maeda,H., Tokiyoshi,Y. and Eda,Y.
  TITLE     Novel canine cytokine protein
  JOURNAL   Patent: JP 2002241398-A 2 28-AUG-2002;
            CHEMO SERO THERAPEUT RES INST
COMMENT     OS   Canine splenocyte
            PN   JP 2002241398-A/2
            PD   28-AUG-2002
            PF   03-JUN-1997 JP 1997161936
            PI   TAKAYUKI IMAMURA,HIROAKI MAEDA,YUKIO TOKIYOSHI,YASUYUKI EDA PC
              C07K14/52,A61K38/00,A61K39/395,C07K16/24,C12N5/10,C12N15/09, PC
            C12P21/02//
            PC   C12P21/08,(C12P21/02,C12R1:91),A61K37/02,C12N5/00,C12N15/00 CC
              Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES                Location/Qualifiers
     source             1. .924
                        /organism="unidentified"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32644"
ORIGIN

  Query Match             7.2%;  Score 66;  DB 2;  Length 924;
  Best Local Similarity   100.0%;  Pred. No. 2e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 533

Qy        531 CTGCCC 536
              ||||||
Db        534 CTGCCC 539


RESULT 31
AR595969
LOCUS       AR595969                987 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 58 from patent US 6818444.
ACCESSION   AR595969
VERSION     AR595969.1  GI:56646950
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 58 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES                Location/Qualifiers
     source             1. .987
                        /organism="unknown"
                        /mol_type="genomic DNA"
ORIGIN

  Query Match             7.2%;  Score 66;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        531 CTGCCC 536
              ||||||
Db        597 CTGCCC 602


RESULT 32
AR595970/c
LOCUS       AR595970                987 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 60 from patent US 6818444.
ACCESSION   AR595970
VERSION     AR595970.1  GI:56646951
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 60 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES                Location/Qualifiers
     source             1. .987
                        /organism="unknown"
                        /mol_type="genomic DNA"
ORIGIN

  Query Match             7.2%;  Score 66;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy        531 CTGCCC 536
              ||||||
Db        391 CTGCCC 386


RESULT 33
AR151061
LOCUS       AR151061                990 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 1 from patent US 6231850.
ACCESSION   AR151061
VERSION     AR151061.1  GI:15117111
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12
  JOURNAL   Patent: US 6231850-A 1 15-MAY-2001;
FEATURES                Location/Qualifiers
     source             1. .990
                        /organism="unknown"
                        /mol_type="unassigned DNA"
ORIGIN

  Query Match             7.2%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        531 CTGCCC 536
              ||||||
Db        597 CTGCCC 602
```

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RESULT 34
AR151071
LOCUS       AR151071                990 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 11 from patent US 6231850.
ACCESSION   AR151071
VERSION     AR151071.1  GI:15117121
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12
  JOURNAL   Patent: US 6231850-A 11 15-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             7.2%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        531 CTGCCC 536
              ||||||
Db        597 CTGCCC 602


RESULT 35
BD014653
LOCUS       BD014653                990 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy.
ACCESSION   BD014653
VERSION     BD014653.1  GI:22555436
KEYWORDS    JP 2001161378-A/1.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F.
  TITLE     Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy
  JOURNAL   Patent: JP 2001161378-A 1 19-JUN-2001;
            TORAY INDUSTRIES INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 2001161378-A/1
            PD   19-JUN-2001
            PF   26-SEP-2000 JP 2000292946
            PI   FUMIYOSHI OKANO
            PC   C12N15/09,A61K38/00,A61P17/00,A61P17/00,A61P31/04,A61P31/04,
            PC   A61P35/00,
            PC   A61P37/00,C07K1/18,C07K1/22,C07K14/54,C12P21/02//(C12P21/02,
            PC   C12R1:91),
            PC   (C12P21/02,C12R1:93),C12N15/00,A61K37/02
            CC   Process for producing highly pure protein, interleukin 12,  CC
                 protein
            CC   inhibiting interleukin-12 activity, remedies for mammalian  CC
                 immunopathy and
            CC   method of treating immunopathy
            FH   Key             Location/Qualifiers
            FT   CDS             (1). .(987)
            FT   mat_peptide     (67). .(987).
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="Canis sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9616"
ORIGIN

  Query Match             7.2%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        531 CTGCCC 536
              ||||||
Db        597 CTGCCC 602


RESULT 36
BD014663
LOCUS       BD014663                990 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy.
ACCESSION   BD014663
VERSION     BD014663.1  GI:22555446
KEYWORDS    JP 2001161378-A/11.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F.
  TITLE     Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy
  JOURNAL   Patent: JP 2001161378-A 11 19-JUN-2001;
            TORAY INDUSTRIES INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 2001161378-A/11
            PD   19-JUN-2001
            PF   26-SEP-2000 JP 2000292946
            PI   FUMIYOSHI OKANO
            PC   C12N15/09,A61K38/00,A61P17/00,A61P17/00,A61P31/04,A61P31/04,
            PC   A61P35/00,
            PC   A61P37/00,C07K1/18,C07K1/22,C07K14/54,C12P21/02//(C12P21/02,
            PC   C12R1:91),
            PC   (C12P21/02,C12R1:93),C12N15/00,A61K37/02
            CC   Process for producing highly pure protein, interleukin 12,  CC
                 protein
            CC   inhibiting interleukin-12 activity, remedies for mammalian  CC
                 immunopathy and
            CC   method of treating immunopathy
            FH   Key             Location/Qualifiers
            FT   CDS             (1). .(987)
            FT   mat_peptide     (67). .(987).
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="Canis sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9616"
ORIGIN

  Query Match             7.2%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
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Qy        531 CTGCCC 536
              ||||||
Db        597 CTGCCC 602


RESULT 37
E15017
LOCUS       E15017                   990 bp    DNA     linear   PAT 28-JUL-1999
DEFINITION  Canine mRNA for interleukin 12 40kDa subunit,complete cds.
ACCESSION   E15017
VERSION     E15017.1  GI:5709700
KEYWORDS    JP 1998036397-A/1.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F.
  TITLE     CANINE INTERLEUKIN 12 AND ITS PRODUCTION
  JOURNAL   Patent: JP 1998036397-A 1 10-FEB-1998;
            TORAY IND INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 1998036397-A/1
            PD   10-FEB-1998
            PF   08-NOV-1996 JP 1996296789
            PR   08-NOV-1995 JP 95P   289729, 23-MAY-1996 JP 96P   128104 PI
            OKANO FUMIYOSHI
            PC   C07K14/54,C07H21/04,C12N5/10,C12N15/09,C12P21/02,(C12N5/10, PC
              C12R1:91),
            PC   (C12P21/02,C12R1:91);
            CC   strandedness: Double;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .990
            FT                   /organism='Canis sp.'
            FT                   /tissue_type='liver'
            FT   CDS             1. .990
            FT                   /product='interleukin 12 40kDa subunit'.
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="Canis sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9616"
ORIGIN

  Query Match             7.2%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        531 CTGCCC 536
              ||||||
Db        597 CTGCCC 602


RESULT 38
AR316460
LOCUS       AR316460                 990 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 1 from patent US 6562334.
ACCESSION   AR316460
VERSION     AR316460.1  GI:33695288
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12 administration as an immune disease treatment
  JOURNAL   Patent: US 6562334-A 1 13-MAY-2003;
            Toray Industries, Inc.;;
            JPX;
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             7.2%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        531 CTGCCC 536
              ||||||
Db        597 CTGCCC 602


RESULT 39
AR316470
LOCUS       AR316470                 990 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 11 from patent US 6562334.
ACCESSION   AR316470
VERSION     AR316470.1  GI:33695298
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12 administration as an immune disease treatment
  JOURNAL   Patent: US 6562334-A 11 13-MAY-2003;
            Toray Industries, Inc.;;
            JPX;
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             7.2%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        531 CTGCCC 536
              ||||||
Db        597 CTGCCC 602


RESULT 40
AR595973
LOCUS       AR595973                1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 66 from patent US 6818444.
ACCESSION   AR595973
VERSION     AR595973.1  GI:56646954
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 66 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
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     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             7.2%;  Score 66;  DB 2;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy        531 CTGCCC 536
              ||||||
Db        531 CTGCCC 536


RESULT 41
AR595974/c
LOCUS       AR595974               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 68 from patent US 6818444.
ACCESSION   AR595974
VERSION     AR595974.1  GI:56646955
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 68 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             7.2%;  Score 66;  DB 2;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy        531 CTGCCC 536
              ||||||
Db       1003 CTGCCC 998


RESULT 42
AR595971
LOCUS       AR595971               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 61 from patent US 6818444.
ACCESSION   AR595971
VERSION     AR595971.1  GI:56646952
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 61 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             7.2%;  Score 66;  DB 2;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        531 CTGCCC 536
              ||||||
Db        597 CTGCCC 602


RESULT 43
AR595972/c
LOCUS       AR595972               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 63 from patent US 6818444.
ACCESSION   AR595972
VERSION     AR595972.1  GI:56646953
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 63 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             7.2%;  Score 66;  DB 2;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy        531 CTGCCC 536
              ||||||
Db       1003 CTGCCC 998


RESULT 44
BD171281
LOCUS       BD171281               2154 bp    DNA     linear   PAT 18-FEB-2003
DEFINITION  Novel canine cytokine protein.
ACCESSION   BD171281
VERSION     BD171281.1  GI:28412571
KEYWORDS    JP 2002241398-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 2154)
  AUTHORS   Imamura,T., Maeda,H., Tokiyoshi,Y. and Eda,Y.
  TITLE     Novel canine cytokine protein
  JOURNAL   Patent: JP 2002241398-A 1 28-AUG-2002;
            CHEMO SERO THERAPEUT RES INST
COMMENT     OS   Canine splenocyte
            PN   JP 2002241398-A/1
            PD   28-AUG-2002
            PF   03-JUN-1997 JP 1997161936
            PI   TAKAYUKI IMAMURA,HIROAKI MAEDA,YUKIO TOKIYOSHI,YASUYUKI EDA PC
              C07K14/52,A61K38/00,A61K39/395,C07K16/24,C12N5/10,C12N15/09, PC
            C12P21/02//
            PC   C12P21/08,(C12P21/02,C12R1:91),A61K37/02,C12N5/00,C12N15/00 CC
              Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
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FEATURES             Location/Qualifiers
     source          1. .2154
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             7.2%;  Score 66;  DB 2;  Length 2154;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 650

Qy        531 CTGCCC 536
              ||||||
Db        651 CTGCCC 656


RESULT 45
AR596011
LOCUS       AR596011                2267 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 107 from patent US 6818444.
ACCESSION   AR596011
VERSION     AR596011.1  GI:56646992
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2267)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 107 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .2267
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             7.2%;  Score 66;  DB 2;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 749

Qy        531 CTGCCC 536
              ||||||
Db        750 CTGCCC 755


RESULT 46
AR596012/c
LOCUS       AR596012                2267 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 109 from patent US 6818444.
ACCESSION   AR596012
VERSION     AR596012.1  GI:56646993
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2267)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 109 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .2267
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             7.2%;  Score 66;  DB 2;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1578 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1519

Qy        531 CTGCCC 536
              ||||||
Db       1518 CTGCCC 1513


RESULT 47
AF349536
LOCUS       AF349536                 588 bp    mRNA    linear   MAM 17-MAY-2001
DEFINITION  Canis familiaris interleukin-12 subunit p40 mRNA, partial cds.
ACCESSION   AF349536
VERSION     AF349536.1  GI:14133584
KEYWORDS    .
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 588)
  AUTHORS   Fonfara,S., Groene,A., Koenig,M. and Baumgaertner,W.
  TITLE     Sequence of canine interleukin-12-p40 mRNA in DH82-cells
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 588)
  AUTHORS   Fonfara,S., Groene,A., Koenig,M. and Baumgaertner,W.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-FEB-2001) Institute of Pathology,
            Justus-Liebig-University, Frankfurter Str. 96, Giessen 35392,
            Germany
FEATURES             Location/Qualifiers
     source          1. .588
                     /organism="Canis familiaris"
                     /mol_type="mRNA"
                     /db_xref="taxon:9615"
                     /cell_line="DH82"
     CDS             <1. .>588
                     /codon_start=3
                     /product="interleukin-12 subunit p40"
                     /protein_id="AAK54070.1"
                     /db_xref="GI:14133585"
                     /translation="QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVV
                     LTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIH
                     KKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFS
                     DPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGS"
ORIGIN

  Query Match             6.8%;  Score 63;  DB 14;  Length 588;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-22;
  Matches   63;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         22 GTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACC 81
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 GTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACC 140

Qy         82 TGC 84
              |||
Db        141 TGC 143


RESULT 48
CFU49100
LOCUS       CFU49100                1015 bp    mRNA    linear   MAM 13-MAR-1996
DEFINITION  Canis familiaris interleukin-12 p40 subunit mRNA, complete cds.
ACCESSION   U49100
VERSION     U49100.1  GI:1223907
```

```
KEYWORDS    .
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 1015)
  AUTHORS   Belke-Louis,G.F. and Buettner,M.
  TITLE     Cloning and sequence analysis of the p35 and p40 subunits of canine
            interleukin-12
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1015)
  AUTHORS   Belke-Louis,G.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-FEB-1996) Georg F. Belke-Louis, Institute of Med.
            Microbiology, Veterinaerstr. 13, Muenchen, D-80539, Germany
FEATURES             Location/Qualifiers
     source          1. .1015
                     /organism="Canis familiaris"
                     /mol_type="mRNA"
                     /db_xref="taxon:9615"
     CDS             1. .990
                     /codon_start=1
                     /product="interleukin-12 p40 subunit"
                     /protein_id="AAA92059.1"
                     /db_xref="GI:1223908"
                     /translation="MHPQQLVISWFSLVLLASSLMTIWELEKDVYVVELDWHPDAPGE
                     MVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLL
                     LIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSR
                     GFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHK
                     LKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCV
                     QAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSDWASVSCS"
ORIGIN

  Query Match             6.8%;  Score 63;  DB 14;  Length 1015;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-22;
  Matches   63;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         22 GTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACC 81
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 GTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACC 147

Qy         82 TGC 84
              |||
Db        148 TGC 150


RESULT 49
BV242752
LOCUS       BV242752                621 bp    DNA     linear   STS 19-JAN-2005
DEFINITION  S234P6134RD4.T0 EnglishShepherd Canis familiaris STS genomic,
            sequence tagged site.
ACCESSION   BV242752
VERSION     BV242752.1  GI:57305294
KEYWORDS    STS.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 621)
  AUTHORS   Lindblad-Toh,K.
  TITLE     The genome sequence of Canis familiaris
  JOURNAL   Unpublished (2004)
COMMENT
            Contact: Kerstin Lindblad-Toh
            Whitehead Institute for Biomedical Research, Center for Genome
            Research
            320 Charles Street, Cambridge, MA 02141, USA
            Tel: 6172521477
            Fax: 6172580903
            Email: kersli@genome.wi.mit.edu
            Primer A: No sequence submitted
            Primer B: No sequence submitted
            STS size: 621
            Protocol:
            WGS-discovery (WGS):
            Paired-end low-coverage whole genome shotgun reads were generated
            from 9 breeds
            (German Shepherd, Rottweiler, Bedlington Terrier, Beagle, Labrador
            Retriever, English
            Shepherd, Italian Greyhound, Alaskan Malamute and the Portuguese
            Water Dog -100,000 each)
            and five other canids (Chinese, Alaskan, Indian and Spanish Gray
            Wolf as well as the
            Californian Coyote).
            The WGS reads were placed uniquely on the CanFam1.0 boxer assembly
            and SNP detection was
            carried out by SSAHA-SNP. 863872 reads were annotated as STSs and
            485941 SNPs were
            annotated with alleles from the boxer and the breed or canid from
            which the particular
            read came. The validation rate for these SNPs was estimated at
            approximately 98%.
            WGA-discovery (WGA) of Boxer/Poodle SNPs:
            A second set of SNPs was generated using a similar methodology
            except that the contigs
            from the 1.5x poodle assembly (Kirkness 2003) were used instead of
            WGS reads. Since this
            sequence lacked base quality scores, arbitrary quality scores of
            phred 40 were assigned
            before the poddle seqeunce was placed uniquely on the CanFam1.0
            boxer assembly and SNP
            detection was carried out by SSAHA-SNP. 1637780 SNPs were annotated
            with alleles from the
            boxer and the poodle. The validation rate for these SNPs was
            estimated at approximately TBD%.
            Internal-WGA-discovery (I-WGA):
            A third set of SNPs were discovered by comparing reads in the WGA
            assembly. SNPs were
            defined as mismatch positions that had a base quality of >= 30 on
            both reads in a region
            that aligned without gaps, and with at most one additional mismatch
            in the ten flanking
            bases. For each allele, at least one additional read had to confirm
            it. 731476 SNPs were
            annotated with alleles between the two boxer alleles. The
            validation rate for these SNPs
            was estimated at approximately TBD%.
FEATURES             Location/Qualifiers
     source          1. .621
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /strain="EnglishShepherd"
                     /db_xref="taxon:9615"
                     /map="+ 4 22-568 54361767-54362313"
                     /clone_lib="EnglishShepherd"
     STS             <1. .>621
ORIGIN

  Query Match             6.6%;  Score 61;  DB 7;  Length 621;
  Best Local Similarity   100.0%;  Pred. No. 1e-20;
  Matches   61;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        807 CGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGC 866
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 CGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGC 328

Qy        867 C 867
              |
Db        329 C 329


RESULT 50
AX154598
LOCUS       AX154598                984 bp    DNA     linear   PAT 22-JUN-2001
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```
DEFINITION  Sequence 2 from Patent WO0140257.
ACCESSION   AX154598
VERSION     AX154598.1  GI:14536181
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 2 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .984
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match             6.6%;  Score 61;  DB 2;  Length 984;
  Best Local Similarity   100.0%;  Pred. No. 9.2e-21;
  Matches   61;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        607 ACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTG 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        673 ACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTG 732

Qy        667 A 667
              |
Db        733 A 733


RESULT 51
AX154599
LOCUS       AX154599                984 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 3 from Patent WO0140257.
ACCESSION   AX154599
VERSION     AX154599.1  GI:14536182
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 3 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .984
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match             6.5%;  Score 60;  DB 2;  Length 984;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-20;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAAC 657
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAAC 723


RESULT 52
AX154602
LOCUS       AX154602                975 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 6 from Patent WO0140257.
ACCESSION   AX154602
VERSION     AX154602.1  GI:14536185
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 6 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .975
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match             5.8%;  Score 53;  DB 2;  Length 975;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-16;
  Matches   53;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        829 GTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTA 881
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 GTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTA 926


RESULT 53
AF333121
LOCUS       AF333121                452 bp    mRNA    linear   MAM 06-FEB-2001
DEFINITION  Canis familiaris interleukin 12 subunit p40 mRNA, partial cds.
ACCESSION   AF333121
VERSION     AF333121.1  GI:12667429
KEYWORDS    .
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 452)
  AUTHORS   Markus,S. and Baumgaertner,W.
  TITLE     Expression of canine interleukin-12 subunit p40 mRNA in a
            continuous macrophage cell line
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 452)
  AUTHORS   Markus,S. and Baumgaertner,W.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-JAN-2001) Department of Veterinary Pathology,
            Justus-Liebig-University of Giessen, Frankfurter Strasse 96,
            Giessen 35392, Germany
FEATURES             Location/Qualifiers
     source          1. .452
                     /organism="Canis familiaris"
                     /mol_type="mRNA"
                     /db_xref="taxon:9615"
                     /cell_line="DH 82"
                     /cell_type="macrophage"
                     /note="amplified using primer pair p77s/p34as"
     CDS             <1. .>452
                     /codon_start=2
                     /product="interleukin 12 subunit p40"
                     /protein_id="AAK01441.1"
                     /db_xref="GI:12667430"
                     /translation="TCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHK
                     GGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAIST
                     DLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGS"
ORIGIN

  Query Match             5.5%;  Score 51;  DB 14;  Length 452;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-15;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGA 521
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGA 444
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RESULT 54
RNU16674
LOCUS       RNU16674                821 bp    mRNA    linear   ROD 07-NOV-1994
DEFINITION  Rattus norvegicus interleukin-12p40 mRNA, partial cds.
ACCESSION   U16674
VERSION     U16674.1  GI:565093
KEYWORDS    .
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 821)
  AUTHORS   Goodman,R.E. and Toews,G.B.
  TITLE     A partial cDNA of the coding region of rat IL-12p40, cloned by
            RT/PCR from Staphlococcal endotoxin stimulated splenocytes
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 821)
  AUTHORS   Goodman,R.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-OCT-1994) Richard E. Goodman, Internal
            Medicine/Pulmonary, University of Michigan, 1150 W. Medical Center
            Dr., 3311 Med. Sci. I, Ann Arbor, MI 48109-0652, USA
FEATURES             Location/Qualifiers
     source          1. .821
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Fischer"
                     /db_xref="taxon:10116"
                     /tissue_type="cultured splenocytes (SEA plus SEB
                     stimulation)"
     CDS             17. .>821
                     /note="encodes the N-terminal 268 amino acids of the
                     expected 335 amino acids encoded by the mouse gene"
                     /codon_start=1
                     /product="interleukin-12p40"
                     /protein_id="AAA52229.1"
                     /db_xref="GI:565094"
                     /translation="MCHQKLTFSWFAMVLLVSPLMAMWELEKDVYVVEVDWRPDAPGE
                     TVTLTCDSPEEDDITWTSDQRRGVIGSGKTLTITVREFLDAGQYTCHRGGETLSHSHL
                     LLHKKENGIWSTEILKNFKNKTFLKREAPNYSGRFTCSWLVHRNTDLKFNIKSSSSSP
                     ESRAVTCGAASLSAEKVTLNQRDYEKYSVACQEDVTCPTAEETLPIELVVEAQQQNKY
                     ENYSTSFFIRDIIKPDPPKNLQVKPLKNSQVEVSWEYPDSWSTPHSYFSL"
ORIGIN

  Query Match             5.5%;  Score 51;  DB 6;  Length 821;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-15;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        612 CAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCA 662
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 CAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCA 735


RESULT 55
AF133197
LOCUS       AF133197                1008 bp    mRNA    linear   ROD 08-APR-1999
DEFINITION  Rattus norvegicus interleukin-12 p40 precursor, mRNA, complete cds.
ACCESSION   AF133197
VERSION     AF133197.1  GI:4574731
KEYWORDS    .
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 1008)
  AUTHORS   Khalife,J., Pierrot,C., Cocude,C., Cetre,C., Godin,C. and Capron,A.
  TITLE     Molecular cloning and sequencing of the rat interleukin-12 p40 gene
  JOURNAL   Eur. Cytokine Netw. 9 (1), 69-73 (1998)
   PUBMED   9613680
REFERENCE   2  (bases 1 to 1008)
  AUTHORS   Khalife,J., Pierrot,C., Cocude,C., Cetre,C., Godin,C. and Capron,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAR-1999) InSERM U167, 1, rue du professeur Calmette,
            Lille 59019, France
FEATURES             Location/Qualifiers
     source          1. .1008
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Fischer"
                     /db_xref="taxon:10116"
     CDS             1. .1008
                     /note="IL-12P40"
                     /codon_start=1
                     /product="interleukin-12 p40 precursor"
                     /protein_id="AAD24190.1"
                     /db_xref="GI:4574732"
                     /translation="MCHQKLTFSWFAMVLLVSPLMAMWELEKDVYVVEVDWRPDAPGE
                     TVTLTCDSPEEDDITWTSDQRRGVIGSGKTLTITVREFLDAGQYTCHRGGETLSHSHL
                     LLHKKENGIWSTEILKNFKNKTFLKCEAPNYSGRFTCSWLVHRNTDLKFNIKSSSSSP
                     ESRAVTCGRASLSAEKVTLNQRDYEKYSVACQEDVTCPTAEETLPIELVVEAQQQNKY
                     ENYSTSFFIRDIIKPDPPKNLQVKPLKNSQVEVSWEYPDSWSTPHSYFSLKFFVRIQR
                     KKEKTKETEEECNQKGAFLVEKTSAEVQCKGANICVQAQDRYYNSSCSKWTCVPCRGR
                     S"
ORIGIN

  Query Match             5.5%;  Score 51;  DB 6;  Length 1008;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-15;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        612 CAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCA 662
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 CAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCA 719


RESULT 56
AX154600
LOCUS       AX154600                984 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 4 from Patent WO0140257.
ACCESSION   AX154600
VERSION     AX154600.1  GI:14536183
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 4 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .984
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match             5.3%;  Score 49;  DB 2;  Length 984;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-14;
  Matches   49;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        385 GATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAG 433
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAG 499


RESULT 57
AF421395
LOCUS       AF421395                1425 bp    mRNA    linear   ROD 07-JUL-2004
DEFINITION  Sigmodon hispidus interleukin 12 p40 subunit precursor, mRNA,
            complete cds.
ACCESSION   AF421395
VERSION     AF421395.1  GI:16304138
```

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KEYWORDS    .
SOURCE      Sigmodon hispidus (hispid cotton rat)
  ORGANISM  Sigmodon hispidus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Cricetidae; Sigmodontinae; Sigmodon.
REFERENCE   1  (bases 1 to 1425)
  AUTHORS   Blanco,J.C., Pletneva,L., Boukhvalova,M., Richardson,J.Y.,
            Harris,K.A. and Prince,G.A.
  TITLE     The cotton rat: an underutilized animal model for human infectious
            diseases can now be exploited using specific reagents to cytokines,
            chemokines, and interferons
  JOURNAL   J. Interferon Cytokine Res. 24 (1), 21-28 (2004)
   PUBMED   14980081
REFERENCE   2  (bases 1 to 1425)
  AUTHORS   Pletneva,L.M., Bacot,S., Blanco,J.C., Langley,R.J. and Prince,G.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-SEP-2001) Molecular Biology, Virion Systems Inc.,
            9610 Medical Center Drive, Suite 100, Rockville, MD 20850, USA
FEATURES             Location/Qualifiers
     source          1. .1425
                     /organism="Sigmodon hispidus"
                     /mol_type="mRNA"
                     /db_xref="taxon:42415"
     CDS             25. .1008
                     /codon_start=1
                     /product="interleukin 12 p40 subunit precursor"
                     /protein_id="AAL16936.1"
                     /db_xref="GI:16304139"
                     /translation="MCHQKLTISWFAMVLLVSPLMAIWELEKDVYVVEVDWSPGAPGE
                     RVVLTCDTSEEDDIIWTSDQSSEVVGSGKTLIVQVKEFSDAGQYTCHKGGETLSHSRL
                     LLHKKEDGIWSTDILKDQKDPKNKTFLKCEAANYSGRFTCWWLTAVSTDLKFSLKSSS
                     SSSDSRSVTCGAASLSTEKVTVDQRDYNKYSVACQEDITCPTAEETLPIELVMEAQHK
                     YKYENYSTGFFIRDIIKPDPPKNLQLKPLKSSQVEVSWEYPDSWSTPHSYFSLKFFVQ
                     VYRKKEKKGESLLVDKPSAKIRCSKGGEVRVRAQDHYYNSSWSEWASVSCN"
ORIGIN

  Query Match             5.3%;  Score 49;  DB 6;  Length 1425;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-14;
  Matches   49;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        614 GCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCA 662
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        704 GCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCA 752


RESULT 58
DQ152965
LOCUS       DQ152965                224 bp    mRNA    linear   MAM 07-NOV-2005
DEFINITION  Ovis aries interleukin-12 p40 subunit precursor (IL-12) mRNA,
            partial cds.
ACCESSION   DQ152965
VERSION     DQ152965.1  GI:77744673
KEYWORDS    .
SOURCE      Ovis aries (sheep)
  ORGANISM  Ovis aries
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Caprinae; Ovis.
REFERENCE   1  (bases 1 to 224)
  AUTHORS   Ingham,A.B., Menzies,M.L. and Kijas,J.W.
  TITLE     Sequence diversity and rates of molecular evolution between sheep
            and cattle genes
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 224)
  AUTHORS   Ingham,A.B., Menzies,M.L. and Kijas,J.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-2005) Livestock Industries, CSIRO, QBP 306
            Carmody Rd, St Lucia, Queensland 4067, Australia
FEATURES             Location/Qualifiers
     source          1. .224
                     /organism="Ovis aries"
                     /mol_type="mRNA"
                     /db_xref="taxon:9940"
     gene            <1. .>224
                     /gene="IL-12"
     CDS             <1. .>224
                     /gene="IL-12"
                     /codon_start=2
                     /product="interleukin-12 p40 subunit precursor"
                     /protein_id="ABB02298.1"
                     /db_xref="GI:77744674"
                     /translation="IEVVMEAVHKLKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQ
                     VEVSWEYPDTWSTPHSYFSLTFCVQVQGKN"
ORIGIN

  Query Match             4.8%;  Score 44;  DB 14;  Length 224;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db         41 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 84


RESULT 59
CEU10160
LOCUS       CEU10160                525 bp    mRNA    linear   MAM 09-JUL-1994
DEFINITION  Cervus elaphus interleukin 12 mRNA, partial cds.
ACCESSION   U10160
VERSION     U10160.1  GI:508867
KEYWORDS    .
SOURCE      Cervus elaphus (red deer)
  ORGANISM  Cervus elaphus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Cervidae; Cervinae; Cervus.
REFERENCE   1  (bases 1 to 525)
  AUTHORS   Lockhart,E.A.
  TITLE     Cloning and sequencing of cervine IL-12
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 525)
  AUTHORS   Lockhart,E.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-MAY-1994) Euan A. Lockhart, Microbiology, Deer
            Research Laboratory, University of Otago, Union St., Dunedin, New
            Zealand
FEATURES             Location/Qualifiers
     source          1. .525
                     /organism="Cervus elaphus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9860"
     CDS             <1. .>525
                     /standard_name="IL-12"
                     /codon_start=2
                     /product="interleukin 12"
                     /protein_id="AAA19658.1"
                     /db_xref="GI:508868"
                     /translation="AGQYTCHKGGEVLSRSLLLLHKKEDGIWSTDILKDQKEPKAKSF
                     LKCEAKDYSGHFTCWWLTAISTDLKFSVKSSRGSSDPRGVTCGAMSLSTEKVIVDHRE
                     YKKYTVECQEGSACPAAEESLPIEVVVEAVHKLKYENYTSSFFIRDIIKPDPPKNLQL
                     RPLKNSRQVEVSWE"
ORIGIN

  Query Match             4.8%;  Score 44;  DB 14;  Length 525;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        413 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 456


RESULT 60
BD021808
LOCUS       BD021808                906 bp    DNA     linear   PAT 27-AUG-2002
```

```
DEFINITION  Natural killer stimulatory factor.
ACCESSION   BD021808
VERSION     BD021808.1  GI:22563031
KEYWORDS    JP 2001245678-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 906)
  AUTHORS   Trinchieri,G., Perussia,B., Kobayashi,M., Clark,S.C., Wong,G.G. and
            Hewick,R.M.
  TITLE     Natural killer stimulatory factor
  JOURNAL   Patent: JP 2001245678-A 1 11-SEP-2001;
            GENETICS INSTITUTE INC,THE WISTAR INSTITUTE
COMMENT     OS   Unidentified
            PN   JP 2001245678-A/1
            PD   11-SEP-2001
            PF   10-JAN-2001 JP 2001002839
            PR   10-NOV-1988 US       269945,07-FEB-1989 US       307817 PI
            GIORGIO TRINCHIERI,BICE PERUSSIA,MICHIKO KOBAYASHI,STEVEN C  PI
            CLARK,
            PI   GORDON G WONG,RODNEY M HEWICK
            PC   C12N15/09,A61K38/00,A61K39/395,A61P35/00,A61P35/02,A61P37/04,
            PC   A61P43/00,
            PC   C07K16/24,G01N33/53//C07K14/52,C12N15/00,A61K37/02 CC
            Natural killer stimulatory factor
            FH   Key             Location/Qualifiers
            FT   source          1. .906
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .906
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             4.8%;  Score 44;  DB 2;  Length 906;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        693 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 736


RESULT 61
BD021809
LOCUS       BD021809                906 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Natural killer stimulatory factor.
ACCESSION   BD021809
VERSION     BD021809.1  GI:22563032
KEYWORDS    JP 2001245678-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 906)
  AUTHORS   Trinchieri,G., Perussia,B., Kobayashi,M., Clark,S.C., Wong,G.G. and
            Hewick,R.M.
  TITLE     Natural killer stimulatory factor
  JOURNAL   Patent: JP 2001245678-A 2 11-SEP-2001;
            GENETICS INSTITUTE INC,THE WISTAR INSTITUTE
COMMENT     OS   Unidentified
            PN   JP 2001245678-A/2
            PD   11-SEP-2001
            PF   10-JAN-2001 JP 2001002839
            PR   10-NOV-1988 US       269945,07-FEB-1989 US       307817 PI
            GIORGIO TRINCHIERI,BICE PERUSSIA,MICHIKO KOBAYASHI,STEVEN C  PI
            CLARK,
            PI   GORDON G WONG,RODNEY M HEWICK
            PC   C12N15/09,A61K38/00,A61K39/395,A61P35/00,A61P35/02,A61P37/04,
            PC   A61P43/00,
            PC   C07K16/24,G01N33/53//C07K14/52,C12N15/00,A61K37/02 CC
            Natural killer stimulatory factor
            FH   Key             Location/Qualifiers
            FT   source          1. .906
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .906
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             4.8%;  Score 44;  DB 2;  Length 906;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        693 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 736


RESULT 62
AX154601
LOCUS       AX154601                969 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 5 from Patent WO0140257.
ACCESSION   AX154601
VERSION     AX154601.1  GI:14536184
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 5 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .969
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match             4.8%;  Score 44;  DB 2;  Length 969;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        649 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 692


RESULT 63
AF004024
LOCUS       AF004024                984 bp    mRNA    linear   MAM 14-NOV-2000
DEFINITION  Ovis aries interleukin-12 p40 subunit precursor, mRNA, complete
            cds.
ACCESSION   AF004024
VERSION     AF004024.2  GI:5870870
KEYWORDS    .
SOURCE      Ovis aries (sheep)
  ORGANISM  Ovis aries
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Caprinae; Ovis.
REFERENCE   1  (bases 1 to 984)
  AUTHORS   Swinburne,S.J., Russ,G.R. and Krishnan,R.
  TITLE     Ovine interleukin 12 has biological activity on ovine and human
            activated peripheral blood mononuclear cells
  JOURNAL   Cytokine 12 (10), 1546-1552 (2000)
   PUBMED   11023671
REFERENCE   2  (bases 1 to 984)
  AUTHORS   Swinburne,S.J., Russ,G.R. and Krishnan,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-MAY-1997) Transplantation Immunology Laboratory,
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            Queen Elizabeth Hospital, 28 Woodville Road, Adelaide, South
            Australia 5011, Australia
REFERENCE   3  (bases 1 to 984)
  AUTHORS   Swinburne,S.J., Russ,G.R. and Krishnan,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-SEP-1999) Transplantation Immunology Laboratory, The
            Queen Elizabeth Hospital, 28 Woodville Rd., Adelaide, South
            Australia, Australia
  REMARK    Sequence update by submitter
COMMENT     On Sep 13, 1999 this sequence version replaced gi:2199555.
FEATURES             Location/Qualifiers
     source          1. .984
                     /organism="Ovis aries"
                     /mol_type="mRNA"
                     /db_xref="taxon:9940"
                     /cell_type="peripheral blood mononuclear"
     CDS             1. .984
                     /function="cytokine"
                     /note="IL-12"
                     /codon_start=1
                     /product="interleukin-12 p40 subunit precursor"
                     /protein_id="AAB61368.2"
                     /db_xref="GI:5870871"
                     /translation="MHPQQLVVSWFSLVLLASPIVAIWELEKNVYVVELDWYPNAPGE
                     TVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSRSLL
                     LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCSWLTAISTNLKFSVKSSR
                     GSSDPRGVTCGAASLSAEKVSMDHREYNKYTVECQEGSACPAAEESLPIEVVMEAVHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                     QVQGKNKREKKLFTDQTSAKVTCHKDANIRVQARDRYYSSFWSEWASVSCS"
     sig_peptide     1. .66
     mat_peptide     67. .981
                     /product="interleukin-12 p40 subunit"
ORIGIN

  Query Match             4.8%;  Score 44;  DB 14;  Length 984;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707


RESULT 64
AF209435
LOCUS       AF209435                984 bp    mRNA    linear   MAM 03-FEB-2000
DEFINITION  Ovis aries interleukin 12 p40 subunit precursor (IL-12 p40) mRNA,
            complete cds.
ACCESSION   AF209435
VERSION     AF209435.1  GI:6636341
KEYWORDS    .
SOURCE      Ovis aries (sheep)
  ORGANISM  Ovis aries
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Caprinae; Ovis.
REFERENCE   1  (bases 1 to 984)
  AUTHORS   De Rose,R., Scheerlinck,J.-P.Y., Casey,G., Wood,P.R., Tennent,J.M.
            and Chaplin,P.J.
  TITLE     Ovine Interleukin 12: Analysis of biological function and species
            comparison
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 984)
  AUTHORS   De Rose,R., Scheerlinck,J.-P.Y., Casey,G., Wood,P.R., Tennent,J.M.
            and Chaplin,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-NOV-1999) Animal Health, CSIRO, Park Drive and
            Flemington Road, Parkville, Victoria 3052, Australia
FEATURES             Location/Qualifiers
     source          1. .984
                     /organism="Ovis aries"
                     /mol_type="mRNA"
                     /strain="Merino"
                     /db_xref="taxon:9940"
                     /cell_type="mononuclear"
                     /tissue_type="peripheral blood"
     gene            1. .984
                     /gene="IL-12 p40"
     CDS             1. .984
                     /gene="IL-12 p40"
                     /note="cytokine; contains 10 cysteine residues"
                     /codon_start=1
                     /product="interleukin 12 p40 subunit precursor"
                     /protein_id="AAF20151.1"
                     /db_xref="GI:6636342"
                     /translation="MHPQQLVVSWFSLVLLASPIVAIWELEKNVYVVELDWYPNAPGE
                     TVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSRSLL
                     LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCSWLTAISTNLKFSVKSSR
                     GSSDPRGVTCGAASLSAEKVSMDHREYNKYTVECQEGSACPAAEESLPIEVVMEAVHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                     QVQGKNKREKKLFADQTSAKVTCHKDANIRVQARDRYYSSFWSEWASVSCS"
     sig_peptide     1. .66
                     /gene="IL-12 p40"
     mat_peptide     67. .981
                     /gene="IL-12 p40"
                     /product="interleukin 12 p40 subunit"
     misc_feature    667. .669
                     /gene="IL-12 p40"
                     /note="putative N-linked site; glycosylation site"
     misc_feature    793. .795
                     /gene="IL-12 p40"
                     /note="putative O-linked site; glycosylation site"
ORIGIN

  Query Match             4.8%;  Score 44;  DB 14;  Length 984;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707


RESULT 65
AR008950
LOCUS       AR008950                987 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 1 from patent US 5756085.
ACCESSION   AR008950
VERSION     AR008950.1  GI:3967755
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Sykes,M. and Wolf,S.F.
  TITLE     Use of interleukin-12 to prevent graft versus host disease
  JOURNAL   Patent: US 5756085-A 1 26-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             4.8%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 66
BD007070
LOCUS       BD007070                987 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  IL-12 gene expression and delivery systems and uses.
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```
ACCESSION   BD007070
VERSION     BD007070.1  GI:18635441
KEYWORDS    JP 2001503257-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Nodosutoromu,J., Freemark,B. and Dishupande,D.
  TITLE     IL-12 gene expression and delivery systems and uses
  JOURNAL   Patent: JP 2001503257-A 1 13-MAR-2001;
            BARENTISU INC,SYNTEX INC
COMMENT     OS   Unidentified
            PN   JP 2001503257-A/1
            PD   13-MAR-2001
            PF   10-OCT-1997 JP 1998519514
            PR   18-OCT-1996 US    60/028676
            PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
            C12N15/09,A61K31/711,A61K38/00,A61K47/18,A61K47/28,A61K48/00, PC
            A61P11/06,
            PC   C12N15/00,A61K37/02
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .987
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             4.8%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 67
BD007076
LOCUS       BD007076                  987 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Gene expression and delivery systems and uses.
ACCESSION   BD007076
VERSION     BD007076.1  GI:18635447
KEYWORDS    JP 2001503258-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Nodosutoromu,J., Freemark,B. and Dishupande,D.
  TITLE     Gene expression and delivery systems and uses
  JOURNAL   Patent: JP 2001503258-A 1 13-MAR-2001;
            BARENTISU INC
COMMENT     OS   Unidentified
            PN   JP 2001503258-A/1
            PD   13-MAR-2001
            PF   10-OCT-1997 JP 1998519520
            PR   18-OCT-1996 US    60/028687
            PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
            C12N15/09,A61K48/00,A61P11/06,A61P35/00,A61P43/00//C07K14/54, PC
            C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .987
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             4.8%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 68
BD105974
LOCUS       BD105974                  987 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Animal model for evaluation of vaccines.
ACCESSION   BD105974
VERSION     BD105974.1  GI:23200792
KEYWORDS    JP 2002501375-A/24.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Chang,L.J.
  TITLE     Animal model for evaluation of vaccines
  JOURNAL   Patent: JP 2002501375-A 24 15-JAN-2002;
            LUNG JI CHANG
COMMENT     PN   JP 2002501375-A/24
            PD   15-JAN-2002
            PF   09-APR-1998 JP 1998543062
            PR   09-APR-1997 US    08/838702,01-MAY-1997 US    08/848760 PR
            09-DEC-1997 US    60/069163
            PI   LUNG JI CHANG
            PC   A01K67/027,C12N7/01,C12N1/10,C07K14/16,A61K39/008,C12N1/36, PC
              C12N7/04,
            PC   A61K39/21
            CC   Strandedness: Double;
            CC   Topology: Linear;
            CC   /desc = 'DNA'
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             4.8%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 69
BD136034
LOCUS       BD136034                  987 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Interferon alpha plasmid and delivery system and method of
            preparing and using the same.
ACCESSION   BD136034
VERSION     BD136034.1  GI:23230979
KEYWORDS    JP 2002506647-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.
  TITLE     Interferon alpha plasmid and delivery system and method of
            preparing and using the same
```

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  JOURNAL   Patent: JP 2002506647-A 1 05-MAR-2002;
            VALENTIS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002506647-A/1
            PD   05-MAR-2002
            PF   12-MAR-1999 JP 2000536861
            PR   19-MAR-1998 US    60/078654
            PI   JEFF NORDSTROM,FEDERICA PERICLE,ALAIN ROLLAND,ROBERT RALSTON
            PC   C12N15/09,A61K38/21,A61K48/00,A61P35/00,C07K14/54,C07K14/56,
            PC   C12N1/15,
            PC   C12N1/19,C12N1/21,C12N5/10//A61K9/127,C12N15/00,A61K37/66, PC
             C12N5/00
            CC   Interferon alpha plasmid and delivery system and method of  CC
                   preparing and
            CC   using the same
            FH   Key             Location/Qualifiers
            FT   source          1. .987
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             4.8%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 70
CQ803342
LOCUS       CQ803342                 987 bp    DNA     linear   PAT 10-MAY-2004
DEFINITION  Sequence 2 from Patent WO2004035799.
ACCESSION   CQ803342
VERSION     CQ803342.1  GI:47110208
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Waehler,R. and Schnieders,F.
  TITLE     Viral vectors and the use of the same for gene therapy
  JOURNAL   Patent: WO 2004035799-A 2 29-APR-2004;
            Universitaetsklinikum Hamburg-Eppendorf (DE)
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             4.8%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 71
CS131491
LOCUS       CS131491                 987 bp    DNA     linear   PAT 02-AUG-2005
DEFINITION  Sequence 10 from Patent WO2005066348.
ACCESSION   CS131491
VERSION     CS131491.1  GI:71794159
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Gillies,S.
  TITLE     Compounds for targeting
  JOURNAL   Patent: WO 2005066348-A 10 21-JUL-2005;
            Antisoma PLC (GB); EMD Lexigen Research Center Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HuIL12 p40 subunit"
ORIGIN

  Query Match             4.8%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 72
I28591
LOCUS       I28591                   987 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 1 from patent US 5573764.
ACCESSION   I28591
VERSION     I28591.1  GI:1819367
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Sykes,M. and Wolf,S.F.
  TITLE     Use of interleukin-12 to prevent graft versus host disease
  JOURNAL   Patent: US 5573764-A 1 12-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             4.8%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 73
AR533404
LOCUS       AR533404                 987 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 24 from patent US 6730512.
ACCESSION   AR533404
VERSION     AR533404.1  GI:53923070
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Chang,L.-J.
  TITLE     Combination immunogene therapy
  JOURNAL   Patent: US 6730512-A 24 04-MAY-2004;
            Amdl, Inc.; Tustin, CA
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unknown"
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                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             4.8%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 74
AX154633
LOCUS       AX154633                 987 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 37 from Patent WO0140257.
ACCESSION   AX154633
VERSION     AX154633.1  GI:14536197
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 37 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             4.8%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 75
AY603406
LOCUS       AY603406                 993 bp    mRNA    linear   MAM 18-JUL-2004
DEFINITION  Capra hircus interleukin 12 p40 subunit precursor, mRNA, complete
            cds.
ACCESSION   AY603406
VERSION     AY603406.1  GI:50261479
KEYWORDS    .
SOURCE      Capra hircus (goat)
  ORGANISM  Capra hircus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Caprinae; Capra.
REFERENCE   1  (bases 1 to 993)
  AUTHORS   Rasool,T.J., Hosamani,M., Shebannavar,S., Sreekumar,E. and
            Singh,R.K.
  TITLE     cloning and sequencing of goat cytokines
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 993)
  AUTHORS   Rasool,T.J., Hosamani,M., Shebannavar,S., Sreekumar,E. and
            Singh,R.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-APR-2004) Division of Virology, Indian Veterinary
            Research Institute, Mukteswar, Nainital, Uttaranchal 263138, India
FEATURES             Location/Qualifiers
     source          1. .993
                     /organism="Capra hircus"
                     /mol_type="mRNA"
                     /isolation_source="peripheral blood mononuclear cells
                     stimulated with Concanavalin A"
                     /db_xref="taxon:9925"
                     /note="breed: Pashmina"
     CDS             1. .984
                     /note="cytokine"
                     /codon_start=1
                     /product="interleukin 12 p40 subunit precursor"
                     /protein_id="AAT72316.1"
                     /db_xref="GI:50261480"
                     /translation="MHPQQLVVSWFSLVLLASPIVAIWELEKNVYVVELDWYPNAPGE
                     TVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSRSLL
                     LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCSWLTAISTNLKFSVKSSR
                     GSSDPRGVTCGAASLSAEKVSMDHREYNKYTVECQEGSACPAAEESLPIEVVMEAVHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                     QVQGKNKREKKLFTDQTSAKVTCHKDANIRVQARDRYYSSFWSEWASVSCS"
ORIGIN

  Query Match             4.8%;  Score 44;  DB 14;  Length 993;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707


RESULT 76
CEU57752
LOCUS       CEU57752                 993 bp    mRNA    linear   MAM 28-OCT-1999
DEFINITION  Cervus elaphus interleukin-12 p40 subunit mRNA, complete cds.
ACCESSION   U57752
VERSION     U57752.1  GI:1373387
KEYWORDS    .
SOURCE      Cervus elaphus (red deer)
  ORGANISM  Cervus elaphus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Cervidae; Cervinae; Cervus.
REFERENCE   1  (bases 1 to 993)
  AUTHORS   Lockhart,E., Slobbe,L. and Buchan,G.
  TITLE     The characterisation of a cervine immunoregulatory cytokine,
            interleukin 12
  JOURNAL   DNA Seq. 10 (2), 139-148 (1999)
   PUBMED   10376218
REFERENCE   2  (bases 1 to 993)
  AUTHORS   Lockhart,E.A. and Buchan,G.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-MAY-1996) Euan A. Lockhart, Microbiology, University
            of Otago, Cumberland St, Dunedin, New Zealand
FEATURES             Location/Qualifiers
     source          1. .993
                     /organism="Cervus elaphus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9860"
                     /cell_type="peripheral blood mononuclear cells"
     CDS             1. .984
                     /codon_start=1
                     /product="interleukin-12 p40 subunit"
                     /protein_id="AAB02258.1"
                     /db_xref="GI:1373388"
                     /translation="MHPQQLVVSWFSLVLLTSPIVAIWELEKNVYVVELDWYPDAPGE
                     TVVLRCDTPEEDGITWTSDQSSEVLGSGKTLTVQVKEFGDAGQYTCHKGGEVLSRSLL
                     LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCWWLTAISTDLKFSVKSSR
                     GSSDPRGVTCGAASLSTEKVIVDHREYKKYTVECQEGSACPAAEESLPIEVVVEAVHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                     QVQGKNKREKKLFMDQTSAKVTCHKDASIRVQARDRYYNSFWSEWASVSCS"
     primer_bind     1. .33
     primer_bind     complement(961. .993)
ORIGIN

  Query Match             4.8%;  Score 44;  DB 14;  Length 993;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-11;
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  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707


RESULT 77
AY234218
LOCUS       AY234218               1005 bp    mRNA    linear   PRI 07-APR-2003
DEFINITION  Papio anubis interleukin-12 alpha p40 subunit precursor (IL12a)
            mRNA, complete cds.
ACCESSION   AY234218
VERSION     AY234218.1  GI:29569754
KEYWORDS    .
SOURCE      Papio anubis (olive baboon)
  ORGANISM  Papio anubis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Papio.
REFERENCE   1  (bases 1 to 1005)
  AUTHORS   Villinger,F.
  TITLE     Nonhuman primate cytokines
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1005)
  AUTHORS   Villinger,F.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-FEB-2003) Pathology & Laboratory Medicine, Emory
            University School of Medicine, Woodruff Memorial Building Rm 2339,
            1639 Pierce Drive, Atlanta, GA 30322, USA
FEATURES             Location/Qualifiers
     source          1. .1005
                     /organism="Papio anubis"
                     /mol_type="mRNA"
                     /db_xref="taxon:9555"
     gene            1. .1005
                     /gene="IL12a"
     CDS             9. .995
                     /gene="IL12a"
                     /codon_start=1
                     /product="interleukin-12 alpha p40 subunit precursor"
                     /protein_id="AAO85331.1"
                     /db_xref="GI:29569755"
                     /translation="MCHQQLVISWFSLVFLASPLMAIWELKKDVYVVELDWYPDAPGE
                     MVVLTCDTPEEDGITWTLDQSGEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSHSLL
                     LLHKKEDGIWSTDVLKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                     GSSNPQGVTCGAVTLSAERVRGDNKEYEYSVECQEDSACPAAEERLPIEVMVDAIHKL
                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQAEVSWEYPDTWSTPHSYFSLTFCIQ
                     VQGKSKREKKDRIFTDKTSATVICRKNASFSVQAQDRYYSSSWSEWASVPCS"
     sig_peptide     9. .74
                     /gene="IL12a"
     mat_peptide     75. .992
                     /gene="IL12a"
                     /product="interleukin-12 alpha p40 subunit"
ORIGIN

  Query Match             4.8%;  Score 44;  DB 5;  Length 1005;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        669 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 712


RESULT 78
CTU19834
LOCUS       CTU19834               1005 bp    mRNA    linear   PRI 03-FEB-1996
DEFINITION  Cercocebus torquatus interleukin-12 alpha p40 subunit (IL-12a)
            mRNA, complete cds.
ACCESSION   U19834
VERSION     U19834.1  GI:644785
KEYWORDS    .
SOURCE      Cercocebus torquatus (red-crowned mangabey)
  ORGANISM  Cercocebus torquatus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Cercocebus.
REFERENCE   1  (bases 1 to 1005)
  AUTHORS   Villinger,F., Brar,S.S., Mayne,A., Chikkala,N. and Ansari,A.A.
  TITLE     Comparative sequence analysis of cytokine genes from human and
            nonhuman primates
  JOURNAL   J. Immunol. 155 (8), 3946-3954 (1995)
   PUBMED   7561102
REFERENCE   2  (bases 1 to 1005)
  AUTHORS   Villinger,F.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JAN-1995) Francois J. Villinger, Emory University,
            Pathology, 1327 Clifton Rd, Atlanta, GA 30322, USA
FEATURES             Location/Qualifiers
     source          1. .1005
                     /organism="Cercocebus torquatus"
                     /mol_type="mRNA"
                     /sub_species="atys"
                     /db_xref="taxon:9530"
                     /clone="FPn IL-12a"
                     /cell_type="peripheral blood mononuclear cells"
                     /tissue_type="blood"
     gene            1. .1005
                     /gene="IL-12a"
     CDS             9. .995
                     /gene="IL-12a"
                     /function="NK cell stimulatory factor"
                     /codon_start=1
                     /product="interleukin-12 alpha p40 subunit"
                     /protein_id="AAA86701.1"
                     /db_xref="GI:644786"
                     /translation="MCHQQLVISWFSLVFLASPLMAIWELKKDVYVVELDWYPDAPGE
                     MVVLTCDTPEEDGITWTLDQSGEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSHSLL
                     LPHKKEDGIWSTDILKDQKEPKNETFLRCEAKNYSGRITCWWLSTISTDLTFSIISSR
                     GSSNPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEERLPIEVMVDAIHKL
                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCIQ
                     VQGKSKREKKDRIFTDKTSATVICRKNASFSVQAQDRYYSSSWNEWTSVPCS"
ORIGIN

  Query Match             4.8%;  Score 44;  DB 5;  Length 1005;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        669 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 712


RESULT 79
AF180563
LOCUS       AF180563               1007 bp    mRNA    linear   PRI 26-SEP-1999
DEFINITION  Homo sapiens interleukin 12, P40 mRNA, complete cds.
ACCESSION   AF180563
VERSION     AF180563.1  GI:5923854
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1007)
  AUTHORS   Hongyuan,J. and Meiyun,Z.
  TITLE     Cloning and sequence analysis of IL-12 cDNA from Chinese
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1007)
  AUTHORS   Hongyuan,J. and Meiyun,Z.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-AUG-1999) Hepatitis, Institute of Virology, CAPM, 100
            Yingxinjie, Xuanwuqu, Beijing 100052, China
FEATURES             Location/Qualifiers
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     source          1. .1007
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_type="peripheral mononuclear"
     CDS             7. .993
                     /note="NKSF/CLMF; IL12p40; 40kD"
                     /codon_start=1
                     /product="interleukin 12, P40"
                     /protein_id="AAD56386.1"
                     /db_xref="GI:5923855"
                     /translation="MCHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGE
                     MVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLL
                     LLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                     GSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKL
                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
                     VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"
ORIGIN

  Query Match             4.8%;  Score 44;  DB 5;  Length 1007;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        667 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 710


RESULT 80
AB246273
LOCUS       AB246273               1008 bp    mRNA    linear   MAM 13-JAN-2006
DEFINITION  Bubalus carabanensis IL-12p40 mRNA for interleukin-12p40, complete
            cds.
ACCESSION   AB246273
VERSION     AB246273.1  GI:84871695
KEYWORDS    .
SOURCE      Bubalus carabanensis
  ORGANISM  Bubalus carabanensis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bubalus.
REFERENCE   1
  AUTHORS   Mingala,C.N., Raadan,O., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Comparative assessment of Th1 and Th2 cytokines of swamp type
            buffalo and other bubaline breeds by molecular cloning, sequencing
            and phylogenetics
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1008)
  AUTHORS   Mingala,C.N., Odbileg,R., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JAN-2006) Claro N Mingala, Graduate School of
            Veterinary Medicine, Hokkaido University, Department of Disease
            Control, Laboratory of Infectious Diseases; Kita-ku Kita 18 Nishi
            9, Sapporo, Hokkaido 060-0818, Japan (E-mail:cnmingala@hotmail.com,
            Tel:81-11-706-5216, Fax:81-11-706-5217)
FEATURES             Location/Qualifiers
     source          1. .1008
                     /organism="Bubalus carabanensis"
                     /mol_type="mRNA"
                     /db_xref="taxon:346063"
                     /sex="female"
                     /cell_type="PBMC"
     gene            1. .1008
                     /gene="IL-12p40"
     CDS             1. .984
                     /gene="IL-12p40"
                     /codon_start=1
                     /product="interleukin-12p40"
                     /protein_id="BAE75850.1"
                     /db_xref="GI:84871696"
                     /translation="MHPQQLVVSWFSLVLLASPIVAIWELEKNVYIVELDWYPDAPGE
                     TVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSRSLL
                     LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCWWLTAISTDLKFSVKSSR
                     GSSDPRGVTCGAASLSAEKVSVDHREYNKYTVECQEGSTCPAAEESLLIEVVVEAVHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                     QVQGKNKREKKLFMDQTSAKVTCHKDANVRVQARDRYYSSFWSEWASVSCS"
ORIGIN

  Query Match             4.8%;  Score 44;  DB 14;  Length 1008;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707


RESULT 81
AB246353
LOCUS       AB246353               1008 bp    mRNA    linear   MAM 13-JAN-2006
DEFINITION  Bubalus bubalis IL-12p40 mRNA for interleukin-12p40, complete cds.
ACCESSION   AB246353
VERSION     AB246353.1  GI:84871717
KEYWORDS    .
SOURCE      Bubalus bubalis (water buffalo)
  ORGANISM  Bubalus bubalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bubalus.
REFERENCE   1
  AUTHORS   Mingala,C.N., Raadan,O., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Comparative assessment of Th1 and Th2 cytokines of swamp type
            buffalo and other bubaline breeds by molecular cloning, sequencing
            and phylogenetics
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1008)
  AUTHORS   Mingala,C.N., Odbileg,R., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2006) Claro N Mingala, Graduate School of
            Veterinary Medicine, Hokkaido University, Department of Disease
            Control, Laboratory of Infectious Diseases; Kita-ku Kita 18 Nishi
            9, Sapporo, Hokkaido 060-0818, Japan (E-mail:cnmingala@hotmail.com,
            Tel:81-11-706-5216, Fax:81-11-706-5217)
FEATURES             Location/Qualifiers
     source          1. .1008
                     /organism="Bubalus bubalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:89462"
                     /sex="female"
                     /cell_type="PBMC"
                     /note="Bulgarian Murrah buffalo - crossbreed between
                     Mediterranean and Indian buffalo both are Riverine type
                     water buffalo"
     gene            1. .1008
                     /gene="IL-12p40"
     CDS             1. .984
                     /gene="IL-12p40"
                     /codon_start=1
                     /product="interleukin-12p40"
                     /protein_id="BAE75858.1"
                     /db_xref="GI:84871718"
                     /translation="MHPQQLVVSWFSLVLLASPIVAIWELEKNVYVVELDWYPDAPGE
                     TVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSRSLL
                     LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCWWLTAISTDLKFSVKSSR
                     GSSDPRGVTCEAASLSAEKVSVDHREYNKYTVECQEGSTCPAAEESLLIEVVVEAVHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                     QVQGKNKREKKLFMDQTSAKVTCHKDANVRVQARDRYYSSFWSEWASVSCS"
ORIGIN

  Query Match             4.8%;  Score 44;  DB 14;  Length 1008;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
```

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RESULT 82
AB246358
LOCUS       AB246358               1008 bp    mRNA    linear   MAM 14-JAN-2006
DEFINITION  Bubalus bubalis x Bubalus carabanensis IL-12p40 mRNA for
            interleukin-12p40, complete cds.
ACCESSION   AB246358
VERSION     AB246358.1  GI:84875356
KEYWORDS    .
SOURCE      Bubalus bubalis x Bubalus carabanensis
  ORGANISM  Bubalus bubalis x Bubalus carabanensis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bubalus.
REFERENCE   1
  AUTHORS   Mingala,C.N., Raadan,O., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Comparative assessment of Th1 and Th2 cytokines of swamp type
            buffalo and other bubaline breeds by molecular cloning, sequencing
            and phylogenetics
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1008)
  AUTHORS   Mingala,C.N., Odbileg,R., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2006) Claro N Mingala, Graduate School of
            Veterinary Medicine, Hokkaido University, Department of Disease
            Control, Laboratory of Infectious Diseases; Kita-ku Kita 18 Nishi
            9, Sapporo, Hokkaido 060-0818, Japan (E-mail:cnmingala@hotmail.com,
            Tel:81-11-706-5216, Fax:81-11-706-5217)
FEATURES             Location/Qualifiers
     source          1. .1008
                     /organism="Bubalus bubalis x Bubalus carabanensis"
                     /mol_type="mRNA"
                     /db_xref="taxon:365610"
                     /sex="female"
                     /cell_type="PBMC"
                     /note="Philippine carabao crossbreed (CB) - crossbreed
                     between Philippine carabao (Swamp type water buffalo) and
                     Indian Murrah buffalo (Riverine type water buffalo)"
     gene            1. .1008
                     /gene="IL-12p40"
     CDS             1. .984
                     /gene="IL-12p40"
                     /codon_start=1
                     /product="interleukin-12p40"
                     /protein_id="BAE75892.1"
                     /db_xref="GI:84875357"
                     /translation="MHPQQLVVSWFSLVLLASPIVAIWELEKNVYVVELDWYPDAPGE
                     TVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSRSLL
                     LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSEHFTGWWLTAISTNLKFSVKSSR
                     GSSDPRGVTCGAASLSAEKVSVDHREYNKYTVECQEGSTCPAAEESLLIEVVVEAVHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                     QVQGKNKREKKLFMDQTSAKVTCHKDANVRVQARDRYYSSFWSEWASVSCS"
ORIGIN

  Query Match             4.8%;  Score 44;  DB 14;  Length 1008;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707


RESULT 83
AF007576
LOCUS       AF007576               1012 bp    mRNA    linear   MAM 14-JUL-1997
DEFINITION  Capra hircus interleukin 12 p40 subunit (IL-12) mRNA, complete cds.
ACCESSION   AF007576
VERSION     AF007576.1  GI:2253433
KEYWORDS    .
SOURCE      Capra hircus (goat)
  ORGANISM  Capra hircus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Caprinae; Capra.
REFERENCE   1  (bases 1 to 1012)
  AUTHORS   Beyer,J.C., Cheevers,W.P. and Kumpula-McWhirter,N.M.
  TITLE     CLoning of caprine IL-12 40 kDa subunit
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1012)
  AUTHORS   Beyer,J.C., Cheevers,W.P. and Kumpula-McWhirter,N.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JUN-1997) Veterinary Microbiology and Pathology,
            Washington State University, P.O. Box 647040, Pullman, WA
            99164-7040, USA
FEATURES             Location/Qualifiers
     source          1. .1012
                     /organism="Capra hircus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9925"
                     /cell_type="LPS-stimulated microglial cell"
     gene            1. .1012
                     /gene="IL-12"
     CDS             1. .984
                     /gene="IL-12"
                     /codon_start=1
                     /product="interleukin 12 p40 subunit"
                     /protein_id="AAB62945.1"
                     /db_xref="GI:2253434"
                     /translation="MHPQQLVVSWFSLVLLASPIVAIWELEKNVYVVELDWYPNAPGE
                     TVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSRSLL
                     LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCSWLTAISTNLKFSVKSSR
                     GSSDPRGVTCGAASLSAEKVSMDHREYNKYTVECQEGSACPAAEESLPIEVVMEAVHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                     QVQGKNKREKKLFTDQTSAKVTCHKDANIRVQARDRYYSSFWSEWASVSCS"
ORIGIN

  Query Match             4.8%;  Score 44;  DB 14;  Length 1012;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707


RESULT 84
AY198121
LOCUS       AY198121               1012 bp    mRNA    linear   MAM 09-JUN-2005
DEFINITION  Bubalus bubalis interleukin 12 p40 subunit precursor, mRNA,
            complete cds.
ACCESSION   AY198121
VERSION     AY198121.1  GI:28192687
KEYWORDS    .
SOURCE      Bubalus bubalis (water buffalo)
  ORGANISM  Bubalus bubalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bubalus.
REFERENCE   1  (bases 1 to 1012)
  AUTHORS   Premraj,A., Sreekumar,E., Nautiyal,B. and Rasool,T.J.
  TITLE     Interleukin-12 subunits p35 and p40 of Indian water buffalo
            (Bubalus bubalis) maintain high sequence homology with those of
            other ruminants
  JOURNAL   Eur. J. Immunogenet. 32 (3), 179-186 (2005)
REFERENCE   2  (bases 1 to 1012)
  AUTHORS   Premraj,A., Sreekumar,E. and Rasool,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-DEC-2002) Animal Biotechnology, Rajiv Gandhi Center
            for Biotechnology, Jagathy, Thycaud PO, Trivandrum, Kerala 695014,
            India
FEATURES             Location/Qualifiers
     source          1. .1012
                     /organism="Bubalus bubalis"
                     /mol_type="mRNA"
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                     /db_xref="taxon:89462"
     CDS             1. .984
                     /note="cytokine; 40 kDa subunit"
                     /codon_start=1
                     /product="interleukin 12 p40 subunit precursor"
                     /protein_id="AAO25629.1"
                     /db_xref="GI:28192688"
                     /translation="MHPQQLVVSWFSLVLLASPIVAIWELEKNVYIVELDWYPDAPGE
                     TVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSRSLL
                     LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCWWLTAISTDLKFSVKSSR
                     GSADPRGVTCGAASLSAEKVSVDHREYNKYTVECQEGSTCPAAEESLLIEVVVEAVHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                     QVQGKNKREKKLFMDQTSAKVTCHKDANVRVQARDRYYSSFWSEWASVSCS"
ORIGIN

  Query Match             4.8%;  Score 44;  DB 14;  Length 1012;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707


RESULT 85
BTU11815
LOCUS       BTU11815                1012 bp    mRNA    linear   MAM 27-JAN-1996
DEFINITION  Bos taurus interleukin 12 40 kDa subunit mRNA, complete cds.
ACCESSION   U11815
VERSION     U11815.1  GI:555795
KEYWORDS    .
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 1012)
  AUTHORS   Zarlenga,D.S., Canals,A., Aschenbrenner,R.A. and Gasbarre,L.C.
  TITLE     Enzymatic amplification and molecular cloning of cDNA encoding the
            small and large subunits of bovine interleukin 12
  JOURNAL   Biochim. Biophys. Acta 1270 (2-3), 215-217 (1995)
   PUBMED   7727547
REFERENCE   2  (bases 1 to 1012)
  AUTHORS   Zarlenga,D.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JUL-1994) Dante S. Zarlenga, U.S. Department of
            Agriculture, ARS, LPSI, PIL, Beltsville, MD 20705, USA
FEATURES             Location/Qualifiers
     source          1. .1012
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /strain="Holstein"
                     /db_xref="taxon:9913"
                     /clone="BIL12 40"
                     /sex="male"
                     /cell_type="lymphocytes and macrophages"
                     /tissue_type="lymphoid"
     CDS             1. .984
                     /codon_start=1
                     /product="interleukin 12 40 kDa subunit"
                     /protein_id="AAA85792.1"
                     /db_xref="GI:555796"
                     /translation="MHPQQLVVSWFSLVLLASPIVAMWELEKNVYVVELDWYPDAPGE
                     TVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSRSLL
                     LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCWWLTAISTDLKFSVKSSR
                     GSSDPRGVTCGAALLSAEKVSLEHREYNKYTVECQEGSACPAAEESLLIEVVVEAVHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                     QVQGKNKREKKLFMDQTSAKVTCHKDANVRVQARDRYYSSFWSEWASVSCS"
ORIGIN

  Query Match             4.8%;  Score 44;  DB 14;  Length 1012;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707


RESULT 86
AR052857
LOCUS       AR052857                1018 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 194 from patent US 5833975.
ACCESSION   AR052857
VERSION     AR052857.1  GI:5977719
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1018)
  AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
  TITLE     Canarypox virus expressing cytokine and/or tumor-associated antigen
            DNA sequence
  JOURNAL   Patent: US 5833975-A 194 10-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .1018
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             4.8%;  Score 44;  DB 2;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 87
AR288169
LOCUS       AR288169                1018 bp    mRNA    linear   PAT 12-JUN-2003
DEFINITION  Sequence 194 from patent US 6537594.
ACCESSION   AR288169
VERSION     AR288169.1  GI:31675448
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1018)
  AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
  TITLE     Vaccina virus comprising cytokine and/or tumor associated antigen
            genes
  JOURNAL   Patent: US 6537594-A 194 25-MAR-2003;
            Virogenetics Corporation; Troy, NY
FEATURES             Location/Qualifiers
     source          1. .1018
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             4.8%;  Score 44;  DB 2;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 88
AR567156
LOCUS       AR567156                1018 bp    mRNA    linear   PAT 08-OCT-2004
DEFINITION  Sequence 194 from patent US 6780407.
ACCESSION   AR567156
VERSION     AR567156.1  GI:53984798
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1018)
  AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
  TITLE     Pox virus comprising DNA sequences encoding CEA and B7 antigen
  JOURNAL   Patent: US 6780407-A 194 24-AUG-2004;
            Aventis Pasteur; Swiftwater, PA
FEATURES             Location/Qualifiers
     source          1. .1018
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             4.8%;  Score 44;  DB 2;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 89
E35794
LOCUS       E35794                  1019 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Process for producing interleukin 12.
ACCESSION   E35794
VERSION     E35794.1  GI:18624618
KEYWORDS    JP 2000157274-A/6.
SOURCE      Bos sp.
  ORGANISM  Bos sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 1019)
  AUTHORS   Nakamura,M., Takehara,K. and Ohara,E.
  TITLE     Process for producing interleukin 12
  JOURNAL   Patent: JP 2000157274-A 6 13-JUN-2000;
            DAI ICHI SEIYAKU CO LTD
COMMENT     OS   Bos sp. (bovine)
            PN   JP 2000157274-A/6
            PD   13-JUN-2000
            PF   20-NOV-1998 JP 1998331052
            PR
            PI   MASAYUKI NAKAMURA,KAZUAKI TAKEHARA,EIJI OHARA PC
            C12N15/09,C07K14/54,C12N5/10,C12P21/02//(C12N15/09,C12R1:91), PC
            (C12N5/10,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00, PC
            (C12N15/00,C12R1:91),(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .1019
            FT                   /organism='Bos sp. (bovine)'.
FEATURES             Location/Qualifiers
     source          1. .1019
                     /organism="Bos sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:29061"
ORIGIN

  Query Match             4.8%;  Score 44;  DB 2;  Length 1019;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        675 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 718


RESULT 90
CQ829448
LOCUS       CQ829448                1029 bp    DNA     linear   PAT 05-JUL-2004
DEFINITION  Sequence 7 from Patent WO2004052929.
ACCESSION   CQ829448
VERSION     CQ829448.1  GI:49732784
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Vandenbroeck,K. and Alloza,I.
  TITLE     Recombinant cell line
  JOURNAL   Patent: WO 2004052929-A 7 24-JUN-2004;
            The Queen's University of Belfast (GB)
FEATURES             Location/Qualifiers
     source          1. .1029
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="cDNA for beta chain of IL-12"
ORIGIN

  Query Match             4.8%;  Score 44;  DB 2;  Length 1029;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        676 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 719


RESULT 91
BC074723
LOCUS       BC074723                1046 bp    mRNA    linear   PRI 28-JUL-2005
DEFINITION  Homo sapiens interleukin 12B (natural killer cell stimulatory
            factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA
            (cDNA clone MGC:103792 IMAGE:30915173), complete cds.
ACCESSION   BC074723
VERSION     BC074723.2  GI:50960609
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1046)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
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            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1046)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JUN-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
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  REMARK     NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT      On Aug 4, 2004 this sequence version replaced gi:49901500.
             Contact: MGC help desk
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Genome Sequence Centre, British Columbia Cancer
             Center
             cDNA Library Preparation: British Columbia Cancer Research Center
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Genome Sequence Centre,
             BC Cancer Agency, Vancouver, BC, Canada
             info@bcgsc.bc.ca
             Martin Hirst, Thomas Zeng, Ryan Morin, Michelle Moksa, Johnson
             Pang, Diana Mah, Jing Wang, Kieth Fichter, Eric Chuah, Allen
             Delaney, Rob Kirkpatrick, Agnes Baross, Sarah Barber, Mabel
             Brown-John, Steve S. Chand, William Chow, Ryan Babakaiff, Dave
             Wong, Corey Matsuo, Jaclyn Beland, Susan Gibson, Luis delRio, Ruth
             Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
             Kim MacDonald,  Mike R. Mayo, Josh Moran, Diana Palmquist, JR
             Santos, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang,
             Jacquie Schein, Asim Siddiqui,Steven Jones, Rob Holt, Marco Marra.

             Clone distribution: MGC clone distribution information can be found
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ORIGIN

  Query Match             4.8%;  Score 44;  DB 5;  Length 1046;
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  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 92
BC067498
LOCUS       BC067498               1073 bp    mRNA    linear   PRI 28-JUL-2005
DEFINITION  Homo sapiens interleukin 12B (natural killer cell stimulatory
            factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA
            (cDNA clone MGC:79355 IMAGE:6971868), complete cds.
ACCESSION   BC067498
VERSION     BC067498.1  GI:45768642
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1073)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
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            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1073)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 172 Row: d Column: 13
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            passed the following selection criteria: matched mRNA gi: 24497437.
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ORIGIN

  Query Match             4.8%;  Score 44;  DB 5;  Length 1073;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
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Db        665 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 708


RESULT 93
BC067499
LOCUS       BC067499               1073 bp    mRNA    linear   PRI 28-JUL-2005
DEFINITION  Homo sapiens interleukin 12B (natural killer cell stimulatory
            factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA
            (cDNA clone MGC:79356 IMAGE:6971869), complete cds.
ACCESSION   BC067499
VERSION     BC067499.1  GI:45768645
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1073)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
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            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1073)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 172 Row: d Column: 12
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            passed the following selection criteria: matched mRNA gi: 24497437.
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                     /note="synonyms: CLMF2, IL-12B, NKSF, CLMF"
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ORIGIN

  Query Match             4.8%;  Score 44;  DB 5;  Length 1073;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        665 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 708


RESULT 94
BC067500
LOCUS       BC067500               1073 bp    mRNA    linear   PRI 28-JUL-2005
DEFINITION  Homo sapiens interleukin 12B (natural killer cell stimulatory
            factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA
            (cDNA clone MGC:79358 IMAGE:6971872), complete cds.
ACCESSION   BC067500
VERSION     BC067500.1  GI:45768649
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1073)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
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  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1073)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 172 Row: d Column: 21
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 24497437.
FEATURES             Location/Qualifiers
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                     /note="Vector: pDNR-Dual"
     gene            1. .1073
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                     /note="synonyms: CLMF2, IL-12B, NKSF, CLMF"
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                     VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"
ORIGIN

  Query Match             4.8%;  Score 44;  DB 5;  Length 1073;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
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Db        665 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 708


RESULT 95
BC067501
LOCUS       BC067501                1073 bp    mRNA    linear   PRI 28-JUL-2005
DEFINITION  Homo sapiens interleukin 12B (natural killer cell stimulatory
            factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA
            (cDNA clone MGC:79359 IMAGE:6971873), complete cds.
ACCESSION   BC067501
VERSION     BC067501.1  GI:45767736
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1073)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
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            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
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            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1073)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 172 Row: d Column: 22
            This clone was selected for full length sequencing because it
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ORIGIN

  Query Match             4.8%;  Score 44;  DB 5;  Length 1073;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
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Db        665 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 708


RESULT 96
BC067502
LOCUS       BC067502                1073 bp    mRNA    linear   PRI 28-JUL-2005
DEFINITION  Homo sapiens interleukin 12B (natural killer cell stimulatory
            factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA
            (cDNA clone MGC:79360 IMAGE:6971874), complete cds.
ACCESSION   BC067502
VERSION     BC067502.1  GI:45768652
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1073)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
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            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1073)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 172 Row: d Column: 23
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 24497437.
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             4.8%;  Score 44;  DB 5;  Length 1073;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
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Db        665 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 708


RESULT 97
MMU19841
LOCUS       MMU19841                1080 bp    mRNA    linear   PRI 03-FEB-1996
DEFINITION  Macaca mulatta interleukin-12 alpha (IL-12a) mRNA, complete cds.
ACCESSION   U19841
VERSION     U19841.1  GI:644799
KEYWORDS    .
SOURCE      Macaca mulatta (rhesus monkey)
  ORGANISM  Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Cercopithecidae; Cercopithecinae; Macaca.
REFERENCE  1  (bases 1 to 1080)
  AUTHORS  Villinger,F., Brar,S.S., Mayne,A., Chikkala,N. and Ansari,A.A.
  TITLE    Comparative sequence analysis of cytokine genes from human and
           nonhuman primates
  JOURNAL  J. Immunol. 155 (8), 3946-3954 (1995)
   PUBMED  7561102
REFERENCE  2  (bases 1 to 1080)
  AUTHORS  Villinger,F.J.
  TITLE    Direct Submission
  JOURNAL  Submitted (13-JAN-1995) Francois J. Villinger, Emory University,
           Pathology, 1327 Clifton Rd, Atlanta, GA 30322, USA
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DEFINITION  Sequence 4 from patent US 6617135.
ACCESSION   AR393788
VERSION     AR393788.1  GI:40120790
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1389)
  AUTHORS   Gillies,S.D. and Lo,K.-M.
  TITLE     Multiple cytokine protein complexes
  JOURNAL   Patent: US 6617135-A 4 09-SEP-2003;
            EMD Lexigen Research Center Corp.; Billerica, MA
FEATURES             Location/Qualifiers
     source          1. .1389
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ORIGIN

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RESULT 99
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LOCUS       AX084106               1389 bp    DNA     linear   PAT 28-FEB-2001
DEFINITION  Sequence 4 from Patent WO0110912.
ACCESSION   AX084106
VERSION     AX084106.1  GI:13185656
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Gillies,S.D. and Lo,K.M.
  TITLE     Multiple cytokine-antibody complexes
  JOURNAL   Patent: WO 0110912-A 4 15-FEB-2001;
            Lexigen Pharmaceuticals Corp. (US)
FEATURES             Location/Qualifiers
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RESULT 100
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LOCUS       BD165800               1397 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Antibody against cytotoxic lymphocyte maturing factors.
ACCESSION   BD165800
VERSION     BD165800.1  GI:27871612
KEYWORDS    JP 2002167400-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
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unclassified sequences.
REFERENCE 1 (bases 1 to 1397)
AUTHORS Chizzonite,R.A., Gately,M.K., Gubler,U.A., Hulmes,J.D., Pan,Y.C.E., Podlanski,F.J. and Stern,A.S.
TITLE Antibody against cytotoxic lymphocyte maturing factors
JOURNAL Patent: JP 2002167400-A 1 11-JUN-2002;
PROTEIN DESIGN LABS INC
COMMENT OS Homo sapiens (human)
PN JP 2002167400-A/1
PD 11-JUN-2002
PF 14-AUG-2001 JP 2001246031
PR 22-DEC-1989 US 455708,09-MAY-1990 US 520935 PR
27-AUG-1990 US 572284
PI RICHARD ANTHONY CHIZZONITE,MAURICE KENT GATELY,ULRICH ANDREAS
PI GUBLER,
PI JEFFREY DAVID HULMES,YU CHING EUGENE PAN,FRANK JOHN PODLANSKI,
PI ALVIN SETH STERN
PC C07K16/24,C12N15/02,C12N15/02,C12P21/08,C12N15/00,C12N15/00 CC
Antibody against cytotoxic lymphocyte maturing factors FH Key
Location/Qualifiers
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ORIGIN

Query Match 4.8%; Score 44; DB 2; Length 1397;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

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Post-processing: Listing first 200 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	4	921	100.0	921	14	ADV34679	Adv34679 Feline si
c	5	921	100.0	1533	6	ABK98954	Abk98954 Feline in
	6	921	100.0	1533	6	ABK98953	Abk98953 Feline in
c	7	921	100.0	1533	14	ADV34697	Adv34697 Feline si
	8	921	100.0	1533	14	ADV34695	Adv34695 Feline si
	9	921	100.0	1599	6	ABK98950	Abk98950 Feline in
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	18	870	94.5	2193	2	AAV56625	Aav56625 Feline FL
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	20	868	94.2	985	6	ABK98961	Abk98961 Feline in
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c	36	66	7.2	987	14	ADV34712	Adv34712 Canine si
	37	66	7.2	987	14	ADV34710	Adv34710 Canine si
	38	66	7.2	990	2	AAV13816	Aav13816 Canine IL
	39	66	7.2	990	2	AAV13817	Aav13817 Canine IL
	40	66	7.2	990	2	AAX03162	Aax03162 Nucleic a
	41	66	7.2	990	2	AAX03152	Aax03152 Nucleic a
	42	66	7.2	990	2	AAX35625	Aax35625 Nucleic a
	43	66	7.2	990	2	AAX35615	Aax35615 Nucleic a
	44	66	7.2	990	4	AAI64378	Aai64378 Canine co
	45	66	7.2	990	4	AAI64388	Aai64388 Canine co
	46	66	7.2	990	11	ADZ25698	Adz25698 Canine in
	47	66	7.2	1533	6	ABK98967	Abk98967 Canine in
c	48	66	7.2	1533	6	ABK98968	Abk98968 Canine in
c	49	66	7.2	1533	14	ADV34718	Adv34718 Canine si
	50	66	7.2	1533	14	ADV34716	Adv34716 Canine si
	51	66	7.2	1599	6	ABK98965	Abk98965 Canine in
c	52	66	7.2	1599	6	ABK98966	Abk98966 Canine in
c	53	66	7.2	1599	14	ADV34715	Adv34715 Canine si
	54	66	7.2	1599	14	ADV34713	Adv34713 Canine si
	55	66	7.2	2154	2	AAX18176	Aax18176 Canine fu
c	56	66	7.2	2267	6	ABK99006	Abk99006 Canine in
	57	66	7.2	2267	6	ABK99005	Abk99005 Canine in
	58	66	7.2	2267	14	ADV34757	Adv34757 Canine si
c	59	66	7.2	2267	14	ADV34759	Adv34759 Canine si
	60	63	6.8	1015	13	ADT04849	Adt04849 Canine in
	61	61	6.6	984	5	AAD15204	Aad15204 Modified
	62	60	6.5	984	5	AAD15205	Aad15205 Modified
	63	53	5.8	975	5	AAD15208	Aad15208 Modified
	64	49	5.3	984	5	AAD15206	Aad15206 Modified
	65	44	4.8	906	2	AAQ04701	Aaq04701 Sequence
	66	44	4.8	969	5	AAD15207	Aad15207 Modified
	67	44	4.8	979	2	AAQ12149	Aaq12149 Cytotoxic
	68	44	4.8	984	2	AAT50759	Aat50759 Sequence
	69	44	4.8	984	12	ADG39430	Adg39430 Human CLM
	70	44	4.8	985	10	ADK98707	Adk98707 Human int
	71	44	4.8	987	2	AAQ97484	Aaq97484 Human int
	72	44	4.8	987	2	AAV07273	Aav07273 Human Int
	73	44	4.8	987	2	AAV07217	Aav07217 DNA encod
	74	44	4.8	987	2	AAZ40404	Aaz40404 Human int
	75	44	4.8	987	2	AAV83199	Aav83199 Interleuk
	76	44	4.8	987	5	AAD15210	Aad15210 Human cyt
	77	44	4.8	987	6	ACC47592	Acc47592 Human int
	78	44	4.8	987	12	ADF77276	Adf77276 Human IL-
	79	44	4.8	987	12	ADO07653	Ado07653 Human int
	80	44	4.8	987	13	ADS00006	Ads00006 Human int
	81	44	4.8	987	14	ADV42753	Adv42753 Human psy
	82	44	4.8	987	14	ADW97242	Adw97242 Human p40
	83	44	4.8	987	14	AEB48822	Aeb48822 Human int
	84	44	4.8	1007	5	AAD18585	Aad18585 Human int
	85	44	4.8	1018	2	AAQ67879	Aaq67879 EPV 42 kD
	86	44	4.8	1018	2	AAZ08510	Aaz08510 EPV 42 kD
	87	44	4.8	1018	13	ADR21886	Adr21886 EPV 42kDa
	88	44	4.8	1019	3	AAA70709	Aaa70709 Bovine in
	89	44	4.8	1029	12	ADP88402	Adp88402 Human int
	90	44	4.8	1389	4	AAF76880	Aaf76880 Human p40
	91	44	4.8	1397	2	AAT77849	Aat77849 40 kDa su

	92	44	4.8	1397	2	AAT97969 Aat97969 40 kDa su
	93	44	4.8	1397	2	AAV00401 Aav00401 40 kDa su
	94	44	4.8	1397	2	AAV37767 Aav37767 Cytotoxic
	95	44	4.8	1397	12	ADG39387 Adg39387 Human cyt
	96	44	4.8	1397	12	ADO03758 Ado03758 Human CLM
	97	44	4.8	1399	3	AAZ40021 Aaz40021 Human p40
	98	44	4.8	1399	14	ADY86632 Ady86632 Human int
	99	44	4.8	1580	12	ADQ14472 Adq14472 DNA encod
	100	44	4.8	2300	3	AAA92406 Aaa92406 Human int
	101	44	4.8	2318	8	ACA61267 Aca61267 DNA encod
	102	44	4.8	2318	10	ABX33940 Abx33940 Human cDN
	103	44	4.8	2336	14	AEE03207 Aee03207 Human int
	104	44	4.8	2347	12	ACF57534 Acf57534 Human IL1
	105	44	4.8	2347	12	ADJ62892 Adj62892 Human int
	106	44	4.8	2347	14	ADZ26728 Adz26728 Human IL1
	107	44	4.8	2362	2	AAQ23586 Aaq23586 Natural k
	108	44	4.8	2362	2	AAT48098 Aat48098 Human int
	109	44	4.8	2362	2	AAV42535 Aav42535 Human int
	110	44	4.8	2362	2	AAV15227 Aav15227 Heterodim
	111	44	4.8	2362	3	AAZ28862 Aaz28862 Human int
	112	44	4.8	2362	4	AAF56280 Aaf56280 IL-12 vac
	113	44	4.8	4727	14	AEA40942 Aea40942 T-DNA reg
	114	44	4.8	5686	2	AAZ40415 Aaz40415 Plasmid p
	115	44	4.8	5686	12	ADF77239 Adf77239 Human IL-
	116	44	4.8	6139	3	AAZ40023 Aaz40023 Interleuk
	117	44	4.8	8578	6	AAD31546 Aad31546 pIRES-hB7
	118	44	4.8	8578	6	AAD31545 Aad31545 pIRES-hB7
	119	44	4.8	8608	6	AAD31548 Aad31548 pIRES-hB7
	120	44	4.8	8623	6	AAD31547 Aad31547 pIRES-hB7
	121	44	4.8	8629	6	AAD31552 Aad31552 pIRES-IL1
	122	44	4.8	8638	6	AAD31549 Aad31549 pIRES-hB7
	123	44	4.8	8644	6	AAD31551 Aad31551 pIRES-IL1
	124	44	4.8	8659	6	AAD31550 Aad31550 pIRES-IL1
	125	44	4.8	11453	10	ADG25152 Adg25152 Vector pS
	126	44	4.8	11569	10	ADG25150 Adg25150 Vector pA
	127	39	4.2	1007	10	ACD26421 Acd26421 cDNA enco
	128	39	4.2	2390	12	ADM29103 Adm29103 Human int
	129	39	4.2	18110	6	ABK15357 Abk15357 Human int
	130	39	4.2	18340	5	AAD19368 Aad19368 Mammalian
c	131	35	3.8	270	12	ACH83638 Ach83638 Human gen
c	132	35	3.8	556	12	ACH69938 Ach69938 Human gen
	133	35	3.8	975	5	AAD15203 Aad15203 Modified
c	134	30	3.3	30	3	AAA48905 Aaa48905 Probe 12.
	135	30	3.3	73	4	AAS15322 Aas15322 Mouse IL-
	136	30	3.3	600	2	AAX78397 Aax78397 IL-12p40
	137	30	3.3	600	2	AAX25947 Aax25947 Interleuk
	138	30	3.3	1008	13	ADS00008 Ads00008 Murine in
	139	30	3.3	1008	14	ADW97243 Adw97243 Murine p4
	140	30	3.3	1056	2	AAV28472 Aav28472 Murine in
	141	30	3.3	1061	2	AAT35200 Aat35200 Mouse int
	142	30	3.3	1409	4	AAF76879 Aaf76879 Murine p4
	143	30	3.3	1472	4	AAF76878 Aaf76878 Murine p4
	144	30	3.3	1569	4	AAF76888 Aaf76888 Single-ch
	145	30	3.3	1610	12	ADQ14470 Adq14470 DNA encod
	146	30	3.3	1840	8	ACA61265 Aca61265 DNA encod
	147	30	3.3	2013	4	AAF76887 Aaf76887 Murine p3
	148	30	3.3	2334	14	AEE03206 Aee03206 Murine in
	149	30	3.3	2438	12	ADO43004 Ado43004 DNA encod
	150	30	3.3	2709	4	AAF76889 Aaf76889 Coding se
	151	30	3.3	5252	12	ADO07652 Ado07652 Tricistro
	152	30	3.3	5966	2	AAZ40417 Aaz40417 Plasmid p
	153	30	3.3	5966	12	ADF77241 Adf77241 Mouse IL-
	154	30	3.3	5985	12	ADQ82718 Adq82718 Anticance
	155	30	3.3	6295	2	AAV02043 Aav02043 Plasmid p
	156	30	3.3	7287	2	AAV02042 Aav02042 Plasmid p
	157	30	3.3	9049	12	ADO07661 Ado07661 Viral vec
	158	30	3.3	10633	12	ADO07660 Ado07660 Viral vec
	159	30	3.3	11458	10	ADG25151 Adg25151 Vector pA
	160	30	3.3	11746	12	ADO07659 Ado07659 Viral vec
	161	30	3.3	28191	14	AEE03204 Aee03204 Adenovira
	162	30	3.3	28892	14	AEE03202 Aee03202 Adenovira
	163	30	3.3	38246	12	ADO07662 Ado07662 Viral vec
c	164	25	2.7	25	6	ABK98986 Abk98986 Feline PC
c	165	25	2.7	25	14	ADV34736 Adv34736 Feline IL
c	166	25	2.7	25	14	AEC56176 Aec56176 Antisense
c	167	24	2.6	26	2	AAX78412 Aax78412 Rat GADPH
c	168	24	2.6	26	2	AAX25927 Aax25927 IL12 p40
	169	24	2.6	987	2	AAZ40406 Aaz40406 Human int
	170	24	2.6	987	2	AAZ40405 Aaz40405 Human int
	171	24	2.6	987	12	ADF77278 Adf77278 Human IL-
	172	24	2.6	987	12	ADF77277 Adf77277 Human IL-
	173	23	2.5	200	2	AAV03357 Aav03357 Homo sapi
c	174	22	2.4	25	6	ABK98988 Abk98988 Feline PC
c	175	22	2.4	25	14	ADV34738 Adv34738 Feline IL
	176	22	2.4	399	14	AEE14792 Aee14792 Hamster S
	177	22	2.4	399	14	AEE11150 Aee11150 Hamster c
c	178	22	2.4	87350	2	AAX83003 Aax83003 Human WRN
c	179	22	2.4	87543	7	ADJ84092 Adj84092 Human WRN
	180	21	2.3	21	3	AAA48904 Aaa48904 Reverse p
c	181	21	2.3	21	3	AAA48903 Aaa48903 Forward p
	182	21	2.3	21	12	ADG14584 Adg14584 IL-12p40
	183	21	2.3	23	2	AAX78422 Aax78422 Rat GADPH
	184	21	2.3	23	2	AAX25940 Aax25940 IL12 p40
	185	21	2.3	44	2	AAV56632 Aav56632 Feline FL
	186	20	2.2	20	5	AAD19313 Aad19313 Mammalian
c	187	20	2.2	20	10	ABX33973 Abx33973 Human int
c	188	20	2.2	20	10	ABX33972 Abx33972 Human int
c	189	20	2.2	20	10	ABX33959 Abx33959 Human int
c	190	20	2.2	20	10	ABX33954 Abx33954 Human int
c	191	20	2.2	20	10	ABX33971 Abx33971 Human int
c	192	20	2.2	20	10	ABX33963 Abx33963 Human int
c	193	20	2.2	20	10	ABX33960 Abx33960 Human int
	194	20	2.2	20	12	ADH50946 Adh50946 Interleuk
c	195	20	2.2	32	2	AAV56631 Aav56631 Feline FL
	196	20	2.2	419	5	AAD19240 Aad19240 Mammalian
	197	20	2.2	419	5	AAD19239 Aad19239 Mammalian
	198	20	2.2	2341	12	ADQ25468 Adq25468 Human sof
	199	20	2.2	2341	12	ADQ24153 Adq24153 Human sof
	200	20	2.2	2752	6	AAL39635 Aal39635 Human sec

ALIGNMENTS

```
RESULT 1
ABK98942
ID   ABK98942 standard; cDNA; 921 BP.
XX
AC   ABK98942;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p40-921 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69302.
XX
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PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 49-50; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 921 BP; 277 A; 227 C; 230 G; 187 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 921;  DB 6;  Length 921;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 2
ABK98943/c
ID   ABK98943 standard; cDNA; 921 BP.
XX
AC   ABK98943;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p40-921 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Disclosure; Page 51; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 921 BP; 187 A; 230 C; 227 G; 277 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 921;  DB 6;  Length 921;
  Best Local Similarity  100.0%;  Pred. No. 0;
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  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCAGT 1


RESULT 3
ADV34681/c
ID   ADV34681 standard; DNA; 921 BP.
XX
AC   ADV34681;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain mature IL-12p40 complementary DNA, nFeIL-12p40 921.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 28; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain mature IL-12p40 subunit
CC   complementary DNA.
XX
SQ   Sequence 921 BP; 187 A; 230 C; 227 G; 277 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 921;  DB 14;  Length 921;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502
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Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        781 AACAGAGAAAAGAAAGAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCAGT 1
```

```
RESULT 4
ADV34679
ID   ADV34679 standard; cDNA; 921 BP.
XX
AC   ADV34679;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain mature IL-12p40 protein cDNA, nFeIL-12p40 921.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .921
FT                   /*tag=  a
FT                   /product= "PFeIL-12p40 307 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34680.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 23; SEQ ID NO 26; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain mature IL-12p40 subunit
CC   protein encoding cDNA.
XX
SQ   Sequence 921 BP; 277 A; 227 C; 230 G; 187 T; 0 U; 0 Other;
```

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  Query Match           100.0%;  Score 921;  DB 14;  Length 921;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
```

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Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921
```

```
RESULT 5
ABK98954/c
ID   ABK98954 standard; cDNA; 1533 BP.
XX
AC   ABK98954;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1533 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 66-67; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 921;  DB 6;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613
```

```
RESULT 6
ABK98953
ID   ABK98953 standard; cDNA; 1533 BP.
XX
AC   ABK98953;
XX
DT   21-OCT-2002  (first entry)
```

XX
DE Feline interleukin-12 nFeIL-12-1533 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69307.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 63-64; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

Query Match 100.0%; Score 921; DB 6; Length 1533;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921
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RESULT 7
ADV34697/c
ID ADV34697 standard; DNA; 1533 BP.
XX
AC ADV34697;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain IL-12 complementary DNA, nFeIL-12 1533.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Felis catus.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.

```
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 45; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 complementary DNA.
XX
SQ   Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 921;  DB 14;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613


RESULT 8
ADV34695
ID   ADV34695 standard; cDNA; 1533 BP.
XX
AC   ADV34695;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1533
FT                   /*tag=  a
FT                   /product= "PFeIL-12 511 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34696.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 43; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 921;  DB 14;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
                 |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 9
ABK98950
ID   ABK98950 standard; cDNA; 1599 BP.
XX
AC   ABK98950;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1599 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69306.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 58-60; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 921;  DB 6;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
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Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987
```

```
RESULT 10
ABK98951/c
ID   ABK98951 standard; cDNA; 1599 BP.
XX
AC   ABK98951;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1599 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 61-62; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;
```

```
  Query Match           100.0%;  Score 921;  DB 6;  Length 1599;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814
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Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613
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RESULT 11
ADV34691
ID   ADV34691 standard; cDNA; 1599 BP.
XX
AC   ADV34691;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1599
FT                   /*tag=  a
FT                   /product= "PFeIL-12p533 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34692.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 38; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;
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Query Match 100.0%; Score 921; DB 14; Length 1599;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987
```

```
RESULT 12
ADV34693/c
ID   ADV34693 standard; DNA; 1599 BP.
XX
AC   ADV34693;
```

```
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 complementary DNA, nFeIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 40; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 complementary DNA.
XX
SQ   Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 921;  DB 14;  Length 1599;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613


RESULT 13
AAV56626
ID   AAV56626 standard; cDNA; 921 BP.
XX
AC   AAV56626;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp40 cDNA mature transcript #1.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP001824.
XX
PR   04-JUN-1996;   96JP-00165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76174.
XX
PT   Novel feline cytokine protein - useful for treating feline auto:immune
PT   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS   Claim 20; Page 55; 94pp; Japanese.
XX
```

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CC   This sequence encodes a novel feline cytokine mature protein, FLAFp40.
CC   This protein can be used in the production of a FLAFp35/FLAFp40
CC   heterodimer which can potentiate the cytotoxic activity of feline
CC   cytotoxic T lymphocyte cells. Such proteins are used for treatment of
CC   feline autoimmune diseases e.g. as caused by feline herpes virus or
CC   feline calcivirus
XX
SQ   Sequence 921 BP; 276 A; 227 C; 231 G; 187 T; 0 U; 0 Other;

  Query Match            94.5%;  Score 870;  DB 2;  Length 921;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 14
ABK98944
ID   ABK98944 standard; cDNA; 987 BP.
XX
AC   ABK98944;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p40-987 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69303.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 51-53; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 987 BP; 283 A; 250 C; 246 G; 208 T; 0 U; 0 Other;

  Query Match            94.5%;  Score 870;  DB 6;  Length 987;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987


RESULT 15
ABK98945/c
ID   ABK98945 standard; cDNA; 987 BP.
XX
AC   ABK98945;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p40-987 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 3; Page 54; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 987 BP; 208 A; 246 C; 250 G; 283 T; 0 U; 0 Other;

  Query Match             94.5%;  Score 870;  DB 6;  Length 987;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCAGT 1


RESULT 16
ADV34682
ID   ADV34682 standard; cDNA; 987 BP.
XX
AC   ADV34682;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12p40 full-length cDNA, nFeIL-12p40 987.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .987
FT                   /*tag=  a
FT                   /product= "PFeIL-12p40 329 protein "
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34683.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 23; SEQ ID NO 29; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12p40 subunit protein
CC   encoding full-length cDNA.
XX
SQ   Sequence 987 BP; 283 A; 250 C; 246 G; 208 T; 0 U; 0 Other;

  Query Match             94.5%;  Score 870;  DB 14;  Length 987;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
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Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987


RESULT 17
ADV34684/c
ID   ADV34684 standard; DNA; 987 BP.
XX
AC   ADV34684;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12p40 complementary DNA, nFeIL-12p40 987.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 31; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12p40 subunit full-length
CC   complementary DNA.
XX
SQ   Sequence 987 BP; 208 A; 246 C; 250 G; 283 T; 0 U; 0 Other;

  Query Match             94.5%;  Score 870;  DB 14;  Length 987;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCAGT 1


RESULT 18
AAV56625
ID   AAV56625 standard; cDNA; 2193 BP.
XX
AC   AAV56625;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp40 cDNA.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             64. .1053
FT                   /*tag=  a
FT   sig_peptide     64. .129
```

```
FT                   /*tag=  b
FT   mat_peptide     130. .1050
FT                   /*tag=  c
FT                   /product= "FLAFp40"
FT                   /note= "feline cytokine"
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP001824.
XX
PR   04-JUN-1996;   96JP-00165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76173.
XX
PT   Novel feline cytokine protein - useful for treating feline auto:immune
PT   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS   Claim 19; Page 52-54; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine protein, FLAFp40. This
CC   protein can be used in the production of a FLAFp35/FLAFp40 heterodimer
CC   which can potentiate the cytotoxic activity of feline cytotoxic T
CC   lymphocyte cells. Such proteins are used for treatment of feline
CC   autoimmune diseases e.g. as caused by feline herpes virus or feline
CC   calcivirus
XX
SQ   Sequence 2193 BP; 680 A; 451 C; 493 G; 569 T; 0 U; 0 Other;

  Query Match             94.5%;  Score 870;  DB 2;  Length 2193;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 189

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 249

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 309

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 369

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 429

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 489

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 549

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        550 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 609

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        610 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 669

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 729

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 789

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 849

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 909

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 969

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 1029

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db       1030 TGGGCATCCGTGTCCTGCAGT 1050


RESULT 19
ABK98962/c
ID   ABK98962 standard; cDNA; 985 BP.
XX
AC   ABK98962;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p40-N985 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 3; Page 75-76; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
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CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 985 BP; 207 A; 245 C; 250 G; 283 T; 0 U; 0 Other;

  Query Match             94.2%;  Score 868;  DB 6;  Length 985;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 860

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 800

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 740

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 680

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 620

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 560

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 500

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 440

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 380

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 320

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 260

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 200

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 140

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 80

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         79 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 20

Qy        901 TGGGCATCCGTGTCCTGCA 919
              ||||||||||||||||||||
Db         19 TGGGCATCCGTGTCCTGCA 1


RESULT 20
ABK98961
ID   ABK98961 standard; cDNA; 985 BP.
XX
AC   ABK98961;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p40-N985 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69311.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 3; Page 73-74; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 985 BP; 283 A; 250 C; 245 G; 207 T; 0 U; 0 Other;

  Query Match             94.2%;  Score 868;  DB 6;  Length 985;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
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Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCA 919
              ||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCA 985
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RESULT 21
ADV34707
ID   ADV34707 standard; cDNA; 985 BP.
XX
AC   ADV34707;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline N-terminal IL-12p40 protein encoding cDNA, nFeIL-12p40-N985.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .984
FT                   /*tag= a
FT                   /product= "PCaIL-12P40-N328 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34708.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 55; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline N-terminal single chain IL-12p40 protein
CC   encoding cDNA.
XX
SQ   Sequence 985 BP; 283 A; 250 C; 245 G; 207 T; 0 U; 0 Other;
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  Query Match             94.2%;  Score 868;  DB 14;  Length 985;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
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                |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCA 919
                ||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCA 985


RESULT 22
ADV34709/c
ID   ADV34709 standard; DNA; 985 BP.
XX
AC   ADV34709;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline N-terminal IL-12p40 protein complementary DNA, nFeIL-12p40-N985.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 57; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline N-terminal single chain IL-12p40
CC   complementary DNA.
XX
SQ   Sequence 985 BP; 207 A; 245 C; 250 G; 283 T; 0 U; 0 Other;

  Query Match             94.2%;  Score 868;  DB 14;  Length 985;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 860

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 800

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 740

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 680

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 620

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 560

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 500

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 440

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 380

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 320

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 260

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 200

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 140

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 80

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db         79 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 20

Qy        901 TGGGCATCCGTGTCCTGCA 919
              ||||||||||||||||||
Db         19 TGGGCATCCGTGTCCTGCA 1


RESULT 23
AAV56627
ID   AAV56627 standard; cDNA; 921 BP.
XX
AC   AAV56627;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp40 cDNA mature transcript #2.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP001824.
XX
PR   04-JUN-1996;   96JP-00165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76174.
XX
PT   Novel feline cytokine protein - useful for treating feline auto:immune
PT   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS   Claim 21; Page 56-57; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine mature protein, FLAFp40.
CC   This protein can be used in the production of a FLAFp35/FLAFp40
CC   heterodimer which can potentiate the cytotoxic activity of feline
CC   cytotoxic T lymphocyte cells. Such proteins are used for treatment of
CC   feline autoimmune diseases e.g. as caused by feline herpes virus or
CC   feline calcivirus
XX
SQ   Sequence 921 BP; 276 A; 228 C; 230 G; 187 T; 0 U; 0 Other;

  Query Match             88.9%;  Score 819;  DB 2;  Length 921;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches  919;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 24
AAF26082
ID   AAF26082 standard; DNA; 990 BP.
XX
AC   AAF26082;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p40 encoding DNA SEQ ID 8.
XX
KW   Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW   interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS   Felis sp.
XX
PN   WO200104280-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002262.
XX
PR   08-JUL-1999;   99CH-00001258.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
XX
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PI   Leutenegger C,  Schroff M,  Wittig B,  Lutz H;
XX
DR   WPI; 2001-147190/15.
XX
PT   Vaccine for treating or preventing lentivirus infection in cats, contains
PT   nucleic acid sequence encoding viral protein under control of eukaryotic
PT   promoter.
XX
PS   Claim 14; Page 36; 37pp; German.
XX
CC   This invention describes a novel vaccine (A) for prevention or treatment
CC   of lentivirus infection in felines which comprises an immunizing nucleic
CC   acid sequence (I) that contains, or comprises, at least part of a gene
CC   encoding a protein (II) of the virus, under control of a eukaryotic
CC   promoter functional in the relevant animal. (II) is especially the
CC   envelope (env) protein. The invention also describes (1) vaccine (A)
CC   containing an immunizing protein, or fragment, from a lentivirus plus at
CC   least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC   lentivirus protein, or fragment, especially derived from feline immune
CC   deficiency virus (FIV), by expressing the corresponding nucleic acid
CC   sequence in a host cell. The products of the invention have antiviral
CC   activity. The vaccine (A) and related protein-based vaccines, are
CC   particularly used to treat or prevent lentivirus infections in domestic
CC   cats, especially feline immune deficiency virus (FIV). Vaccination with
CC   (A) allows differentiation between vaccinated and infected animals, from
CC   the antibody status. The vaccines may be formulated with an adjuvant
CC   (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC   immune response, particularly a Th1 response
XX
SQ   Sequence 990 BP; 283 A; 249 C; 248 G; 210 T; 0 U; 0 Other;

  Query Match             83.4%;  Score 768;  DB 4;  Length 990;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987


RESULT 25
AAF26085
ID   AAF26085 standard; DNA; 990 BP.
XX
AC   AAF26085;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p40 encoding DNA.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS   Felis sp.
XX
PN   WO200104155-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002263.
XX
PR   08-JUL-1999;   99CH-00001259.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Lutz H,  Leutenegger C,  Pedersen N,  Schroff M,  Wittig B;
XX
DR   WPI; 2001-147178/15.
XX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs.
XX
PS   Claim 3; Page 30; 35pp; German.
XX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
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CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
CC   following: (i) as immunostimulant, for preventative or therapeutic use;
CC   and (ii) treating tumors and autoimmune diseases, or diseases associated
CC   with a Th1 defect, especially pre-existing infections by feline immune
CC   deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ   Sequence 990 BP; 283 A; 249 C; 248 G; 210 T; 0 U; 0 Other;

  Query Match             83.4%;  Score 768;  DB 4;  Length 990;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987


RESULT 26
AAF26076
ID   AAF26076 standard; DNA; 4522 BP.
XX
AC   AAF26076;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p40 encoding DNA SEQ ID 2.
XX
KW   Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW   interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS   Felis sp.
XX
PN   WO200104280-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002262.
XX
PR   08-JUL-1999;   99CH-00001258.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
XX
PI   Leutenegger C,  Schroff M,  Wittig B,  Lutz H;
XX
DR   WPI; 2001-147190/15.
XX
PT   Vaccine for treating or preventing lentivirus infection in cats, contains
PT   nucleic acid sequence encoding viral protein under control of eukaryotic
PT   promoter.
XX
PS   Disclosure; Page 29-31; 37pp; German.
XX
CC   This invention describes a novel vaccine (A) for prevention or treatment
CC   of lentivirus infection in felines which comprises an immunizing nucleic
CC   acid sequence (I) that contains, or comprises, at least part of a gene
CC   encoding a protein (II) of the virus, under control of a eukaryotic
CC   promoter functional in the relevant animal. (II) is especially the
CC   envelope (env) protein. The invention also describes (1) vaccine (A)
CC   containing an immunizing protein, or fragment, from a lentivirus plus at
CC   least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC   lentivirus protein, or fragment, especially derived from feline immune
CC   deficiency virus (FIV), by expressing the corresponding nucleic acid
CC   sequence in a host cell. The products of the invention have antiviral
CC   activity. The vaccine (A) and related protein-based vaccines, are
CC   particularly used to treat or prevent lentivirus infections in domestic
CC   cats, especially feline immune deficiency virus (FIV). Vaccination with
CC   (A) allows differentiation between vaccinated and infected animals, from
CC   the antibody status. The vaccines may be formulated with an adjuvant
CC   (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC   immune response, particularly a Th1 response
XX
SQ   Sequence 4522 BP; 1180 A; 1126 C; 1106 G; 1110 T; 0 U; 0 Other;

  Query Match             83.4%;  Score 768;  DB 4;  Length 4522;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
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Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3113 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 3172

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       3173 GGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 3232

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3233 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 3292

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3293 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 3352

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3353 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 3412

Qy        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3413 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 3472

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3473 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 3532

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       3533 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 3592

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3593 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 3652

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3653 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 3712

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3713 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 3772

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3773 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 3832

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3833 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 3892

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3893 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 3952

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       3953 AAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGGAGCAAC 4012

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db       4013 TGGGCATCCGTGTCCTGCAGT 4033
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RESULT 27
AAF26094
ID   AAF26094 standard; DNA; 4522 BP.
XX
AC   AAF26094;
XX
DT   24-APR-2001  (first entry)
XX
DE   Plasmid pMol-fil12p40 DNA SEQ ID 10.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS   Synthetic.
XX
PN   WO200104155-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002263.
XX
PR   08-JUL-1999;   99CH-00001259.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Lutz H, Leutenegger C, Pedersen N, Schroff M, Wittig B;
XX
DR   WPI; 2001-147178/15.
XX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs.
XX
PS   Example 1c; Page 33-35; 35pp; German.
XX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
CC   following: (i) as immunostimulant, for preventative or therapeutic use;
CC   and (ii) treating tumors and autoimmune diseases, or diseases associated
CC   with a Th1 defect, especially pre-existing infections by feline immune
CC   deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ   Sequence 4522 BP; 1180 A; 1126 C; 1106 G; 1110 T; 0 U; 0 Other;

  Query Match           83.4%;  Score 768;  DB 4;  Length 4522;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3113 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 3172

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       3173 GGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 3232

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3233 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 3292

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3293 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 3352
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Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3353 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 3412

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3413 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 3472

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3473 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 3532

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       3533 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 3592

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3593 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 3652

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3653 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 3712

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3713 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 3772

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3773 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 3832

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3833 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 3892

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3893 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 3952

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       3953 AAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGGAGCAAC 4012

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db       4013 TGGGCATCCGTGTCCTGCAGT 4033
```

```
RESULT 28
AAD15209
ID   AAD15209 standard; DNA; 990 BP.
XX
AC   AAD15209;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p40 encoding DNA from clone R16-51.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p40; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
FT                   /product= "Modified p40 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .987
FT                   /*tag=  c
FT                   /product= "Mature modified p40 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08602.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 1; Page 137-138; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p40 protein encoding
CC   DNA
XX
SQ   Sequence 990 BP; 270 A; 250 C; 254 G; 216 T; 0 U; 0 Other;

  Query Match             9.0%;  Score 83;  DB 5;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-31;
  Matches   83;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        799 AGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGC 858
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 AGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGC 924

Qy        859 GTGCAAGCCAGAGACCGCTACTA 881
              |||||||||||||||||||||||
Db        925 GTGCAAGCCAGAGACCGCTACTA 947
```

```
RESULT 29
ABK98959
ID   ABK98959 standard; cDNA; 921 BP.
XX
AC   ABK98959;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p40-921 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
```

```
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69310.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 71; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 921 BP; 272 A; 221 C; 234 G; 194 T; 0 U; 0 Other;

  Query Match             7.2%;  Score 66;  DB 6;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy        531 CTGCCC 536
              ||||||
Db        531 CTGCCC 536


RESULT 30
ABK98960/c
ID   ABK98960 standard; cDNA; 921 BP.
XX
AC   ABK98960;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p40-921 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Disclosure; Page 73; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 921 BP; 194 A; 234 C; 221 G; 272 T; 0 U; 0 Other;

  Query Match             7.2%;  Score 66;  DB 6;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy        531 CTGCCC 536
              ||||||
Db        391 CTGCCC 386


RESULT 31
ADV34706/c
ID   ADV34706 standard; DNA; 921 BP.
XX
AC   ADV34706;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain mature IL-12p40 complementary DNA, nCaIL-12p40 921.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
```

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XX
PS   Disclosure; SEQ ID NO 54; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p40 subunit reverse
CC   complementary DNA.
XX
SQ   Sequence 921 BP; 194 A; 234 C; 221 G; 272 T; 0 U; 0 Other;

  Query Match             7.2%;  Score 66;  DB 14;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy        531 CTGCCC 536
              ||||||
Db        391 CTGCCC 386


RESULT 32
ADV34704
ID   ADV34704 standard; cDNA; 921 BP.
XX
AC   ADV34704;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain mature IL-12p40 protein cDNA, nCaIL-12p40 921.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .921
FT                   /*tag=  a
FT                   /product= "PCaIL-12P40 307 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34705.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 52; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p40 subunit protein
CC   encoding cDNA.
XX
SQ   Sequence 921 BP; 272 A; 221 C; 234 G; 194 T; 0 U; 0 Other;

  Query Match             7.2%;  Score 66;  DB 14;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy        531 CTGCCC 536
              ||||||
Db        531 CTGCCC 536


RESULT 33
AAX18177
ID   AAX18177 standard; cDNA; 924 BP.
XX
AC   AAX18177;
XX
DT   07-MAY-1999  (first entry)
XX
DE   Canine mature CLAF p40 subunit coding sequence.
XX
KW   CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW   viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW   canine infectious hepatitis; ds.
XX
OS   Canis sp.
XX
PN   WO9855511-A1.
XX
PD   10-DEC-1998.
XX
PF   26-MAY-1998;   98WO-JP002295.
XX
PR   03-JUN-1997;   97JP-00161936.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Tokiyoshi S,  Eda Y;
XX
DR   WPI; 1999-070260/06.
DR   P-PSDB; AAW74323.
XX
PT   Canine cytokine protein which activates canine cytotoxic T lymphocytes -
PT   is useful for treatment of viral and autoimmune diseases in dogs.
XX
PS   Claim 8; Page 32; 51pp; Japanese.
XX
CC   This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC   the invention. CLAF activates lymphocytes, especially canine cytotoxic T
CC   cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC   recognising it may be used in the treatment of viral diseases in dogs
CC   (such as canine distemper, canine parvovirus and canine infectious
CC   hepatitis). The antibodies may also be used in isolation of CLAF from
CC   culture of the transformant host cells by affinity chromatography. The
CC   p40 homodimer can be used for the treatment of autoimmune diseases in
CC   dogs
XX
SQ   Sequence 924 BP; 273 A; 222 C; 234 G; 195 T; 0 U; 0 Other;

  Query Match             7.2%;  Score 66;  DB 2;  Length 924;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-22;
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```
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 533

Qy        531 CTGCCC 536
              ||||||
Db        534 CTGCCC 539


RESULT 34
ABK98963
ID   ABK98963 standard; cDNA; 987 BP.
XX
AC   ABK98963;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p40-987 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69312.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 76-77; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 987 BP; 279 A; 244 C; 248 G; 216 T; 0 U; 0 Other;

  Query Match             7.2%;  Score 66;  DB 6;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        531 CTGCCC 536
              ||||||
Db        597 CTGCCC 602


RESULT 35
ABK98964/c
ID   ABK98964 standard; cDNA; 987 BP.
XX
AC   ABK98964;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p40-987 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 4; Page 78; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 987 BP; 216 A; 248 C; 244 G; 279 T; 0 U; 0 Other;

  Query Match             7.2%;  Score 66;  DB 6;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy        531 CTGCCC 536
              ||||||
Db        391 CTGCCC 386


RESULT 36
ADV34712/c
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```
ID   ADV34712 standard; DNA; 987 BP.
XX
AC   ADV34712;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p40 complementary DNA, nCaIL-12p40 987.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 60; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p40 subunit full-length
CC   complementary DNA.
XX
SQ   Sequence 987 BP; 216 A; 248 C; 244 G; 279 T; 0 U; 0 Other;

  Query Match             7.2%;  Score 66;  DB 14;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy        531 CTGCCC 536
              ||||||
Db        391 CTGCCC 386


RESULT 37
ADV34710
ID   ADV34710 standard; cDNA; 987 BP.
XX
AC   ADV34710;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p40 full-length cDNA, nCaIL-12p40 987.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .987
FT                   /*tag=  a
FT                   /product= "PCaIL-12P40-329 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34711.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 58; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p40 subunit protein
CC   encoding full-length cDNA.
XX
SQ   Sequence 987 BP; 279 A; 244 C; 248 G; 216 T; 0 U; 0 Other;

  Query Match             7.2%;  Score 66;  DB 14;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        531 CTGCCC 536
              ||||||
Db        597 CTGCCC 602


RESULT 38
AAV13816
ID   AAV13816 standard; cDNA to mRNA; 990 BP.
XX
AC   AAV13816;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P40 subunit cDNA.
XX
KW   Canine; interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour;
KW   antiviral; vaccine adjuvant; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
```

```
FT                   /product= "interleukin-12_P40_subunit"
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-00296789.
XX
PR   08-NOV-1995;   95JP-00289729.
PR   23-MAY-1996;   96JP-00128104.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   P-PSDB; AAW41790.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected.
XX
PS   Claim 8; Page 8; 12pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin-12 (IL-12) P40 subunit.
CC   A canine IL-12 comprising a P40 and P35 subunit is capable of inducing an
CC   antiviral activating factor and the expression of class II MHC molecules
CC   in canine tumour cells, stimulating proliferation of canine blastogenic
CC   lymphocytes and activating canine leukocytes to inhibit canine tumour
CC   cells. The canine IL-12 can be used in veterinary medicines, e.g.
CC   antitumour, antivirus and vaccine adjuvant activities are expected
XX
SQ   Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 U; 0 Other;

  Query Match             7.2%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        531 CTGCCC 536
              ||||||
Db        597 CTGCCC 602


RESULT 39
AAV13817
ID   AAV13817 standard; cDNA to mRNA; 990 BP.
XX
AC   AAV13817;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P40 subunit cDNA.
XX
KW   Canine; interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour;
KW   antiviral; vaccine adjuvant; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
FT                   /product= "interleukin-12_P40_subunit"
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-00296789.
XX
PR   08-NOV-1995;   95JP-00289729.
PR   23-MAY-1996;   96JP-00128104.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   P-PSDB; AAW41791.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected.
XX
PS   Claim 10; Page 10-11; 12pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin-12 (IL-12) P40 subunit.
CC   A canine IL-12 comprising a P40 and P35 subunit is capable of inducing an
CC   antiviral activating factor and the expression of class II MHC molecules
CC   in canine tumour cells, stimulating proliferation of canine blastogenic
CC   lymphocytes and activating canine leukocytes to inhibit canine tumour
CC   cells. The canine IL-12 can be used in veterinary medicines, e.g.
CC   antitumour, antivirus and vaccine adjuvant activities are expected
XX
SQ   Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 U; 0 Other;

  Query Match             7.2%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        531 CTGCCC 536
              ||||||
Db        597 CTGCCC 602


RESULT 40
AAX03162
ID   AAX03162 standard; cDNA to mRNA; 990 BP.
XX
AC   AAX03162;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Nucleic acid encoding canine interleukin 12.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
FT                   /product= "interleukin_12"
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP002031.
XX
PR   16-MAY-1997;   97JP-00127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
```

```
DR   WPI; 1999-070100/06.
DR   P-PSDB; AAW84373.
XX
PT   New therapeutic and prophylactic agents - comprise genetically-engineered
PT   canine interleukin 12, used to treat, e.g. canine and feline
PT   immunological diseases.
XX
PS   Claim 1; Page 30-32; 45pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin 12 (IL-12) protein. The
CC   IL-12 protein can be used in therapeutic or prophylactic agents. The
CC   agents can be used to prevent and treat canine and feline immunological
CC   diseases including dog and cat tumours, skin diseases, viral infections
CC   and allergic diseases, especially tumours, breast tumour, oesinophilic
CC   granuloma, epidermoid tumour, skin tumour, lipoma, othematoma,
CC   pneumonoedema, skin soft pedicled soft tumour and anal tumour; skin
CC   diseases, otitis externa, dermatitis, eczema, fungal diseases of the
CC   skin, pyoderma, allergic dermatitis, nettle rash, traumatic dermatitis
CC   and hair loss; infections; dog Parvovirus infection and distemper virus,
CC   cat plaque virus infection and feline leukaemia, and allergic diseases,
CC   e.g. pollinosis
XX
SQ   Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 U; 0 Other;

  Query Match             7.2%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        531 CTGCCC 536
              ||||||
Db        597 CTGCCC 602


RESULT 41
AAX03152
ID   AAX03152 standard; cDNA to mRNA; 990 BP.
XX
AC   AAX03152;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Nucleic acid encoding canine interleukin 12.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
FT                   /product= "interleukin_12"
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP002031.
XX
PR   16-MAY-1997;   97JP-00127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   P-PSDB; AAW84371.
XX
PT   New therapeutic and prophylactic agents - comprise genetically-engineered
PT   canine interleukin 12, used to treat, e.g. canine and feline
PT   immunological diseases.
XX
PS   Claim 1; Page 23-25; 45pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin 12 (IL-12) protein. The
CC   IL-12 protein can be used in therapeutic or prophylactic agents. The
CC   agents can be used to prevent and treat canine and feline immunological
CC   diseases including dog and cat tumours, skin diseases, viral infections
CC   and allergic diseases, especially tumours, breast tumour, oesinophilic
CC   granuloma, epidermoid tumour, skin tumour, lipoma, othematoma,
CC   pneumonoedema, skin soft pedicled soft tumour and anal tumour; skin
CC   diseases, otitis externa, dermatitis, eczema, fungal diseases of the
CC   skin, pyoderma, allergic dermatitis, nettle rash, traumatic dermatitis
CC   and hair loss; infections; dog Parvovirus infection and distemper virus,
CC   cat plaque virus infection and feline leukaemia, and allergic diseases,
CC   e.g. pollinosis
XX
SQ   Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 U; 0 Other;

  Query Match             7.2%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        531 CTGCCC 536
              ||||||
Db        597 CTGCCC 602


RESULT 42
AAX35625
ID   AAX35625 standard; cDNA to mRNA; 990 BP.
XX
AC   AAX35625;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-00133345.
XX
PR   16-MAY-1997;   97JP-00127690.
PR   07-AUG-1997;   97JP-00213755.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   P-PSDB; AAY02342.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) - for
```

```
PT   prevention and treatment of dog and cat immune diseases.
XX
PS   Claim 1; Page 14-15; 16pp; Japanese.
XX
CC   The present sequence encodes canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment of dog
CC   and cat immune diseases. The treatment used an agent comprising dog IL-12
CC   (CaIL12) proteins to form a heterodimer. The agent is useful for
CC   preventing and treating dog and cat immune diseases, including tumours,
CC   skin diseases, infectious diseases and allergic diseases
XX
SQ   Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 U; 0 Other;

  Query Match             7.2%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        531 CTGCCC 536
              ||||||
Db        597 CTGCCC 602


RESULT 43
AAX35615
ID   AAX35615 standard; cDNA to mRNA; 990 BP.
XX
AC   AAX35615;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-00133345.
XX
PR   16-MAY-1997;   97JP-00127690.
PR   07-AUG-1997;   97JP-00213755.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   P-PSDB; AAY02339.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) - for
PT   prevention and treatment of dog and cat immune diseases.
XX
PS   Claim 1; Page 12; 16pp; Japanese.
XX
CC   The present sequence encodes canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment of dog
CC   and cat immune diseases. The treatment used an agent comprising dog IL-12
CC   (CaIL12) proteins to form a heterodimer. The agent is useful for
CC   preventing and treating dog and cat immune diseases, including tumours,
CC   skin diseases, infectious diseases and allergic diseases
XX
SQ   Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 U; 0 Other;

  Query Match             7.2%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        531 CTGCCC 536
              ||||||
Db        597 CTGCCC 602


RESULT 44
AAI64378
ID   AAI64378 standard; DNA; 990 BP.
XX
AC   AAI64378;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine coding sequence #1.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
FT                   /product= "Canine protein #1"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .987
FT                   /*tag=  c
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-00292946.
XX
PR   01-OCT-1999;   99JP-00281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   P-PSDB; AAG66480.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian.
XX
PS   Claim 6; Page 14; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention
XX
SQ   Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 U; 0 Other;

  Query Match             7.2%;  Score 66;  DB 4;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        531 CTGCCC 536
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```
              ||||||
Db        597 CTGCCC 602


RESULT 45
AAI64388
ID   AAI64388 standard; DNA; 990 BP.
XX
AC   AAI64388;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine coding sequence #3.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
FT                   /product= "Canine protein #1"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .987
FT                   /*tag=  c
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-00292946.
XX
PR   01-OCT-1999;   99JP-00281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   P-PSDB; AAG66482.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian.
XX
PS   Claim 6; Page 16-17; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention
XX
SQ   Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 U; 0 Other;

  Query Match             7.2%;  Score 66;  DB 4;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        531 CTGCCC 536
              ||||||
Db        597 CTGCCC 602


RESULT 46
ADZ25698
ID   ADZ25698 standard; cDNA; 990 BP.
XX
AC   ADZ25698;
XX
DT   16-JUN-2005  (first entry)
XX
DE   Canine interleukin 12 P40 encoding cDNA SEQ ID NO:3.
XX
KW   interleukin-12; antiviral; gene; ss.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  b
FT                   /product= "interleukin-12 P40"
FT   sig_peptide     1. .66
FT                   /*tag=  a
FT   mat_peptide     67. .987
FT                   /*tag=  c
FT                   /product= "interleukin-12 P40"
XX
PN   JP2003284585-A.
XX
PD   07-OCT-2003.
XX
PF   28-MAR-2002; 2002JP-00090161.
XX
PR   28-MAR-2002; 2002JP-00090161.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2003-885430/82.
DR   P-PSDB; ADZ25702.
XX
PT   Large scale production of interleukin-12 for pharmaceutical applications,
PT   comprises infecting an insect cell with a recombinant virus containing
PT   gene encoding IL-12, and producing IL-12 by carrying out spinner culture
PT   of insect cell.
XX
PS   Example; SEQ ID NO 3; 8pp; Japanese.
XX
CC   The invention related to the large scale production of interleukin-12 (IL
CC   -12), which involves infecting an insect cell with a recombinant virus
CC   containing a gene encoding IL-12, and producing IL-12 by carrying out
CC   spinner culture of insect cell. The method is useful for producing IL-12,
CC   preferably canine IL-12. IL-12 has pharmaceutical applications. The
CC   present sequence encodes canine IL-12 P40, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 U; 0 Other;

  Query Match             7.2%;  Score 66;  DB 11;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        531 CTGCCC 536
              ||||||
Db        597 CTGCCC 602


RESULT 47
ABK98967
ID   ABK98967 standard; cDNA; 1533 BP.
XX
AC   ABK98967;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1533 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
```

```
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69314.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 83-85; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 446 A; 368 C; 369 G; 350 T; 0 U; 0 Other;

  Query Match             7.2%;  Score 66;  DB 6;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy        531 CTGCCC 536
              ||||||
Db        531 CTGCCC 536


RESULT 48
ABK98968/c
ID   ABK98968 standard; cDNA; 1533 BP.
XX
AC   ABK98968;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1533 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 86-87; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

  Query Match             7.2%;  Score 66;  DB 6;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy        531 CTGCCC 536
              ||||||
Db       1003 CTGCCC 998


RESULT 49
ADV34718/c
ID   ADV34718 standard; DNA; 1533 BP.
XX
AC   ADV34718;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12 complementary DNA, nCaIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
```

PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 4; SEQ ID NO 68; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the canine single chain IL-12 complementary DNA.
XX
SQ Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

Query Match 7.2%; Score 66; DB 14; Length 1533;
Best Local Similarity 100.0%; Pred. No. 2.6e-22;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy 531 CTGCCC 536
||||||
Db 1003 CTGCCC 998

RESULT 50
ADV34716
ID ADV34716 standard; cDNA; 1533 BP.
XX
AC ADV34716;
XX
DT 24-FEB-2005 (first entry)
XX
DE Canine single chain IL-12 protein cDNA, nCaIL-12 1533.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; gene; ss.
XX
OS Canis familiaris.
XX
FH Key Location/Qualifiers
FT CDS 1. .1533
FT /*tag= a
FT /product= "PCaIL-12 511 protein"
FT /partial
FT /note= "No start and stop codon"
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
DR P-PSDB; ADV34717.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 4; SEQ ID NO 66; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the canine single chain IL-12 protein encoding cDNA.
XX
SQ Sequence 1533 BP; 446 A; 368 C; 369 G; 350 T; 0 U; 0 Other;

Query Match 7.2%; Score 66; DB 14; Length 1533;
Best Local Similarity 100.0%; Pred. No. 2.6e-22;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy 531 CTGCCC 536
||||||
Db 531 CTGCCC 536

RESULT 51
ABK98965
ID ABK98965 standard; cDNA; 1599 BP.
XX
AC ABK98965;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12-1599 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69313.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 79-80; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,

```
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 452 A; 392 C; 383 G; 372 T; 0 U; 0 Other;

  Query Match             7.2%;  Score 66;  DB 6;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        531 CTGCCC 536
              ||||||
Db        597 CTGCCC 602


RESULT 52
ABK98966/c
ID   ABK98966 standard; cDNA; 1599 BP.
XX
AC   ABK98966;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1599 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 82-83; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 372 A; 383 C; 392 G; 452 T; 0 U; 0 Other;

  Query Match             7.2%;  Score 66;  DB 6;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy        531 CTGCCC 536
              ||||||
Db       1003 CTGCCC 998


RESULT 53
ADV34715/c
ID   ADV34715 standard; DNA; 1599 BP.
XX
AC   ADV34715;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12 complementary DNA, nCaIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 63; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 complementary DNA.
XX
SQ   Sequence 1599 BP; 372 A; 383 C; 392 G; 452 T; 0 U; 0 Other;

  Query Match             7.2%;  Score 66;  DB 14;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004
```

```
Qy        531 CTGCCC 536
              ||||||
Db       1003 CTGCCC 998


RESULT 54
ADV34713
ID   ADV34713 standard; cDNA; 1599 BP.
XX
AC   ADV34713;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12 protein cDNA, nCaIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1599
FT                   /*tag=  a
FT                   /product= "PCaIL-12 533 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34714.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 61; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1599 BP; 452 A; 392 C; 383 G; 372 T; 0 U; 0 Other;

  Query Match             7.2%;  Score 66;  DB 14;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        531 CTGCCC 536
              ||||||
Db        597 CTGCCC 602


RESULT 55
AAX18176
ID   AAX18176 standard; cDNA; 2154 BP.
XX
AC   AAX18176;
XX
DT   07-MAY-1999  (first entry)
XX
DE   Canine full length CLAF p40 subunit coding sequence.
XX
KW   CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW   viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW   canine infectious hepatitis; ds.
XX
OS   Canis sp.
XX
PN   WO9855511-A1.
XX
PD   10-DEC-1998.
XX
PF   26-MAY-1998;   98WO-JP002295.
XX
PR   03-JUN-1997;   97JP-00161936.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Tokiyoshi S,  Eda Y;
XX
DR   WPI; 1999-070260/06.
DR   P-PSDB; AAW74322.
XX
PT   Canine cytokine protein which activates canine cytotoxic T lymphocytes -
PT   is useful for treatment of viral and autoimmune diseases in dogs.
XX
PS   Claim 8; Page 30-31; 51pp; Japanese.
XX
CC   This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC   the invention. CLAF activates lymphocytes, especially canine cytotoxic T
CC   cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC   recognising it may be used in the treatment of viral diseases in dogs
CC   (such as canine distemper, canine parvovirus and canine infectious
CC   hepatitis). The antibodies may also be used in isolation of CLAF from
CC   culture of the transformant host cells by affinity chromatography. The
CC   p40 homodimer can be used for the treatment of autoimmune diseases in
CC   dogs
XX
SQ   Sequence 2154 BP; 663 A; 448 C; 477 G; 566 T; 0 U; 0 Other;

  Query Match             7.2%;  Score 66;  DB 2;  Length 2154;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 650

Qy        531 CTGCCC 536
              ||||||
Db        651 CTGCCC 656


RESULT 56
ABK99006/c
ID   ABK99006 standard; cDNA; 2267 BP.
XX
AC   ABK99006;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p40-2267 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
```

```
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 4; Page 99-100; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 2267 BP; 591 A; 504 C; 468 G; 704 T; 0 U; 0 Other;

  Query Match             7.2%;  Score 66;  DB 6;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1578 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1519

Qy        531 CTGCCC 536
              ||||||
Db       1518 CTGCCC 1513


RESULT 57
ABK99005
ID   ABK99005 standard; cDNA; 2267 BP.
XX
AC   ABK99005;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p40-2267 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69317.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 4; Page 97-98; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 2267 BP; 704 A; 468 C; 504 G; 591 T; 0 U; 0 Other;

  Query Match             7.2%;  Score 66;  DB 6;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 749

Qy        531 CTGCCC 536
              ||||||
Db        750 CTGCCC 755


RESULT 58
ADV34757
ID   ADV34757 standard; cDNA; 2267 BP.
XX
AC   ADV34757;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p40 protein cDNA, nCaIL-12p40 2267.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             154. .1143
FT                   /*tag=  a
FT                   /product= "PCaIL-12p40 329 protein"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
```

```
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34758.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 107; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p40 subunit protein
CC   encoding cDNA.
XX
SQ   Sequence 2267 BP; 704 A; 468 C; 504 G; 591 T; 0 U; 0 Other;

  Query Match             7.2%;  Score 66;  DB 14;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 749

Qy        531 CTGCCC 536
              ||||||
Db        750 CTGCCC 755


RESULT 59
ADV34759/c
ID   ADV34759 standard; DNA; 2267 BP.
XX
AC   ADV34759;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p40 complementary DNA, nCaIL-12p35 2267.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 109; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p40 subunit
CC   complementary DNA.
XX
SQ   Sequence 2267 BP; 591 A; 504 C; 468 G; 704 T; 0 U; 0 Other;

  Query Match             7.2%;  Score 66;  DB 14;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1578 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1519

Qy        531 CTGCCC 536
              ||||||
Db       1518 CTGCCC 1513


RESULT 60
ADT04849
ID   ADT04849 standard; DNA; 1015 BP.
XX
AC   ADT04849;
XX
DT   13-JAN-2005  (first entry)
XX
DE   Canine interleukin-12 (IL-12) p40 DNA.
XX
KW   gene expression; insect; ds; interleukin-12; IL-12.
XX
OS   Canis familiaris.
XX
PN   JP2004290182-A.
XX
PD   21-OCT-2004.
XX
PF   06-FEB-2004; 2004JP-00030183.
XX
PR   10-MAR-2003; 2003JP-00062907.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2004-740760/73.
XX
PT   Novel gene vector for expression in insect useful for expression of
PT   foreign gene such as dog interleukin 12 gene, comprises two promoters.
XX
PS   Claim 4; SEQ ID NO 5; 13pp; Japanese.
XX
CC   The invention relates to a novel gene vector for expression in an insect
CC   comprising at least two promoters, particularly the polyhedrin promoter
CC   and p10 promoter. The vector contains at least two types of foreign
CC   protein expression gene and the gene product of the vector is produced
CC   using a gene recombinant baculovirus, particularly a recombinant silkworm
CC   nuclear polyhedrosis virus. The baculovirus is proliferated in a
CC   silkworm. The vector of the invention may be useful for expression of a
CC   foreign gene, such as canine interleukin 12. Within the vector, two types
CC   of foreign protein expression genes are integrated simultaneously for
CC   their simultaneous expression. The current sequence is that of the canine
CC   interleukin-12 (IL-12) p40 DNA of the invention.
XX
```

```
SQ   Sequence 1015 BP; 285 A; 251 C; 254 G; 225 T; 0 U; 0 Other;

  Query Match             6.8%;  Score 63;  DB 13;  Length 1015;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-21;
  Matches   63;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         22 GTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACC 81
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 GTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACC 147

Qy         82 TGC 84
              |||
Db        148 TGC 150


RESULT 61
AAD15204
ID   AAD15204 standard; DNA; 984 BP.
XX
AC   AAD15204;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p40 encoding DNA from clone B8-96.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p40; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .984
FT                   /*tag=  a
FT                   /product= "Modified p40 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .981
FT                   /*tag=  c
FT                   /product= "Mature modified p40 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08597.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 1; Page 136; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p40 protein encoding
CC   DNA
XX
SQ   Sequence 984 BP; 270 A; 249 C; 259 G; 206 T; 0 U; 0 Other;

  Query Match             6.6%;  Score 61;  DB 5;  Length 984;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-20;
  Matches   61;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        607 ACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTG 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        673 ACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTG 732

Qy        667 A 667
              |
Db        733 A 733


RESULT 62
AAD15205
ID   AAD15205 standard; DNA; 984 BP.
XX
AC   AAD15205;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p40 encoding DNA from clone B2-52.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p40; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .984
FT                   /*tag=  a
FT                   /product= "Modified p40 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .981
FT                   /*tag=  c
FT                   /product= "Mature modified p40 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08598.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 1; Page 136-137; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
```

```
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p40 protein encoding
CC   DNA
XX
SQ   Sequence 984 BP; 267 A; 246 C; 254 G; 217 T; 0 U; 0 Other;

  Query Match             6.5%;  Score 60;  DB 5;  Length 984;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-19;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAAC 657
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAAC 723


RESULT 63
AAD15208
ID   AAD15208 standard; DNA; 975 BP.
XX
AC   AAD15208;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p40 encoding DNA from clone A16-94.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p40; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .975
FT                   /*tag=  a
FT                   /product= "Modified p40 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .972
FT                   /*tag=  c
FT                   /product= "Mature modified p40 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08601.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 1; Page 137; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p40 protein encoding
CC   DNA
XX
SQ   Sequence 975 BP; 261 A; 250 C; 255 G; 209 T; 0 U; 0 Other;

  Query Match             5.8%;  Score 53;  DB 5;  Length 975;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-16;
  Matches   53;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        829 GTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTA 881
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 GTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTA 926


RESULT 64
AAD15206
ID   AAD15206 standard; DNA; 984 BP.
XX
AC   AAD15206;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p40 encoding DNA from clone B1-81.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p40; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .984
FT                   /*tag=  a
FT                   /product= "Modified p40 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .981
FT                   /*tag=  c
FT                   /product= "Mature modified p40 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08599.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 1; Page 137; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p40 protein encoding
CC   DNA
XX
```

```
SQ   Sequence 984 BP; 272 A; 254 C; 247 G; 211 T; 0 U; 0 Other;

  Query Match             5.3%;  Score 49;  DB 5;  Length 984;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-14;
  Matches   49;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        385 GATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAG 433
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAG 499


RESULT 65
AAQ04701
ID   AAQ04701 standard; DNA; 906 BP.
XX
AC   AAQ04701;
XX
DT   25-MAR-2003  (revised)
DT   11-OCT-1990  (first entry)
XX
DE   Sequence encoding natural killer cell stimulatory factor (NKSF).
XX
KW   Natural killer cell stimulatory factor; NKSF; cancer; leukopaenia;
KW   anaemia; radiation; bone marrow transplantation; ds.
XX
OS   Homo sapiens.
XX
PN   WO9005147-A.
XX
PD   17-MAY-1990.
XX
PF   10-NOV-1988;   88US-00269945.
XX
PR   10-NOV-1988;   88US-00269945.
PR   07-FEB-1989;   89US-00307817.
XX
PA   (GEMY ) GENETICS INST INC.
PA   (WIST-) WISTAR INST.
XX
PI   Trinchieri G,  Perussia B,  Kobayashi M,  Clark SC,  Wong GG;
XX
DR   WPI; 1990-178800/23.
DR   P-PSDB; AAR05171.
XX
PT   New natural killer cell stimulatory factor - useful for treating cancer
PT   and e.g. leukopenia, bacterial and viral infections, anaemia and B or T
PT   cell deficiencies.
XX
PS   Claim 16; Page 60; 69pp; English.
XX
CC   Natural killer cell stimulatory factor (NKSF) is useful in treating
CC   cancer and other disease states which respond to NK cell activity. Such
CC   states may arise from immune or haematopoietic-cell deficiency following
CC   a bone marrow translpantation, exposure to radiation and disease.
CC   (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
CC   correct PA field.)
XX
SQ   Sequence 906 BP; 244 A; 220 C; 238 G; 204 T; 0 U; 0 Other;

  Query Match             4.8%;  Score 44;  DB 2;  Length 906;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        693 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 736


RESULT 66
AAD15207
ID   AAD15207 standard; DNA; 969 BP.
XX
AC   AAD15207;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p40 encoding DNA from clone A3-48.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p40; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .969
FT                   /*tag=  a
FT                   /product= "Modified p40 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .966
FT                   /*tag=  c
FT                   /product= "Mature modified p40 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08599.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 1; Page 137; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p40 protein encoding
CC   DNA
XX
SQ   Sequence 969 BP; 263 A; 249 C; 251 G; 206 T; 0 U; 0 Other;

  Query Match             4.8%;  Score 44;  DB 5;  Length 969;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        649 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 692


RESULT 67
AAQ12149
ID   AAQ12149 standard; DNA; 979 BP.
XX
AC   AAQ12149;
XX
DT   10-SEP-1991  (first entry)
```

```
XX
DE   Cytotoxic lymphocyte maturation factor (40 kD subunit) gene.
XX
KW   Cytotoxic lymphocyte maturation factor; CLMF; probe; antitumour;
KW   monoclonal antibodies; T cell; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             41. .979
FT                   /*tag=  a
FT                   /product= "CLMF"
FT   sig_peptide     41. .106
FT                   /*tag=  b
FT                   /note= "hydrophobic signal peptide"
FT   mat_peptide     107. .979
FT                   /*tag=  c
XX
PN   EP433827-A.
XX
PD   26-JUN-1991.
XX
PF   09-DEC-1990;   90EP-00123670.
XX
PR   22-DEC-1989;   89US-00455708.
PR   09-MAY-1990;   90US-00520935.
PR   27-AUG-1990;   90US-00572284.
XX
PA   (HOFF ) HOFFMANN-LA ROCHE AG.
XX
PI   Chizzonite RA,  Gately MK,  Gubler UA,  Hulmes JD,  Pan YCE;
PI   Podlaski FJ,  Stern AS;
XX
DR   WPI; 1991-186715/26.
DR   P-PSDB; AAR12493.
XX
PT   New cytotoxic lymphocyte maturation factor - used as antitumour agent and
PT   monoclonal antibodies used in transplantation to block proliferation and
PT   activation of cytotoxic T cells.
XX
PS   Disclosure; Fig 25 (a-c); 90pp; English.
XX
CC   The natural CLMF protein is a 75 kD heterodimer comprising two
CC   polypeptide subunits, a 40 kD and a 35 kD subunit (AAQ12150). The
CC   subunits are bonded together via one or more disulfide bonds. The CLMF
CC   can interact with IL-2 to synergistically induce the cytolytic activity
CC   of Lymphokine Activated Killer (LAK) cells. It is also capable of
CC   stimulating T-cell growth. It can be used for the prepn. of LAK- and T-
CC   cell activator and antitumour compsns. and for stimulating Natural Killer
CC   (NK) cells
XX
SQ   Sequence 979 BP; 261 A; 245 C; 257 G; 216 T; 0 U; 0 Other;

  Query Match             4.8%;  Score 44;  DB 2;  Length 979;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        701 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 744


RESULT 68
AAT50759
ID   AAT50759 standard; cDNA; 984 BP.
XX
AC   AAT50759;
XX
DT   17-OCT-2003  (revised)
DT   24-SEP-1997  (first entry)
XX
DE   Sequence of ovine IL-12 40 kD sununit cDNA.
XX
KW   Cytokine; ovine; sheep; interleukin-5; interleukin-12; IL-5; IL-12;
KW   livestock; cow; stress; transport; vaccine adjuvant; veterinary; cancer;
KW   immunosuppression; allergy; reproductive system; growth; early maturity;
KW   antibody; diagnosis; immunopotentiator;
KW   early haematopoietic progenitor cell; cytotoxic cell; thymocyte;
KW   secretion; IgM; IgA; bacterial endotoxin; gamma-interferon; ss.
XX
OS   Ovis aries.
XX
PN   WO9700321-A1.
XX
PD   03-JAN-1997.
XX
PF   14-JUN-1996;   96WO-AU000360.
XX
PR   14-JUN-1995;   95AU-00003502.
PR   27-OCT-1995;   95AU-00006244.
XX
PA   (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
PI   Seow H,  Wood P;
XX
DR   WPI; 1997-077528/07.
DR   P-PSDB; AAW08483.
XX
PT   Nucleic acid encoding ovine interleukin-5 or -12 - used as vaccine
PT   adjuvants and to treat or prevent microbial infections in livestock.
XX
PS   Claim 10; Page 49-51; 78pp; English.
XX
CC   The sequences given in AAT50757-59 encode ovine interleukin-12 (IL-12) 35
CC   kD subunit (partial and full length sequence) and the 40 kD subunit.
CC   Ovine IL-5 or IL-12 are used to treat and/or prevent infections in
CC   livestock (esp. cows and sheep), particularly where the animals are
CC   stressed, e.g. during transport. IL-5 and IL-12 can also be used as
CC   adjuvants in vaccines for veterinary use (partic. weakly immunogenic
CC   subunit or synthetic peptide vaccines). They may also be used to treat
CC   cancer, immunosuppression and allergy, to enhance/suppress the
CC   reproductive system and to promote growth or early maturity. Optionally
CC   interleukin can be delivered from constructs or delivery cells and
CC   antibodies are useful in enzyme immunoassays for rapid diagnosis of
CC   infection. The interleukins are immunopotentiators, especially IL-5
CC   promotes growth of early haematopoietic progenitor cells and generation
CC   of cytotoxic cells from thymocytes, also it stimulates production and
CC   secretion of IgM and IgA (in synergism with bacterial endotoxin). IL-12
CC   induces production of gamma-interferon by, and proliferation of, T and NK
CC   cells and increases the (non-)specific cytolytic lymphocyte response. The
CC   genetic constructs can also be used for in vitro production of IL-5 or -
CC   12. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ   Sequence 984 BP; 273 A; 243 C; 253 G; 215 T; 0 U; 0 Other;

  Query Match             4.8%;  Score 44;  DB 2;  Length 984;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707


RESULT 69
ADG39430
ID   ADG39430 standard; DNA; 984 BP.
XX
AC   ADG39430;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human CLMF 40 kDa subunit DNA.
XX
KW   human; cytotoxic lymphocyte maturation factor; CLMF;
KW   activated T-cell stimulator; natural killer cell stimulator;
```

```
KW   immunoenhancer; antitumour; tumour; cancer; ds; gene.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             67. .984
FT                   /*tag=  a
FT                   /partial
FT                   /product= "CLMF 40 kDa subunit"
FT                   /note= "No start or stop codon given"
XX
PN   US2003204059-A1.
XX
PD   30-OCT-2003.
XX
PF   08-OCT-2002; 2002US-00267565.
XX
PR   22-DEC-1989;   89US-00455708.
PR   09-MAY-1990;   90US-00520935.
PR   27-AUG-1990;   90US-00572284.
PR   24-MAR-1992;   92US-00857023.
PR   02-MAR-1994;   94US-00205011.
PR   02-JUN-1995;   95US-00459151.
PR   22-SEP-1999;   99US-00401839.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CIE SA F.
XX
PI   Gately MK,  Gubler UA,  Hulmes JD,  Podlaski FJ,  Stern AS;
PI   Chizzonite RA,  Pan YE;
XX
DR   WPI; 2004-010534/01.
DR   P-PSDB; ADG39429.
XX
PT   Novel protein comprising cytotoxic lymphocyte maturation factor in
PT   substantially pure form or protein which exhibits cytotoxic lymphocyte
PT   maturation factor activity, useful as antitumor and immunoenhancing
PT   agent.
XX
PS   Claim 17; Page 28-29; 74pp; English.
XX
CC   The invention relates to a protein which comprises a cytotoxic lymphocyte
CC   maturation factor (CLMF). The protein is useful for stimulating activated
CC   T-cells which involves treating T-cells with the protein. The method
CC   further involves treating the activated T-cells with IL2 or its
CC   biologically active fragment. The protein is useful for stimulating
CC   natural killer cells which involves treating the natural killer cells
CC   with the protein. The protein has immunoenhancing and antitumour effects
CC   when used as single therapeutic agent in vivo. The present sequence is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 984 BP; 263 A; 243 C; 258 G; 220 T; 0 U; 0 Other;

  Query Match             4.8%;  Score 44;  DB 12;  Length 984;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 70
ADK98707
ID   ADK98707 standard; DNA; 985 BP.
XX
AC   ADK98707;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human interleukin-12 (IL-12) P40 subunit DNA.
XX
KW   human; recombinant interleukin-12; IL-12; P35 subunit; P40 subunit; ds.
XX
OS   Homo sapiens.
XX
PN   CN1408727-A.
XX
PD   09-APR-2003.
XX
PF   29-SEP-2001; 2001CN-00126923.
XX
PR   29-SEP-2001; 2001CN-00126923.
XX
PA   (ZHON-) ZHONGXIN GUOJIAN PHARM CO LTD SHANGHAI.
XX
PI   Wan G,  Li C;
XX
DR   WPI; 2003-664076/63.
XX
PT   Method for efficiently expressing recombinant human interleukin 12 in
PT   eukaryotic cell.
XX
PS   Example 2; SEQ ID NO 2; 14pp; Chinese.
XX
CC   The invention describes the process of producing human recombinant
CC   interleukin-12 (IL-12) includes: providing a nucleotide sequence
CC   corresponding to the P35 subunit with the first signal peptide and a
CC   nucleotide sequence corresponding to the P40 subunit; inserting the
CC   nucleotide sequences into an expression vector; converting the eukaryotic
CC   cell with the expression vector; and culturing the transfected eukaryotic
CC   cell in condition suitable for recombinant human IL-12 expression. The
CC   process balances the expression amount of both P35 and P40 subunits and
CC   thus raises the expression amount of IL-12 with bioactivity via raising
CC   the expression strength of P35 subunit. This sequence represents the
CC   human interleukin-12 (IL-12) P40 subunit polynucleotide.
XX
SQ   Sequence 985 BP; 264 A; 242 C; 258 G; 221 T; 0 U; 0 Other;

  Query Match             4.8%;  Score 44;  DB 10;  Length 985;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        659 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 702


RESULT 71
AAQ97484
ID   AAQ97484 standard; cDNA; 987 BP.
XX
AC   AAQ97484;
XX
DT   25-MAR-2003  (revised)
DT   22-DEC-1995  (first entry)
XX
DE   Human interleukin-12 40 kD subunit.
XX
KW   Interleukin-12; IL-12; cytokine; gamma-interferon; T cell;
KW   natural killer cell; graft vs. host disease; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .987
FT                   /*tag=  a
XX
PN   WO9519786-A1.
XX
PD   27-JUL-1995.
XX
PF   20-JAN-1995;   95WO-US000879.
XX
PR   21-JAN-1994;   94US-00186529.
XX
PA   (GEMY ) GENETICS INST INC.
```

PA (GEHO) GEN HOSPITAL CORP.
XX
PI Wolf SF, Sykes M;
XX
DR WPI; 1995-269273/35.
DR P-PSDB; AAR79186.
XX
PT Control of graft versus host disease using interleukin 12 - partic.
PT admin. at the time of bone marrow transplant.
XX
PS Disclosure; Page 21-22; 32pp; English.
XX
CC AAQ97484 and AAQ97485 are from human lymphoblast cell line RMPI 8866. IL-
CC 12 is a heterodimeric cytokine which was originally identified as a
CC factor which induces gamma-interferon from T cells and natural killer
CC cells as set forth in PCT/US91/06332, published April 2 1992, and
CC incorporated by reference. EP 433827, published June 26 1991, disclosed
CC IL-12 as a cytotoxin lymphocyte maturation factor. In the patent, IL-12
CC is defined as a heterodimeric glycoprotein comprised of two covalently
CC linked subunits having mol. wts of about 40 kD and 35 kD. The two
CC subunits may be disulfide-bonded. IL-12 is administered to prevent or
CC ameliorate GVHD. Dosage is 1 ng-0.1 mg (esp. 1.0 ng-1 microg)/kg daily
CC for 3 days, the first dose given 1 hr. after transplant. IL-12 can be
CC used as the native heterodimer or as subunits. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

Query Match 4.8%; Score 44; DB 2; Length 987;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
||||||||||||||||||||||||||||||||||||||||||||
Db 661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704

RESULT 72
AAV07273
ID AAV07273 standard; cDNA; 987 BP.
XX
AC AAV07273;
XX
DT 25-SEP-1998 (first entry)
XX
DE Human Interleukin-12 p40 gene.
XX
KW IL-12 subunit; expression construct; treatment; asthma;
KW microbial infection; viral infection; cancer; Human; Interleukin; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .987
FT /*tag= a
FT /product= "IL-12 p40"
XX
PN WO9817689-A2.
XX
PD 30-APR-1998.
XX
PF 10-OCT-1997; 97WO-US018779.
XX
PR 18-OCT-1996; 96US-0028676P.
XX
PA (GENE-) GENEMEDICINE INC.
XX
PI Nordstrom J, Freimark B, Deshpande D;
XX
DR WPI; 1998-261428/23.
DR P-PSDB; AAW51311.
XX
PT Constructs for expression of interleukin-12 sub-units - are used for
PT delivery of IL-12 sub-units for treating e.g. asthma, microbial or viral
PT infections and certain cancers.
XX
PS Claim 1; Page 34; 80pp; English.
XX
CC The IL-12 subunits AAV07273 and AAV07274 can be expressed using an
CC appropriate expression construct engineered into a plasmid. The plasmids
CC can provide for efficient expression of IL-12 subunits. The products can
CC be used for the treatment of asthma, microbial and viral infections and
CC certain cancers
XX
SQ Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

Query Match 4.8%; Score 44; DB 2; Length 987;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
||||||||||||||||||||||||||||||||||||||||||||
Db 661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704

RESULT 73
AAV07217
ID AAV07217 standard; DNA; 987 BP.
XX
AC AAV07217;
XX
DT 12-AUG-1998 (first entry)
XX
DE DNA encoding human interleukin-12 40kDa subunit.
XX
KW Interleukin-12; IL-12; graft-versus-host disease;
KW GVHD. bone marrow transplantation; graft-versus-leukemia; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .987
FT /*tag= a
FT /product= "Interleukin-12_40kDa_subunit"
XX
PN US5756085-A.
XX
PD 26-MAY-1998.
XX
PF 30-APR-1996; 96US-00640386.
XX
PR 21-JAN-1994; 94US-00186529.
XX
PA (GEMY) GENETICS INST INC.
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Sykes M, Wolf SF;
XX
DR WPI; 1998-321459/28.
DR P-PSDB; AAW51221.
XX
PT Therapy of graft-versus-host disease - by administration of interleukin-
PT 12 to maintain and/or promote graft-versus-leukaemia effects.
XX
PS Disclosure; Col 17-20; 20pp; English.
XX
CC The invention relates to a method for the treatment or prevention of
CC graft-versus-host disease (GVHD) which comprises the administration of
CC interleukin-12 (IL-12) at the time of bone-marrow transplantation to
CC maintain or promote graft-versus-leukaemia effects. Preferably, dosage is
CC 0.001-100 (preferably 1-100) mu g/kg for 3 days starting on the day of
CC the bone marrow transplant. IL-12 is administered daily until there is an
CC improvement in the condition. Administration is oral, cutaneous,
CC subcutaneous, intravenous or by inhalation preferably subcutaneous, or
CC intravenous. The present sequence encodes the human interleukin-12 40kDa
CC subunit

```
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

  Query Match             4.8%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 74
AAZ40404
ID   AAZ40404 standard; DNA; 987 BP.
XX
AC   AAZ40404;
XX
DT   15-FEB-2000  (first entry)
XX
DE   Human interleukin 12 p40 subunit wild type coding sequence.
XX
KW   Wild type; human; interferon-alpha; plasmid; cytomegalovirus; CMV;
KW   promoter; growth hormone; untranslated region; UTR; mammal; disease;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9947678-A2.
XX
PD   23-SEP-1999.
XX
PF   12-MAR-1999;   99WO-US005394.
XX
PR   19-MAR-1998;   98US-0078654P.
XX
PA   (GENE-) GENEMEDICINE INC.
XX
PI   Nordstrom J,  Pericle F,  Rolland A,  Ralston R;
XX
DR   WPI; 1999-562116/47.
DR   P-PSDB; AAY42487.
XX
PT   New plasmids containing an interferon-alpha coding sequence, used for the
PT   treatment of a mammalian condition or disease, particularly cancer.
XX
PS   Claim 11; Page 43-45; 137pp; English.
XX
CC   This sequence represents the wild type coding region for the human
CC   interleukin 12 p40 subunit. The invention relates to a novel plasmid
CC   comprising a cytomegalovirus (CMV) promoter transcriptionally linked with
CC   an interferon alpha (IFN-alpha) coding sequence, and a growth hormone 3'-
CC   untranslated region (UTR). The plasmids can be used for treating a
CC   mammalian condition or disease, particularly cancer
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

  Query Match             4.8%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 75
AAV83199
ID   AAV83199 standard; DNA; 987 BP.
XX
AC   AAV83199;
XX
DT   02-MAR-1999  (first entry)
XX
DE   Interleukin (IL)-12B cDNA.
XX
KW   Mouse; immunodeficient; pathogen; tumour; lymphocyte; antigen;
KW   immunomodulator; vector; vaccine; cancer; HIV; Leishmania; Mycobacterium;
KW   Listeria; Plasmodium; retrovirus; evaluation;
KW   human immunodeficiency virus; ds.
XX
OS   Homo sapiens.
XX
PN   WO9844788-A2.
XX
PD   15-OCT-1998.
XX
PF   09-APR-1998;   98WO-US006944.
XX
PR   09-APR-1997;   97US-00838702.
PR   01-MAY-1997;   97US-00848760.
PR   09-DEC-1997;   97US-0069163P.
XX
PA   (CHAN/) CHANG L.
XX
PI   Chang L;
XX
DR   WPI; 1999-024005/02.
XX
PT   Use of immunodeficient mice comprising human cells - particularly
PT   SCTD/beige mice comprising human immune cells for evaluating vaccines
PT   against cancers or human pathogens, e.g. HIV.
XX
PS   Example 10(c)(i); Page 110; 154pp; English.
XX
CC   Immunodeficient mice comprising human cells can be used for exposure to
CC   human pathogens and/or their components or human tumour cells and human
CC   peripheral blood lymphocytes. Also claimed is a vaccine comprising a cell
CC   modified to express an antigen and an immune-modulating protein, this is
CC   preferably an expression vector comprising a polynucleotide sequence that
CC   encodes the antigen and immune-modulating protein. Such vectors can be
CC   used to treat a subject having a tumour by transferring the expression
CC   vector into the tumour so that the antigen and the immune-modulator are
CC   expressed by at least the tumour. The methods can be used for producing
CC   and evaluating vaccines including cancer vaccines and vaccines directed
CC   against human pathogens, e.g. HIV, Leishmania, Mycobacterium, Listeria or
CC   Plasmodium. Two primers (AAV83197, AAV83198) were used to amplify the IL-
CC   12B for insertion into expression vectors of the invention
XX
SQ   Sequence 987 BP; 264 A; 245 C; 257 G; 221 T; 0 U; 0 Other;

  Query Match             4.8%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 76
AAD15210
ID   AAD15210 standard; DNA; 987 BP.
XX
AC   AAD15210;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Human cytokine p40 DNA.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p40; ds.
XX
OS   Homo sapiens.
XX
```

```
FH   Key             Location/Qualifiers
FT   CDS             1. .987
FT                   /*tag= a
FT                   /product= "p40 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag= b
FT   mat_peptide     67. .984
FT                   /*tag= c
FT                   /product= "Mature p40 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08603.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 5; Page 142; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is human p40 protein encoding DNA
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

  Query Match             4.8%;  Score 44;  DB 5;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 77
ACC47592
ID   ACC47592 standard; DNA; 987 BP.
XX
AC   ACC47592;
XX
DT   12-JUN-2003  (first entry)
XX
DE   Human interleukin 12 (hIL-12) P40 subunit gene.
XX
KW   Human; interleukin 12; hIL-12; baculovirus vector;
KW   recombinant production; AcNPV-hIL12;
KW   Autographa california nuclear polyhedrosis virus; tumour; cancer;
KW   infection; bacterial; viral; cytostatic; P40 subunit; gene; ds.
XX
OS   Homo sapiens.
XX
PN   CN1357622-A.
XX
PD   10-JUL-2002.
XX
PF   02-NOV-2001; 2001CN-00133631.
XX
PR   02-NOV-2001; 2001CN-00133631.
XX
PA   (UYWU-) UNIV WUHAN.
XX
PI   Meng X,  Xu J,  Yu Z;
XX
DR   WPI; 2002-741792/81.
XX
PT   Human interleukin-12 recombinant insect virus strain and its preparation.
XX
PS   Claim 5; Fig 7; 17pp; Chinese.
XX
CC   The invention relates to a recombinant baculovirus comprising DNA
CC   encoding human interleukin 12 (hIL-12) and methods for its preparation.
CC   The recombinant baculovirus strain is designated Autographa california
CC   nuclear polyhedrosis virus AcNPV-hIL12 (CCTCC No. 2 V200108). This strain
CC   contains two human IL-12 subunit genes, the IL-12 P35 subunit gene
CC   (ACC47589) and the IL-12 P40 subunit gene (ACC47592) which are
CC   respectively under the control of the viral polyhedrin and P10 promoters.
CC   The baculovirus can be used in the recombinant production of human IL-12
CC   which is suitable for treating tumours and bacterial, viral and other
CC   infections. The present sequence represents the human IL-12 P40 subunit
CC   gene used in construction of the baculovirus vector of the invention
XX
SQ   Sequence 987 BP; 264 A; 245 C; 257 G; 221 T; 0 U; 0 Other;

  Query Match             4.8%;  Score 44;  DB 6;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 78
ADF77276
ID   ADF77276 standard; DNA; 987 BP.
XX
AC   ADF77276;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human IL-12 p40 subunit DNA.
XX
KW   ds; human; interferon alpha expression plasmid; tumour; IL-12.
XX
OS   Homo sapiens.
XX
PN   US2003181405-A1.
XX
PD   25-SEP-2003.
XX
PF   29-APR-2002; 2002US-00136837.
XX
PR   12-MAR-1999;   99US-00268135.
XX
PA   (NORD/) NORDSTROM J L.
PA   (PERI/) PERICLE F.
PA   (ROLL/) ROLLAND A.
PA   (RALS/) RALSTON R O.
XX
PI   Nordstrom JL,  Pericle F,  Rolland A,  Ralston RO;
XX
DR   WPI; 2004-020834/02.
XX
PT   A mammalian interferon alpha expression plasmid is useful in gene therapy
PT   to deliver interferon alpha to cells to modulate tumor activity in the
PT   treatment of cancer.
XX
```

```
PS   Disclosure; Page 14-15; 65pp; English.
XX
CC   The invention relates to a mammalian interferon alpha expression plasmid,
CC   comprising a promoter and a synthetic 5' intron transcriptionally linked
CC   with an interferon alpha coding sequence and a 3' untranslated region.
CC   The mammalian interferon alpha expression plasmid is useful for treating
CC   tumour growth. The present sequence is used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 987 BP; 264 A; 243 C; 258 G; 221 T; 0 U; 1 Other;

  Query Match             4.8%;  Score 44;  DB 12;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 79
ADO07653
ID   ADO07653 standard; DNA; 987 BP.
XX
AC   ADO07653;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Human interleukin-12 40kDa coding sequence.
XX
KW   cytostatic; virucide; anti-HIV; hepatotropic; neuroprotective;
KW   immunostimulant; expression cassette; viral vector; interleukin-12;
KW   co-stimulatory protein; cancer; infection; ds; gene; human.
XX
OS   Homo sapiens.
XX
PN   WO2004035799-A2.
XX
PD   29-APR-2004.
XX
PF   10-OCT-2003; 2003WO-EP011252.
XX
PR   11-OCT-2002; 2002DE-01048141.
XX
PA   (UYHA-) UNIV HAMBURG-EPPENDORF KLINIKUM.
XX
PI   Waehler R,  Schnieders F;
XX
DR   WPI; 2004-357221/33.
XX
PT   Viral vector that expresses single-chain interleukin-12 and costimulator,
PT   useful for treatment of tumors, viral infections, e.g. human
PT   immunodeficiency virus, and prion diseases.
XX
PS   Claim 4; Fig 19; 129pp; German.
XX
CC   The present invention relates to a viral vector that includes a nucleic
CC   acid encoding a single-chain interleukin-12 (IL-12) and a co-stimulatory
CC   protein. Viral vectors and virus particles derived from them are useful
CC   for treatment of tumours, infectious diseases (e.g. HIV, hepatitis A, B
CC   or C, cytomegalovirus or human papilloma virus), or prion diseases. The
CC   present sequence is a human interleukin-12 coding sequence used in the
CC   exemplification of the invention.
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

  Query Match             4.8%;  Score 44;  DB 12;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 80
ADS00006
ID   ADS00006 standard; DNA; 987 BP.
XX
AC   ADS00006;
XX
DT   16-DEC-2004  (first entry)
XX
DE   Human interleukin-23 (IL-23) p40 subunit DNA.
XX
KW   tumour; interleukin-23; IL-23; cytostatic; immunostimulant; cancer;
KW   p40 subunit; ds; gene.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .987
FT                   /*tag=  a
FT                   /product= "Human interleukin-23 (IL-23) p40 subunit
FT                   protein"
XX
PN   JP2004262797-A.
XX
PD   24-SEP-2004.
XX
PF   28-FEB-2003; 2003JP-00052999.
XX
PR   28-FEB-2003; 2003JP-00052999.
XX
PA   (CHIB-) CHIBA PREFECTURE.
XX
DR   WPI; 2004-665614/65.
DR   P-PSDB; ADS00010.
XX
PT   Novel anti-tumor agent comprising interleukin-23 gene, or cell transduced
PT   with interleukin-23 gene, as active ingredient, useful for activating
PT   anti-tumor immune response and treating tumor.
XX
PS   Disclosure; SEQ ID NO 2; 23pp; Japanese.
XX
CC   The invention relates to a novel anti-tumour agent comprising an
CC   interleukin-23 (IL-23) gene, or a cell transduced with an IL-23 gene, as
CC   an active ingredient. The molecules of the invention demonstrate
CC   cytostatic and immunostimulant activities and may be useful within an
CC   anti-tumour agent which activates an anti-tumour immune response. The
CC   agent is safe when used in cancer treatment, may be combined with other
CC   treatments and induces tumour-specific acquired immunity. The current
CC   sequence is that of the human interleukin-23 (IL-23) p40 subunit DNA of
CC   the invention.
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

  Query Match             4.8%;  Score 44;  DB 13;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 81
ADV42753
ID   ADV42753 standard; cDNA; 987 BP.
XX
AC   ADV42753;
XX
DT   10-MAR-2005  (first entry)
XX
DE   Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 381.
XX
```

```
KW   microarray; psychoneuroendocrinimmune; chronic fatigue;
KW   non-insulin dependent diabetes; allergy; immune disorder; inflammation;
KW   cancer; neoplasm; infection; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO2004108899-A2.
XX
PD   16-DEC-2004.
XX
PF   04-JUN-2004; 2004WO-US017686.
XX
PR   04-JUN-2003; 2003US-0475915P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Nicholson A,  Vernon SD;
XX
DR   WPI; 2005-031682/03.
XX
PT   New microarray comprising probes for genes involved in
PT   psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a
PT   condition associated with PNI activity, e.g., inflammatory or infectious
PT   diseases.
XX
PS   Claim 1; SEQ ID NO 381; 254pp; English.
XX
CC   The invention relates to a new microarray which comprises probes for
CC   genes involved in psychoneuroendocrinimmune (PNI) activity. The
CC   microarray is useful in diagnosing a condition associated with PNI
CC   activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
CC   cancer and infection. The present sequence represents a
CC   psychoneuroendocrinimmune gene expressed sequence tag. Note the
CC   specificatio mentions SEQ ID NO of up to 3314 but only sequences up to
CC   SEQ ID NO 1829 are provided.
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

  Query Match             4.8%;  Score 44;  DB 14;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 82
ADW97242
ID   ADW97242 standard; DNA; 987 BP.
XX
AC   ADW97242;
XX
DT   19-MAY-2005  (first entry)
XX
DE   Human p40 gene that inhibits IL-23 immune response Seq 1a.
XX
KW   immune inhibition; transplant rejection; immune disorder;
KW   autoimmune disease; allergy; immunosuppressive; antiallergic; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .987
FT                   /*tag=  a
FT                   /product= "P40 protein"
XX
PN   JP2005060313-A.
XX
PD   10-MAR-2005.
XX
PF   13-AUG-2003; 2003JP-00292937.
XX
PR   13-AUG-2003; 2003JP-00292937.
XX
PA   (CHIB-) CHIBA PREFECTURE.
XX
DR   WPI; 2005-200132/21.
DR   P-PSDB; ADW97244.
XX
PT   Pharmaceutical formulation for inhibiting immune response generated by
PT   interleukin-23 (IL-23) and treating e.g. autoimmune diseases, comprises
PT   p40 molecules or gene encoding p40 molecules.
XX
PS   Claim 3; SEQ ID NO 1; 12pp; Japanese.
XX
CC   This invention relates to a novel pharmaceutical formulation used for
CC   inhibiting the immune response generated by interleukin-23 (IL-23).
CC   Specifically, it refers to a formulation comprising the p40 protein or
CC   the gene encoding this protein thereof. The present invention describes
CC   the p40 gene contained in the form of a viral or non-viral vector that is
CC   capable of expressing and secreting the p40 protein. This vector can be
CC   introduced into a cell such that it can in turn inhibit the immune
CC   response generated by the production of IL-23. Accordingly, this method
CC   is useful for suppressing organ transplant rejection or treating
CC   immunological disorders associated with abnormal immune response with
CC   regard to IL-23. Furthermore, it can be used to treat autoimmune diseases
CC   and allergy. As such, compositions exhibit immunosuppressive and
CC   antiallergic activities. This polynucleotide sequence is the human p40
CC   gene of the invention.
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

  Query Match             4.8%;  Score 44;  DB 14;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 83
AEB48822
ID   AEB48822 standard; cDNA to mRNA; 987 BP.
XX
AC   AEB48822;
XX
DT   22-SEP-2005  (first entry)
XX
DE   Human interleukin-12 p40 domain coding sequence.
XX
KW   Interleukin-12; cytokine; lymphokine; cancer; tumor; glioblastoma;
KW   neoplasm; neurological disease; cytostatic; therapy; immunoconjugate;
KW   fusion protein; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .987
FT                   /*tag=  b
FT   sig_peptide     1. .66
FT                   /*tag=  a
FT   mat_peptide     67. .984
FT                   /*tag=  c
FT                   /product= "Mature interleukin-12 p40 subunit"
XX
PN   WO2005066348-A2.
XX
PD   21-JUL-2005.
XX
PF   05-JAN-2005; 2005WO-GB000007.
XX
PR   05-JAN-2004; 2004US-0534307P.
XX
PA   (EMDL-) EMD LEXIGEN RES CENT CORP.
```

```
PA   (ANTI-) ANTISOMA PLC.
XX
PI   Gillies S,  Lo K,  Lan Y,  Verma R;
XX
DR   WPI; 2005-512669/52.
XX
PT   Novel compound comprising target specific portion having monoclonal
PT   antibody having specificity for oncofetal fibronectin and effector
PT   portion having interleukin-12, useful for treating cancer e.g.
PT   glioblastoma.
XX
PS   Claim 36; SEQ ID NO 10; 83pp; English.
XX
CC   The invention provides a compound comprising a target specific portion
CC   and an effector portion, in which the target specific portion comprises
CC   or consists of a monoclonal antibody having specificity for oncofetal
CC   fibronectin, or its fragment or variant which retains the antigen binding
CC   specificity of the parent monoclonal antibody, and the effector portion
CC   comprises or consists of interleukin-12, or its functional fragment or
CC   variant. The monoclonal antibody binds to a region of oncofetal
CC   fibronectin other than the extra-domain B region. Preferably, the
CC   compound comprises a target specific portion that is capable of binding
CC   to an amino acid sequence present in fibronectin expressed in both fetal
CC   and normal adult tissue, especially the repeat 7 domain of fibronectin,
CC   and is preferably specific for human oncofetal fibronectin. The
CC   monoclonal antibody is preferably a BC1 antibody. The invention also
CC   provides nucleic acids encoding the compounds of the invention and
CC   methods of their use in the production of these compounds, as well as
CC   methods of using the compounds in medicine, especially for the treatment
CC   of cancer in a patient, where the patient is a mammal, preferably a
CC   human, and the patient has a solid tumor. The cancer is a glioblastoma
CC   (claimed) or ovarian, gastric, colorectal or pancreatic cancer. The
CC   present sequence is the coding sequence of the p40 domain of human
CC   interleukin-12. In a claimed compound, the effector portion consists of a
CC   single chain interleukin-12 comprising or consisting of an interleukin-12
CC   p40 domain conjugated to the interleukin-12 and p35 domain AEB48815 via a
CC   disulfide bond. A further claimed compound comprises the p40 sequence
CC   linked by disulfide bond to a fusion protein AEB48818 comprising the BC1
CC   heavy chain fused to human interleukin-12 p35.
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

  Query Match             4.8%;  Score 44;  DB 14;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 84
AAD18585
ID   AAD18585 standard; DNA; 1007 BP.
XX
AC   AAD18585;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human interleukin-12 (IL-12) p40 subunit DNA.
XX
KW   Human; interleukin-12; IL-12; p40 subunit; cytostatic; virucide; AIDS;
KW   Acquired Immune Deficiency Syndrome; immunisation; hepatitis; malaria;
KW   tuberculosis; vaccine; gene therapy; cancer; influenza; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             7. .993
FT                   /*tag=  a
FT                   /product= "Human IL-12p40 subunit protein"
XX
PN   WO200168802-A2.
XX
PD   20-SEP-2001.
XX
PF   15-MAR-2001; 2001WO-KR000408.
XX
PR   15-MAR-2000; 2000KR-00013133.
PR   13-MAR-2001; 2001KR-00012987.
XX
PA   (UYPO-) UNIV POHANG SCI & TECHNOLOGY.
PA   (PROG-) PROGEN CO LTD.
XX
PI   Sung YC,  Lee SH,  Ha SJ,  Song MK,  Chang J;
XX
DR   WPI; 2001-596904/67.
DR   P-PSDB; AAE11198.
XX
PT   Novel human or mouse interleukin (IL)-12p40 subunit mutant genes, that
PT   inhibit secretion of IL-12p40, but normally secrete IL-12p70, useful as
PT   adjuvant for DNA vaccination and gene therapy to AIDS, cancer, malaria.
XX
PS   Claim 1; Page 89-90; 103pp; English.
XX
CC   The invention relates to mutant interleukin (IL)-12p40 subunit genes
CC   which produces highly active human or mouse IL-12p40 sequence. IL-12p40
CC   DNA is useful for DNA immunisation or gene therapy for treating diseases
CC   such as cancer, AIDS, hepatitis C, hepatitis B or influenza, malaria or
CC   tuberculosis, as an therapeutic or prophylactic adjuvant. IL-12p40 DNA
CC   induces immune response by increasing the hydrolysis activity of
CC   cytotoxic T lymphocytes when IL-12p40 subunit gene is injected with the
CC   DNA vaccine, or increasing secretion of interferon (IFN)-gamma from T
CC   helper cells or CD8+ T cells when IL-12p40 subunit gene is injected with
CC   DNA vaccine. IL-12p40 DNA is useful in gene therapy and as a DNA vaccine.
CC   The present sequence is a DNA encoding human Interleukin (IL)-12p40
CC   subunit protein
XX
SQ   Sequence 1007 BP; 270 A; 247 C; 265 G; 225 T; 0 U; 0 Other;

  Query Match             4.8%;  Score 44;  DB 5;  Length 1007;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        667 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 710


RESULT 85
AAQ67879
ID   AAQ67879 standard; DNA; 1018 BP.
XX
AC   AAQ67879;
XX
DT   25-MAR-2003  (revised)
DT   23-MAR-1995  (first entry)
XX
DE   EPV 42 kD promoter/Human IL-12 p40 subunit expression cassette.
XX
KW   Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant;
KW   murine; interleukin-2; IL-2; pRW825; pmut-1; pBS-SK; pMM151; TK vector;
KW   plasmid; vaccinia; H6 promoter; amplify; primer; antigenic response;
KW   polymerase chain reaction; poxvirus; pSD542; immunological response;
KW   pathogen; human; interferon; IFN; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   promoter        1. .31
FT                   /*tag=  a
FT                   /note= "EPV 42 kD promoter"
FT   CDS             32. .1018
FT                   /*tag=  b
FT                   /product= "Human IL-12 p40"
XX
```

PN WO9416716-A1.
XX
PD 04-AUG-1994.
XX
PF 21-JAN-1994; 94WO-US000888.
XX
PR 21-JAN-1993; 93US-00007115.
PR 19-JAN-1994; 94US-00184009.
XX
PA (VIRO-) VIROGENETICS CORP.
XX
PI Paoletti E, Tartaglia J, Cox WI;
XX
DR WPI; 1994-263767/32.
XX
PT Attenuated recombinant virus used for cancer therapy - comprises DNA
PT encoding cytokine and/or tumour associated antigen.
XX
PS Example 27; Fig 33; 232pp; English.
XX
CC The sequences given in AAQ67879-80 are expression cassettes which contain
CC the p40 and p35 subunits of human interleukin-12 (IL-12) under the
CC control of the entomopox virus (EPV) promoter and the vaccinia E3L
CC promoter, respectively. These sequences were used in the construction of
CC an ALVAC-based recombinant virus containing the genes for the two
CC subunits of human IL-12. The p40 subunit was amplified using primers
CC JP202 and JP189 and placed under the control of the entomopox virus (EPV)
CC 42 kD promoter in plasmid PBSHIL12p40II. The p35 subunit was amplified
CC using primers JP186 and JP201 and placed under the control of the
CC vaccinia E3L promoter using primers JP218 and JP220. The expression
CC cassette was isolated and ligated with pBSSK+ generating plasmid
CC PBSHIL12p35II. The p35 and p40 expression cassettes were excised and
CC assembled in pBSSK+ to give PBSHIL12 in which the two expression
CC cassettes are orientated head-to-head relative to each other. The
CC combination casette containing the poxvirus promoted genes for both IL-12
CC subunits was excised from PBSHIL12 and cloned in to ALVAC C6 vector
CC plasmid pC6L to give pC6HIL12. Recombination between this donor plasmid
CC and ALVAC rescuing virus produced recombinant virus ALVAC+IL12, which
CC contains both the human IL-12 genes in the C6 locus. The resulting virus
CC may be used in a composition for inducing an antigenic or immunological
CC response, ie. for immunisation against pathogens. (Updated on 25-MAR-2003
CC to correct PN field.)
XX
SQ Sequence 1018 BP; 283 A; 245 C; 260 G; 230 T; 0 U; 0 Other;

Query Match 4.8%; Score 44; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
||||||||||||||||||||||||||||||||||||||||||||
Db 692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735

RESULT 86
AAZ08510
ID AAZ08510 standard; DNA; 1018 BP.
XX
AC AAZ08510;
XX
DT 19-OCT-1999 (first entry)
XX
DE EPV 42 kDa/human IL-12 P40 expression cassette.
XX
KW Attenuated recombinant virus; cytokine; tumour associated antigen;
KW NYVAC recombinant virus; ALVAC recombinant virus; gene therapy; rabies;
KW cancer; tumour necrosis factor; nuclear phosphoprotein; p53; IL-2; GMCSF;
KW interleukin; interferon; IFN-gamma; IL-4; melanoma associated antigen;
KW carcinoembryonic antigen; immunisation; antigenic; poxvirus; influenza;
KW immunological response; immunotherapy; vaccine; Newcastle Disease; ss.
XX
OS Synthetic.
OS pox virus.
OS Homo sapiens.
OS Unidentified.
XX
PN US5942235-A.
XX
PD 24-AUG-1999.
XX
PF 02-JUN-1995; 95US-00458356.
XX
PR 24-DEC-1981; 81US-00334456.
PR 08-DEC-1982; 82US-00446824.
PR 19-JUN-1984; 84US-00622135.
PR 27-AUG-1987; 87US-00090209.
PR 28-AUG-1987; 87US-00090711.
PR 20-OCT-1987; 87US-00110335.
PR 25-APR-1988; 88US-00186054.
PR 23-AUG-1988; 88US-00234390.
PR 14-JUN-1990; 90US-00537882.
PR 14-JUN-1990; 90US-00537890.
PR 16-DEC-1991; 91US-00805567.
PR 03-MAR-1992; 92US-00847977.
PR 06-MAR-1992; 92US-00847951.
PR 04-MAY-1992; 92US-00881995.
PR 22-JUL-1992; 92US-00918278.
PR 20-JAN-1993; 93US-00007115.
PR 19-JAN-1994; 94US-00184009.
PR 14-APR-1994; 94US-00228926.
PR 13-SEP-1994; 94US-00306259.
XX
PA (HEAL-) HEALTH RES INC.
XX
PI Paoletti E;
XX
DR WPI; 1999-493494/41.
XX
PT Recombinant poxviruses comprising exogenous DNA encoding antigenic
PT determinants useful in immunotherapy to immunize against cancers and
PT other diseases such as influenza, Newcastle Disease and rabies.
XX
PS Example 27; Fig 33; 163pp; English.
XX
CC The present invention describes a recombinant poxvirus (I), comprising
CC exogenous DNA encoding an antigenic determinant of a pathogen which is
CC then expressed in vivo in infected host cells after administration to a
CC patient and therefore induces an immunological response. (I) may be used
CC to vaccinate patients against a wide range of diseases and disorders
CC depending on the type of antigen encoded by the exogenous DNA. (I) may be
CC used to vaccinate against diseases such as rabies, influenza and
CC Newcastle Disease. It is particularly useful for immunising against
CC cancers. The poxvirus (I) also provides a means of manipulating
CC lymphocytes and tumour cells for use in cell-based immunotherapeutic
CC modalities for cancer. (I) also have enhanced safety compared to
CC unattenuated viruses (attenuation reduces the virulence of the viruses)
CC and known recombinant poxvirus vaccines. This increased level of safety
CC reduces the possibility of a 'runaway' infection in the host and reduces
CC the chance of transmission from vaccinated to unvaccinated individuals
CC and contamination of the environment. The present sequence represents a
CC EPV 42 kDa/human IL-12 P40 expression cassette used in the
CC exemplification of the present invention
XX
SQ Sequence 1018 BP; 283 A; 245 C; 260 G; 230 T; 0 U; 0 Other;

Query Match 4.8%; Score 44; DB 2; Length 1018;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
||||||||||||||||||||||||||||||||||||||||||||
Db 692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735

RESULT 87
ADR21886

```
ID   ADR21886 standard; DNA; 1018 BP.
XX
AC   ADR21886;
XX
DT   04-NOV-2004  (first entry)
XX
DE   EPV 42kDa/human IL-12 expression cassette.
XX
KW   Cytostatic; Vaccine; recombinant poxvirus; nonessential region;
KW   attenuated avipox Virus; carcinoembryonic antigen; B7 protein;
KW   cancer therapy; ds; human; IL-12; EPV 42kDa; expression cassette.
XX
OS   Heliothis armigera entomopoxvirus.
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US6780407-B1.
XX
PD   24-AUG-2004.
XX
PF   15-SEP-2000; 2000US-00663667.
XX
PR   08-MAR-1989;   89US-00320471.
PR   14-FEB-1990;   90US-00478179.
PR   07-JAN-1991;   91US-00638080.
PR   07-MAR-1991;   91US-00666056.
PR   11-JUN-1991;   91US-00713967.
PR   16-DEC-1991;   91US-00805567.
PR   03-MAR-1992;   92US-00847977.
PR   06-MAR-1992;   92US-00847951.
PR   21-JAN-1993;   93US-00007115.
PR   19-JAN-1994;   94US-00184009.
PR   30-AUG-1995;   95US-00521016.
XX
PA   (AVET ) AVENTIS PASTEUR.
XX
PI   Paoletti E,  Tartaglia J,  Cox WI;
XX
DR   WPI; 2004-601998/58.
XX
PT   New recombinant poxvirus which is an attenuated avipox Virus that
PT   expresses an exogenous DNA encoding carcinoembryonic antigen and an
PT   exogenous DNA encoding B7 protein, useful for cancer therapy.
XX
PS   Example 27; SEQ ID NO 194; 181pp; English.
XX
CC   The invention describes a recombinant poxvirus containing exogenous DNA
CC   in a nonessential region of the poxvirus, where the poxvirus is an
CC   attenuated avipox Virus that expresses an exogenous DNA encoding
CC   carcinoembryonic antigen and an exogenous DNA encoding B7 protein. Also
CC   described are: a composition comprising a poxvirus above in admixture
CC   with a carrier; and expressing carcinoembryonic antigen and B7 protein in
CC   vivo comprising administering to a mammal the composition above.
CC   Disclosed are: making recombinant poxvirus defined above; recombinant
CC   poxvirus vaccine having an increased level of safety compared to known
CC   recombinant poxvirus vaccines; and a modified vector for expressing a
CC   gene product in a host. The recombinant poxvirus is useful for providing
CC   a recombinant poxvirus vaccine having an increased level of safety
CC   compared to known recombinant poxvirus vaccines. The recombinant poxvirus
CC   is useful for cancer therapy. This sequence represents a human IL-12
CC   expression cassette used in the creation of NYVAC rescue virus and
CC   canarypox virus vector ALVAC comprising the human IL-12 gene.
XX
SQ   Sequence 1018 BP; 283 A; 245 C; 260 G; 230 T; 0 U; 0 Other;

  Query Match             4.8%;  Score 44;  DB 13;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735
```

```
RESULT 88
AAA70709
ID   AAA70709 standard; DNA; 1019 BP.
XX
AC   AAA70709;
XX
DT   15-DEC-2000  (first entry)
XX
DE   Bovine interleukin-12 p40 subunit gene.
XX
KW   Antiinfective; bovine; interleukin 12; IL12; heterodimer; infection; ss.
XX
OS   Bos taurus.
XX
FH   Key             Location/Qualifiers
FT   CDS             12. .995
FT                   /*tag=  a
FT                   /product= "IL-12 p40 subunit"
XX
PN   JP2000157274-A.
XX
PD   13-JUN-2000.
XX
PF   20-NOV-1998;   98JP-00331052.
XX
PR   20-NOV-1998;   98JP-00331052.
XX
PA   (DAUC ) DAIICHI PHARM CO LTD.
XX
DR   WPI; 2000-468201/41.
DR   P-PSDB; AAB15391.
XX
PT   Preparation of bovine interleukin 12 comprising using a vector containing
PT   the gene encoding it, useful for the prevention and treatment of chronic
PT   and opportunistic infections.
XX
PS   Example 1; Page 8-9; 11pp; Japanese.
XX
CC   The invention relates to a method for the preparation of bovine
CC   interleukin 12 (BoIL12). BoIL12 consists of a heterodimer of p35 and p40
CC   subunits. BoIL12 is produced by introducing into a host cell, recombinant
CC   vectors containing genes encoding the p35 and p40 subunits. This sequence
CC   represents the coding region for the bovine IL12 p40 subunit. Interleukin
CC   12 is used for the prevention and treatment of chronic infections and
CC   opportunistic infections
XX
SQ   Sequence 1019 BP; 273 A; 248 C; 271 G; 227 T; 0 U; 0 Other;

  Query Match             4.8%;  Score 44;  DB 3;  Length 1019;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        675 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 718


RESULT 89
ADP88402
ID   ADP88402 standard; cDNA; 1029 BP.
XX
AC   ADP88402;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human interleukin-12 beta chain coding sequence.
XX
KW   antiinflammatory; antiasthmatic; antiallergic; immunosuppressive;
KW   antibacterial; protozoacide; gene therapy; expression vector;
KW   interleukin; ecdysone-inducible promoter; ss; gene; interleukin-12;
KW   human.
XX
```

OS Homo sapiens.
XX
PN WO2004052929-A2.
XX
PD 24-JUN-2004.
XX
PF 08-DEC-2003; 2003WO-IB006404.
XX
PR 06-DEC-2002; 2002GB-00028465.
XX
PA (UYBE-) UNIV QUEENS BELFAST.
XX
PI Vandenbroeck K, Alloza I;
XX
DR WPI; 2004-487887/46.
XX
PT New expression vector comprising DNA encoding a subunit of a dimeric form
PT of interleukin under transcriptional control of an ecdysone-inducible
PT promoter, useful in preparing a composition for treating e.g.,
PT inflammatory disease.
XX
PS Disclosure; Page 86-87; 87pp; English.
XX
CC The present invention relates to an expression vector comprising DNA
CC encoding a subunit of a dimeric form of interleukin under transcriptional
CC control of an ecdysone-inducible promoter. The expression vector is
CC useful in preparing a composition for treating a disease having a
CC pathogenesis which includes endogenous production of cytokine IL-12, IL-
CC 23 or IL-27, e.g., infectious diseases, bacterial, protozoal or virus-
CC induced inflammation, epithelial airway inflammation such as asthma,
CC allergic disease, or autoimmune disease such as multiple sclerosis or
CC inflammatory bowel disease. The present sequence is the coding sequence
CC of the human interleukin-12 beta chain used in the exemplification of the
CC invention.
XX
SQ Sequence 1029 BP; 275 A; 261 C; 267 G; 226 T; 0 U; 0 Other;

Query Match 4.8%; Score 44; DB 12; Length 1029;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
||||||||||||||||||||||||||||||||||||||||||||
Db 676 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 719

RESULT 90
AAF76880
ID AAF76880 standard; DNA; 1389 BP.
XX
AC AAF76880;
XX
DT 15-MAY-2001 (first entry)
XX
DE Human p40-IL-2 coding sequence.
XX
KW Human; p40-IL-2; interleukin-2; IL-2; antiviral; antibacterial;
KW antifungal; cytostatic; antiparasitic; vaccine; gene therapy;
KW fusion protein; protein complex; cytokine; immunoglobulin; cancer;
KW infection; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200110912-A1.
XX
PD 15-FEB-2001.
XX
PF 09-AUG-2000; 2000WO-US021715.
XX
PR 09-AUG-1999; 99US-0147924P.
XX
PA (LEXI-) LEXIGEN PHARM CORP.
XX
PI Gillies SD, Lo KM;
XX
DR WPI; 2001-191523/19.
XX
PT Novel multifunctional fusion protein or protein complexes useful for
PT treating cancer and viral infections, comprise two different cytokine
PT molecules and a targeting group.
XX
PS Example 1; Page 75-76; 90pp; English.
XX
CC The present sequence is given in a specification relating to
CC multifunctional fusion proteins and protein complexes comprising at least
CC two different cytokine molecules and a targeting group such as an
CC immunoglobulin. The fusion proteins and protein complexes are useful for
CC treating cancers, and bacterial, viral, fungal and parasitic infections.
CC They are also useful in gene therapy and as vaccines to prevent or treat
CC various diseases
XX
SQ Sequence 1389 BP; 413 A; 325 C; 327 G; 324 T; 0 U; 0 Other;

Query Match 4.8%; Score 44; DB 4; Length 1389;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
||||||||||||||||||||||||||||||||||||||||||||
Db 661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704

RESULT 91
AAT77849
ID AAT77849 standard; DNA; 1397 BP.
XX
AC AAT77849;
XX
DT 25-MAR-2003 (revised)
DT 18-MAR-1998 (first entry)
XX
DE 40 kDa subunit of human cytotoxic lymphocyte maturation factor DNA.
XX
KW Cytotoxic lymphocyte maturation factor; CLMF; 40 kDa subunit;
KW interleukin-2; T-cell growth; antibody; lymphokine activated killer cell;
KW CLMF bioactivity inhibition; affinity ligand; transplantation;
KW cytotoxic T cell proliferation; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 41. .1027
FT /*tag= a
XX
PN EP790255-A2.
XX
PD 20-AUG-1997.
XX
PF 09-DEC-1990; 97EP-00104656.
XX
PR 22-DEC-1989; 89US-00455708.
PR 09-MAY-1990; 90US-00520935.
PR 27-AUG-1990; 90US-00572284.
PR 09-DEC-1990; 90EP-00123670.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Chizzonite RA, Gately MK, Gubler UA, Hulmes JD, Pan YE;
PI Podlanski FJ, Stern AS;
XX
DR WPI; 1997-404698/38.
DR P-PSDB; AAW24235.
XX
PT Antibodies to cytotoxic lymphocyte maturation factor protein - useful as
PT affinity ligands, assay reagents and medicaments.

```
XX
PS   Disclosure; Fig 25; 80pp; English.
XX
CC   The present DNA sequence encodes the 40 kDa subunit of cytotoxic
CC   lymphocyte maturation factor (CLMF) protein. The natural CLMF protein is
CC   a 75 kDa heterodimer, where the 2 subunits (see AAT77850 for the 35 kDa
CC   subunit) are bonded together via one or more disulphide bonds. CLMF
CC   protein is produced by a human B lyphoblastoid cell line. CLMF
CC   synergistically induces, in the presence of interleukin-2, the cytolytic
CC   activity of lymphokine activated killer cells. CLMF is also capable of
CC   stimulating T-cell growth. A novel antibody directed against an epitope
CC   of CLMF protein (see AAW24237 for epitope) is capable of neutralising
CC   and/or inhibiting CLMF bioactivity. This antibody may be used as an
CC   affinity ligand for purifying the CLMF protein. The antibody can also be
CC   used as an assay reagent for detecting the CLMF protein, and as a
CC   medicament for selectively blocking the proliferation and activation of
CC   cytotoxic T cells, e.g. in transplantation. (Updated on 25-MAR-2003 to
CC   correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 1397 BP; 390 A; 307 C; 333 G; 367 T; 0 U; 0 Other;

  Query Match             4.8%;  Score 44;  DB 2;  Length 1397;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        701 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 744


RESULT 92
AAT97969
ID   AAT97969 standard; DNA; 1397 BP.
XX
AC   AAT97969;
XX
DT   25-MAR-2003  (revised)
DT   18-MAR-1998  (first entry)
XX
DE   40 kDa subunit of human cytotoxic lymphocyte maturation factor DNA.
XX
KW   Cytotoxic lymphocyte maturation factor; CLMF; 40 kDa subunit;
KW   interleukin-2; T-cell growth; antibody; lymphokine activated killer cell;
KW   CLMF bioactivity inhibition; affinity ligand; transplantation;
KW   cytotoxic T cell proliferation; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             41. .1027
FT                   /*tag=  a
XX
PN   EP790308-A1.
XX
PD   20-AUG-1997.
XX
PF   09-DEC-1990;   97EP-00104682.
XX
PR   22-DEC-1989;   89US-00455708.
PR   09-MAY-1990;   90US-00520935.
PR   27-AUG-1990;   90US-00572284.
PR   09-DEC-1990;   90EP-00123670.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Chizzonite RA,  Gately MK,  Gubler UA,  Hulmes JD,  Pan YE;
PI   Podlanski FJ,  Stern AS;
XX
DR   WPI; 1997-404733/38.
DR   P-PSDB; AAW36939.
XX
PT   Sub-unit of cytotoxic lymphocyte maturation factor protein - useful for
PT   producing protein and as antitumour agent.
XX
PS   Disclosure; Fig 25; 83pp; English.
XX
CC   The present DNA sequence encodes a 40 kDa subunit of cytotoxic lymphocyte
CC   maturation factor (CLMF) protein. The natural CLMF protein is a 75 kDa
CC   heterodimer, where the 2 subunits (see AAT97970 for the 35 kDa subunit)
CC   are bonded together via one or more disulphide bonds. CLMF protein is
CC   produced by a human B lyphoblastoid cell line. CLMF synergistically
CC   induces, in the presence of interleukin-2, the cytolytic activity of
CC   lymphokine activated killer cells. CLMF is also capable of stimulating T-
CC   cell growth. The subunits may be used for preparing the CLMF protein and
CC   for preparing medicants for antitumour therapy. (Updated on 25-MAR-2003
CC   to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 1397 BP; 390 A; 307 C; 333 G; 367 T; 0 U; 0 Other;

  Query Match             4.8%;  Score 44;  DB 2;  Length 1397;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        701 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 744


RESULT 93
AAV00401
ID   AAV00401 standard; DNA; 1397 BP.
XX
AC   AAV00401;
XX
DT   25-MAR-2003  (revised)
DT   18-MAR-1998  (first entry)
XX
DE   40 kDa subunit of human cytotoxic lymphocyte maturation factor DNA.
XX
KW   Cytotoxic lymphocyte maturation factor; CLMF; 40 kDa subunit;
KW   interleukin-2; T-cell growth; antibody; lymphokine activated killer cell;
KW   CLMF bioactivity inhibition; affinity ligand; transplantation;
KW   cytotoxic T cell proliferation; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             41. .1027
FT                   /*tag=  a
XX
PN   EP790309-A1.
XX
PD   20-AUG-1997.
XX
PF   09-DEC-1990;   97EP-00104860.
XX
PR   22-DEC-1989;   89US-00455708.
PR   09-MAY-1990;   90US-00520935.
PR   27-AUG-1990;   90US-00572284.
PR   09-DEC-1990;   90EP-00123670.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Chizzonite RA,  Gately MK,  Gubler UA,  Hulmes J,  Pan YE;
PI   Podlanski FJ,  Stern AS,  Witte H;
XX
DR   WPI; 1997-404734/38.
DR   P-PSDB; AAW36941.
XX
PT   Sub-unit of cytotoxic lymphocyte maturation factor protein - useful for
PT   producing CLMF protein and as an antitumour agent.
XX
PS   Disclosure; Fig 25; 83pp; English.
XX
CC   The present DNA sequence encodes a novel 40 kDa subunit of cytotoxic
CC   lymphocyte maturation factor (CLMF) protein. The natural CLMF protein is
```

```
CC   a 75 kDa heterodimer, where the 2 subunits (see AAV00402 for the 35 kDa
CC   subunit) are bonded together via one or more disulphide bonds. CLMF
CC   protein is produced by a human B lyphoblastoid cell line. CLMF
CC   synergistically induces, in the presence of interleukin-2, the cytolytic
CC   activity of lymphokine activated killer cells. CLMF is also capable of
CC   stimulating T-cell growth. The subunits may be used for preparing the
CC   CLMF protein and for preparing medicants for antitumour therapy. (Updated
CC   on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC   PR field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 1397 BP; 390 A; 307 C; 333 G; 367 T; 0 U; 0 Other;

  Query Match             4.8%;  Score 44;  DB 2;  Length 1397;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        701 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 744


RESULT 94
AAV37767
ID   AAV37767 standard; cDNA; 1397 BP.
XX
AC   AAV37767;
XX
DT   17-SEP-1998  (first entry)
XX
DE   Cytotoxic lymphocyte maturation factor 40 kD subunit encoding cDNA.
XX
KW   Cytotoxic lymphocyte maturation factor; CLMF; cytokine; synergize;
KW   interleukin 2; IL-2; human; lymphoblastoid cell; detection; purifying;
KW   proliferation; cytotoxic T cell; transplantation; antibody; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             41. .1027
FT                   /*tag=  a
FT                   /product= "CLMF 40 kD subunit"
XX
PN   US5780597-A.
XX
PD   14-JUL-1998.
XX
PF   02-JUN-1995;   95US-00460061.
XX
PR   22-DEC-1989;   89US-00455708.
PR   09-MAY-1990;   90US-00520935.
PR   27-AUG-1990;   90US-00572284.
PR   24-MAR-1992;   92US-00857023.
PR   02-MAR-1994;   94US-00205011.
XX
PA   (HOFF ) HOFFMANN LA ROCHE INC.
XX
PI   Podlaski FJ,  Stern AS,  Gately MK,  Pan YE,  Hulmes JD;
PI   Chizzonite RA,  Gubler UA;
XX
DR   WPI; 1998-413150/35.
DR   P-PSDB; AAW58725.
XX
PT   New antibodies to cytotoxic lymphocyte maturation factor - useful for
PT   detecting, purifying, and/or blocking proliferation and activation of
PT   cytotoxic T cells, such as in transplantation(s).
XX
PS   Example 10; Fig 25; 71pp; English.
XX
CC   An isolated antibody has been developed which binds specifically to
CC   cytotoxic lymphocyte maturation factor (CLMF) and neutralises CLMF
CC   induced proliferation by more than 50% in a CLMF dependent T cell growth
CC   assay and/or inhibits binding of at least 60% of the factor to
CC   phytohaemagglutinin (PHA) activated peripheral blood lymphocyte (PBL)
CC   blasts as determined in a CLMF receptor binding assay. CLMF is a
CC   heterodimeric protein having a molecular weight band of 75 kD, determined
CC   by sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE)
CC   under non-reducing and/or reducing conditions, providing a first subunit
CC   having a molecular weight band of 40 kD and a second subunit having a
CC   molecular weight of 35 kD. The present sequence encodes the CLMF 40 kD
CC   subunit, from an example of the present invention. The antibody can be
CC   used for the purification and/or detection of CLMF. It is also used in
CC   therapeutic treatments which require selective blocking of proliferation
CC   and activation of cytotoxic T cells (CTLs) such as in transplantation
XX
SQ   Sequence 1397 BP; 390 A; 309 C; 333 G; 365 T; 0 U; 0 Other;

  Query Match             4.8%;  Score 44;  DB 2;  Length 1397;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        701 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 744


RESULT 95
ADG39387
ID   ADG39387 standard; DNA; 1397 BP.
XX
AC   ADG39387;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human cytotoxic lymphocyte maturation factor, CLMF, 40 kDa subunit DNA.
XX
KW   ds; gene; human; cytotoxic lymphocyte maturation factor; CLMF;
KW   activated T-cell stimulator; natural killer cell stimulator;
KW   immunoenhancer; antitumour; tumour; cancer.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             41. .1027
FT                   /*tag=  a
FT                   /product= "CLMF 40 kDa subunit"
XX
PN   US2003204059-A1.
XX
PD   30-OCT-2003.
XX
PF   08-OCT-2002; 2002US-00267565.
XX
PR   22-DEC-1989;   89US-00455708.
PR   09-MAY-1990;   90US-00520935.
PR   27-AUG-1990;   90US-00572284.
PR   24-MAR-1992;   92US-00857023.
PR   02-MAR-1994;   94US-00205011.
PR   02-JUN-1995;   95US-00459151.
PR   22-SEP-1999;   99US-00401839.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CIE SA F.
XX
PI   Gately MK,  Gubler UA,  Hulmes JD,  Podlaski FJ,  Stern AS;
PI   Chizzonite RA,  Pan YE;
XX
DR   WPI; 2004-010534/01.
DR   P-PSDB; ADG39388.
XX
PT   Novel protein comprising cytotoxic lymphocyte maturation factor in
PT   substantially pure form or protein which exhibits cytotoxic lymphocyte
PT   maturation factor activity, useful as antitumor and immunoenhancing
PT   agent.
XX
PS   Disclosure; Fig 25; 74pp; English.
XX
CC   The invention relates to a protein which comprises a cytotoxic lymphocyte
```

```
CC   maturation factor (CLMF). The protein is useful for stimulating activated
CC   T-cells which involves treating T-cells with the protein. The method
CC   further involves treating the activated T-cells with IL2 or its
CC   biologically active fragment. The protein is useful for stimulating
CC   natural killer cells which involves treating the natural killer cells
CC   with the protein. The protein has immunoenhancing and antitumour effects
CC   when used as single therapeutic agent in vivo. The present sequence is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 1397 BP; 390 A; 309 C; 333 G; 365 T; 0 U; 0 Other;

  Query Match             4.8%;  Score 44;  DB 12;  Length 1397;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
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Db        701 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 744


RESULT 96
ADO03758
ID   ADO03758 standard; cDNA; 1397 BP.
XX
AC   ADO03758;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human CLMF 40kDa subunit cDNA.
XX
KW   pharmaceutical composition; T cell growth factor assay; cytokine;
KW   cytokine lymphocyte maturation factor; CLMF; interleukin-12; IL-12;
KW   NC-37 B lymphoblastoid cell; T-cell growth stimulator; human; gene; ss;
KW   40 kDa subunit.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             41. .1027
FT                   /*tag=  b
FT                   /product= "CLMF 40 kDa subunit"
FT                   /note= "Cytotoxic Lymphocyte Maturation Factor"
FT   sig_peptide     41. .106
FT                   /*tag=  a
FT   mat_peptide     107. .1024
FT                   /*tag=  c
FT                   /note= "Mature CLMF 40 kDa subunit"
XX
PN   US6683046-B1.
XX
PD   27-JAN-2004.
XX
PF   02-JUN-1995;   95US-00459151.
XX
PR   22-DEC-1989;   89US-00455708.
PR   09-MAY-1990;   90US-00520935.
PR   27-AUG-1990;   90US-00572284.
PR   24-MAR-1992;   92US-00857023.
PR   02-MAR-1994;   94US-00205011.
XX
PA   (HOFF ) HOFFMANN LA ROCHE INC.
XX
PI   Gately MK,  Gubler UA,  Hulmes JD,  Podlaski FJ,  Stern AS;
PI   Chizzonite RA,  Pan YE;
XX
DR   WPI; 2004-118577/12.
DR   P-PSDB; ADO03759, ADO03795.
XX
PT   Pharmaceutical composition useful for activating T cell growth factors in
PT   assays comprises heterodimeric protein comprising first and second
PT   subunits and carrier.
XX
PS   Disclosure; Fig 25; 72pp; English.
XX
CC   The invention describes a pharmaceutical composition active in a T cell
CC   growth factor assay. The pharmaceutical composition comprises a
CC   heterodimeric protein having a molecular weight of 75 kDa as determined
CC   by Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE)
CC   under non-reducing conditions, and under reducing conditions, providing a
CC   first subunit having a molecular weight of 40 kDa as determined by (SDS-
CC   PAGE), and having a fully defined sequence of 306 amino acids as given in
CC   the specification, and second subunit having a molecular weight of 35 kDa
CC   as determined by (SDS-PAGE). Also described are: a novel cytokine protein
CC   called Cytokine lymphocyte maturation factor (CLMF) or interleukin-12 (IL
CC   -12) synthesised by mammalian cells, particularly human NC-37 B
CC   lymphoblastoid cells, and capable of stimulating T-cell growth; and
CC   monoclonal antibodies directed against (CLMF). (I) is useful as a
CC   pharmaceutical composition which is active in a T cell growth factor
CC   assay. This sequence encodes human cytotoxic lymphocyte maturation factor
CC   (CLMF) 40 kDa subunit.
XX
SQ   Sequence 1397 BP; 390 A; 309 C; 333 G; 365 T; 0 U; 0 Other;

  Query Match             4.8%;  Score 44;  DB 12;  Length 1397;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        701 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 744


RESULT 97
AAZ40021
ID   AAZ40021 standard; DNA; 1399 BP.
XX
AC   AAZ40021;
XX
DT   14-FEB-2000  (first entry)
XX
DE   Human p40 coding sequence.
XX
KW   Interleukin-12; IL-12; fusion protein; IL-12 p35 subunit; B7 protein;
KW   IL-12 p40 subunit; gene therapy; tumour; leukaemia; ss.
XX
OS   Homo sapiens.
XX
PN   US5994104-A.
XX
PD   30-NOV-1999.
XX
PF   08-NOV-1996;   96US-00751767.
XX
PR   08-NOV-1996;   96US-00751767.
XX
PA   (UNLO ) ROYAL FREE HOSPITAL SCHOOL MED.
XX
PI   Anderson RJ,  Prentice HG,  Macdonald ID;
XX
DR   WPI; 2000-038261/03.
DR   P-PSDB; AAY54919.
XX
PT   Nucleic acid constructs encoding interleukin-12 fusion proteins useful
PT   for treating leukemia and other cancers.
XX
PS   Example; Fig 9; 73pp; English.
XX
CC   This sequence encodes the human p40 protein sequence. The invention
CC   relates to an isolated nucleic acid construct (I) comprising a region
CC   encoding an interleukin-12 (IL-12) fusion protein (comprising an IL-12
CC   p35 subunit, an IL-12 p40 subunit and a linker peptide (joining the
CC   subunits)) and a region encoding a B7 protein. (I) may be used to produce
CC   IL-12 fusion proteins according to standard recombinant DNA
CC   methodologies. The fusion proteins may be produced either in vitro in a
CC   fermentation culture or in vivo as part of a gene therapy protocol (in
CC   this case (I) is used to transform a patients cells, which then secrete
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CC   the functional polypeptide to supplement the patients own production of
CC   IL-12 or to rectify mutations which lead to the expression of inactive
CC   polypeptides). The fusion proteins produced in this way may be used to
CC   treat any disease which responds to IL-12 such as tumours (both solid and
CC   dispersed of the kidney, breast, colon, ovarian and cervical tumours and
CC   melanomas) and in particular, tumours of the blood such as leukaemia.
CC   Alternatively, the polypeptides may be used as antigens in the production
CC   of antibodies to IL-12 and to assay for agonists and antagonists of its
CC   activity. The antibodies and antagonists may be used to inhibit the
CC   activity of IL-12. (I) may also be used diagnostically as a probe which
CC   hybridizes to sequences encoding IL-12 and the antibodies may be used to
CC   detect the presence of IL-12 polypeptides in samples. They may be used
CC   diagnostically to quantitate the expression of the polypeptide by
CC   patients and hence which subjects may be in need of restorative therapy
XX
SQ   Sequence 1399 BP; 390 A; 310 C; 333 G; 366 T; 0 U; 0 Other;

  Query Match             4.8%;  Score 44;  DB 3;  Length 1399;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
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Db        703 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 746


RESULT 98
ADY86632
ID   ADY86632 standard; DNA; 1399 BP.
XX
AC   ADY86632;
XX
DT   02-JUN-2005  (first entry)
XX
DE   Human interleukin-12 40 kDa (IL-12 p40) subunit gene.
XX
KW   Gene expression; screening; multiple sclerosis; neuroprotective;
KW   immune disorder; neurological disease; DNA microarray; gene; ds;
KW   interleukin-12; lymphokine; cytokine.
XX
OS   Homo sapiens.
XX
PN   US2005064483-A1.
XX
PD   24-MAR-2005.
XX
PF   30-AUG-2004; 2004US-00929182.
XX
PR   28-AUG-2003; 2003US-0498731P.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   Zang JZ,  Hong J;
XX
DR   WPI; 2005-252668/26.
DR   GENBANK; M65272.
XX
PT   Monitoring multiple sclerosis patient taking beta-interferon or
PT   glatiramer acetate to predict treatment response by determining
PT   expression profile of inflammatory nucleic acids using RNA of patient and
PT   comparing to control.
XX
PS   Claim 1; SEQ ID NO 22; 73pp; English.
XX
CC   The present invention relates to gene expression profiling technology to
CC   quantatively measure the expression profiles of genes selected based on
CC   their role in inflammation and their susceptibility to regulation by
CC   current multiple sclerosis (MS) treatment agents by isolating RNA from
CC   peripheral blood mononuclear cells (PBMC) of patient. The invention is
CC   particularly useful for monitoring a multiple sclerosis patient taking
CC   interferon-beta (IFN-beta) or glatiramer acetate (GA) in order to predict
CC   treatment response. The present sequence is human interleukin-12 40 kDa
CC   (IL-12 p40) subunit gene. This gene is used to illustrate the evaluation
CC   of PBMC responses to in Vitro treatment with IFN-beta or GA agents by
CC   gene expression profiling technology.
XX
SQ   Sequence 1399 BP; 390 A; 310 C; 333 G; 366 T; 0 U; 0 Other;

  Query Match             4.8%;  Score 44;  DB 14;  Length 1399;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        703 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 746


RESULT 99
ADQ14472
ID   ADQ14472 standard; DNA; 1580 BP.
XX
AC   ADQ14472;
XX
DT   07-OCT-2004  (first entry)
XX
DE   DNA encoding human hyperkine protein.
XX
KW   Wound healing; agonist; antagonist; interleukin-23; IL-23; vulnerary;
KW   cytokine; human; hyperkine; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             7. .1572
FT                   /*tag=  a
FT                   /product= "Human hyperkine protein"
XX
PN   WO2004058178-A2.
XX
PD   15-JUL-2004.
XX
PF   18-DEC-2003; 2003WO-US040937.
XX
PR   23-DEC-2002; 2002US-0436274P.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Bowman EP,  Chen S,  Cua DJ;
XX
DR   WPI; 2004-525781/50.
DR   P-PSDB; ADQ14473.
XX
PT   Treating inflammatory skin disorders or improving wound healing comprises
PT   administering to a subject an agonist or antagonist of Interleukin-23.
XX
PS   Example; SEQ ID NO 7; 52pp; English.
XX
CC   The invention relates to a novel method for treating or improving wound
CC   healing. The method comprises administering to a subject an agonist or
CC   antagonist of interleukin (IL)-23. The invention further comprises: an
CC   agonist of IL-23 derived from the binding site of an antibody that
CC   specifically binds to an IL-23 receptor; and a kit comprising the agonist
CC   and a compartment or instructions for use or disposal. The interleukin-23
CC   agents have vulnerary activity. The method is useful for treating or
CC   improving wound healing. This polynucleotide sequence represents the
CC   nucleic acid encoding a hyperkine protein used in the wound healing
CC   method of the invention.
XX
SQ   Sequence 1580 BP; 399 A; 411 C; 426 G; 344 T; 0 U; 0 Other;

  Query Match             4.8%;  Score 44;  DB 12;  Length 1580;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
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```
Db        673 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 716


RESULT 100
AAA92406
ID   AAA92406 standard; cDNA; 2300 BP.
XX
AC   AAA92406;
XX
DT   15-JAN-2001  (first entry)
XX
DE   Human interleukin 2 encoding p35 and p40 proteins.
XX
KW   Human; interleukin 2; IL-2; p35; p40; immune response; tumour;
KW   infectious disease; bacteria; virus; parasite; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             19. .678
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FT                   /product= "p35"
FT   CDS             1304. .2290
FT                   /*tag=  b
FT                   /product= "p40"
XX
PN   CN1258740-A.
XX
PD   05-JUL-2000.
XX
PF   31-DEC-1998;   98CN-00126748.
XX
PR   31-DEC-1998;   98CN-00126748.
XX
PA   (HUAC-) HUACHEN BIOLOGICAL TECHNOLOGY INST SHANG.
XX
PI   Cao X,  Zhang W,  Ju D;
XX
DR   WPI; 2000-558956/52.
DR   P-PSDB; AAB23795, AAB23796.
XX
PT   Recombinant adenovirus expressing human interleukin-12 and its
PT   preparation and use.
XX
PS   Example 3; Fig 4; 27pp; Chinese.
XX
CC   The present invention describes a recombinant adenovirus and its
CC   preparation and use, as well as medicine composite containing the
CC   recombinant adenovirus. The recombinant adenovirus is used clinically,
CC   has the advantages of low cost, easy use and high efficiency and is
CC   especially suitable for immune treatment of tumour and infectious
CC   diseases caused by bacteria, virus and parasite. The present sequence
CC   represents human interleukin 2 (IL-2) cDNA which encodes the p35 and p40
CC   proteins, which is used in an example from the present invention
XX
SQ   Sequence 2300 BP; 598 A; 591 C; 571 G; 540 T; 0 U; 0 Other;

  Query Match             4.8%;  Score 44;  DB 3;  Length 2300;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db       1964 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 2007


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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	2	44	4.8	725	5	CD559454	CD559454 AGENCOURT
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c	4	44	4.8	736	5	CD559453	CD559453 AGENCOURT
c	5	44	4.8	762	5	CD559451	CD559451 AGENCOURT
c	6	44	4.8	766	5	CD559449	CD559449 AGENCOURT
c	7	44	4.8	772	5	CD559450	CD559450 AGENCOURT
c	8	44	4.8	785	5	CD559448	CD559448 AGENCOURT
	9	41	4.5	772	5	CD559604	CD559604 AGENCOURT
	10	39	4.2	724	5	CD559603	CD559603 AGENCOURT
	11	39	4.2	745	5	CD559602	CD559602 AGENCOURT
	12	39	4.2	747	5	CD559607	CD559607 AGENCOURT
c	13	39	4.2	754	5	CD559452	CD559452 AGENCOURT
	14	39	4.2	756	5	CK130264	CK130264 AGENCOURT
	15	39	4.2	1042	5	CD559606	CD559606 AGENCOURT
	16	33	3.6	252	10	DV799576	DV799576 est_t_tru
	17	30	3.3	1839	6	AK162981	AK162981 Mus muscu
	18	30	3.3	2908	6	AK155593	AK155593 Mus muscu
	19	29	3.1	346	4	BY164658	BY164658 BY164658
	20	29	3.1	355	4	BY221814	BY221814 BY221814
	21	29	3.1	375	4	BY222535	BY222535 BY222535
	22	29	3.1	387	4	BY167742	BY167742 BY167742
	23	29	3.1	417	8	CO949904	CO949904 UMC-pd12c
	24	29	3.1	423	4	BY218447	BY218447 BY218447
	25	29	3.1	432	4	BY154173	BY154173 BY154173
	26	29	3.1	475	7	BF704417	BF704417 MI-P-E6-a
c	27	29	3.1	569	11	AZ853726	AZ853726 2M0157M01
	28	29	3.1	649	5	CJ134671	CJ134671 CJ134671
	29	29	3.1	666	4	BY749553	BY749553 BY749553
	30	28	3.0	535	11	AZ441303	AZ441303 1M0232M24
c	31	27	2.9	668	14	AG079702	AG079702 Pan trogl
c	32	24	2.6	414	13	CW885638	CW885638 RPCI42_10
c	33	21	2.3	330	13	CW047416	CW047416 104_285_1
c	34	21	2.3	374	10	T99581	T99581 ye65d08.r1
c	35	21	2.3	508	8	CN071927	CN071927 1021022B0
c	36	21	2.3	509	5	CF059708	CF059708 QCS15g07.
c	37	21	2.3	509	5	CF060247	CF060247 QCS5b05.y
c	38	21	2.3	510	5	CF059885	CF059885 QCS18b04.
c	39	21	2.3	521	2	BI431328	BI431328 949071E08
c	40	21	2.3	523	1	AI491671	AI491671 486020E06
c	41	21	2.3	553	7	AW566435	AW566435 660074D12
	42	21	2.3	566	3	BQ294193	BQ294193 1091026G0
c	43	21	2.3	588	4	CA627255	CA627255 wl1n.pk15
	44	21	2.3	594	7	AW573354	AW573354 660074D12
	45	21	2.3	599	2	BI478972	BI478972 949071E08
c	46	21	2.3	632	4	CA293522	CA293522 SCSGLV100
c	47	21	2.3	633	9	DN207344	DN207344 MEST847_H
c	48	21	2.3	637	3	BQ294192	BQ294192 1091026G0
c	49	21	2.3	692	9	DN222336	DN222336 MEST1126_
c	50	21	2.3	693	9	DN220924	DN220924 MEST1104_
c	51	21	2.3	694	9	DN219584	DN219584 MEST1083_
c	52	21	2.3	716	10	DV622355	DV622355 IV-1091-4
c	53	21	2.3	724	6	AY112414	AY112414 Zea mays
c	54	21	2.3	743	12	CL163765	CL163765 104_357_1
	55	21	2.3	755	14	AG462380	AG462380 Mus muscu
c	56	21	2.3	762	12	CC698019	CC698019 OGWBY19TH
	57	21	2.3	803	12	CG122646	CG122646 PUIMH25TB
c	58	21	2.3	837	12	CG134486	CG134486 PUFSJ61TD
c	59	21	2.3	853	12	CC927699	CC927699 ZMMBBc053
c	60	21	2.3	895	7	BF241716	BF241716 601879850
c	61	21	2.3	983	12	CG033595	CG033595 PUKDR51TB
	62	21	2.3	987	12	BZ782656	BZ782656 PUFDX77TB
c	63	21	2.3	999	12	BZ782662	BZ782662 PUFDX77TD
	64	20	2.2	366	12	CE034167	CE034167 tigr-gss-
	65	20	2.2	376	9	DN901347	DN901347 naq18f07.
	66	20	2.2	454	11	BH772784	BH772784 4CTF CTSS
	67	20	2.2	460	3	BM849607	BM849607 K-EST0129
c	68	20	2.2	467	9	DN504486	DN504486 HL0100090
	69	20	2.2	479	2	BI983815	BI983815 fu08a02.x
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	76	20	2.2	526	3	BQ777940	BQ777940 il39a02.y
c	77	20	2.2	528	13	CW070565	CW070565 104_321_1
	78	20	2.2	535	5	CK902268	CK902268 il39a02.x
	79	20	2.2	545	14	AG826456	AG826456 Sus scrof
c	80	20	2.2	551	14	AG826409	AG826409 Sus scrof
c	81	20	2.2	555	8	CO854235	CO854235 LM_SH5_00
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	85	20	2.2	570	1	AI666909	AI666909 fd16d08.x
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	89	20	2.2	633	1	AL900775	AL900775 AL900775
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	91	20	2.2	649	13	CZ709509	CZ709509 OC__Ba003
	92	20	2.2	654	2	BM096034	BM096034 fv29g12.x

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	95	20	2.2	672	13	DU179885 109855349
c	96	20	2.2	676	14	AG826544 Sus scrof
c	97	20	2.2	681	12	CC008436 PUDHR12TD
c	98	20	2.2	690	11	AZ424475 1M0204A12
c	99	20	2.2	696	11	BZ240832 CH230-272
	100	20	2.2	698	2	BG740695 602631544
c	101	20	2.2	701	10	DT267303 JGI_CAAV1
	102	20	2.2	701	10	DT267304 JGI_CAAV1
c	103	20	2.2	719	10	DT283860 JGI_CAAV1
c	104	20	2.2	724	13	CZ313704 ZMMBF0012
	105	20	2.2	738	14	AG826488 Sus scrof
c	106	20	2.2	742	9	CX704941 gmrtDrNS0
	107	20	2.2	752	9	CX474004 JGI_XZG49
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	109	20	2.2	777	12	CG222535 OG0DT06TH
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	114	20	2.2	815	9	CX966008 JGI_CAAP1
	115	20	2.2	815	14	AG826576 Sus scrof
	116	20	2.2	819	12	CG433498 ZMMBBc004
c	117	20	2.2	826	14	AG825790 Sus scrof
	118	20	2.2	837	12	CG424739 ZMMBBc004
	119	20	2.2	843	14	AG825709 Sus scrof
	120	20	2.2	862	9	CX490517 JGI_XZG33
	121	20	2.2	866	4	BX719908 BX719908
	122	20	2.2	876	11	BZ274756 CH230-450
c	123	20	2.2	879	3	BU134895 603121826
	124	20	2.2	879	12	CG419488 ZMMBBc002
	125	20	2.2	881	8	CR579278 CR579278
	126	20	2.2	884	12	CG152443 PUFQD62TB
	127	20	2.2	885	9	CX414760 JGI_XZT55
	128	20	2.2	890	9	CX375663 JGI_XZT59
	129	20	2.2	893	4	CA792037 AGENCOURT
	130	20	2.2	893	12	CC969890 ZUAGO82TV
c	131	20	2.2	897	11	BZ169807 CH230-463
c	132	20	2.2	900	12	CC001138 PUEAP48TD
	133	20	2.2	905	7	BE533710 601232852
c	134	20	2.2	926	8	CX116780 EI106B21
	135	20	2.2	927	14	DX042542 KBrB042P0
	136	20	2.2	947	12	CG701262 ZMMBBc017
c	137	20	2.2	956	10	DW611860 CLJ265-F0
c	138	20	2.2	959	14	AG826402 Sus scrof
c	139	20	2.2	960	12	CG152445 PUFQD62TD
	140	20	2.2	965	13	CL304216 ZMMBBb009
c	141	20	2.2	985	10	DW657589 CLJ397-G1
c	142	20	2.2	998	14	DU878040 279669 To
c	143	20	2.2	1003	12	CG222548 OG0DT06TV
	144	20	2.2	1048	12	CG698770 ZMMBBc011
	145	20	2.2	1049	10	DW611861 CLJ265-F0
	146	20	2.2	1082	12	CC175278 ZMMBBc029
c	147	20	2.2	1204	9	DN661975 CFW06-B07
	148	20	2.2	1595	2	BG256021 602367310
c	149	19	2.1	224	12	BZ779302 ih87h11.g
	150	19	2.1	234	4	CD131385 MG1-0012T
c	151	19	2.1	236	8	CO314283 EK235626.
	152	19	2.1	293	3	BP949628 BP949628
c	153	19	2.1	300	1	AA714194 nw05h05.s
c	154	19	2.1	328	14	CNS00P65 AL084107 Arabidops
c	155	19	2.1	346	2	BJ694940 BJ694940
c	156	19	2.1	368	3	BU661053 cl67c12.z
	157	19	2.1	369	8	CO362672 RTK1_5_D0
c	158	19	2.1	373	5	CK045056 51163rsic
c	159	19	2.1	378	2	BI594826 As_tgz_44
	160	19	2.1	381	1	AL964966 AL964966
	161	19	2.1	382	8	CN921966 000409AEL
c	162	19	2.1	384	4	BY282227 BY282227
c	163	19	2.1	394	7	AW042400 614028B11
	164	19	2.1	394	9	DR059212 RTNIT1_16
	165	19	2.1	413	9	DR177926 RTMNUT1_8
c	166	19	2.1	415	5	CF917109 CF917109 Bflor498.
	167	19	2.1	429	14	CR204657 Reverse s
c	168	19	2.1	434	4	CB793439 CB793439 AMGNNUC:S
c	169	19	2.1	434	4	CB793440 CB793440 AMGNNUC:S
	170	19	2.1	434	12	CE700465 tigr-gss-
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	172	19	2.1	444	9	CX646589 CX646589 COLD1_10_
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	174	19	2.1	493	8	CN619918 CN619918 TgESTzym9
	175	19	2.1	496	1	AI871624 AI871624 we28d11.x
c	176	19	2.1	505	11	AZ635629 AZ635629 1M0493D09
	177	19	2.1	510	10	DR446638 DR446638 AR1034E03
c	178	19	2.1	511	12	CG991849 CG991849 CH240_151
c	179	19	2.1	512	5	CK057894 CK057894 61316rsic
c	180	19	2.1	512	13	CL955283 CL955283 OsIRUA000
c	181	19	2.1	517	10	DR787178 DR787178 ZM_BFb000
	182	19	2.1	523	14	AG956728 AG956728 Drosophil
c	183	19	2.1	526	8	CO783019 CO783019 BL016D_D1
	184	19	2.1	530	13	CL259985 CL259985 ZMMBBb061
c	185	19	2.1	533	5	CI183750 CI183750
	186	19	2.1	534	5	CK737831 CK737831 TgESTzyj8
	187	19	2.1	535	2	BF922172 BF922172 MR4-NT014
	188	19	2.1	536	7	AW073130 AW073130 wy94a10.x
	189	19	2.1	537	7	BF394460 BF394460 UI-R-CA0-
	190	19	2.1	541	3	BP949994 BP949994 BP949994
	191	19	2.1	543	9	DA100433 DA100433 DA100433
	192	19	2.1	543	9	DA100435 DA100435 DA100435
c	193	19	2.1	543	14	CT107392 CT107392 Sus scrof
	194	19	2.1	551	4	BW536306 BW536306 BW536306
c	195	19	2.1	555	8	CO700056 CO700056 DG32-170e
c	196	19	2.1	562	2	BJ692987 BJ692987 BJ692987
	197	19	2.1	566	3	BQ906981 BQ906981 M023C03 O
	198	19	2.1	571	2	BJ524824 BJ524824 BJ524824
	199	19	2.1	573	9	DA674546 DA674546 DA674546
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ALIGNMENTS

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LOCUS       CE093997                700 bp    DNA     linear   GSS 24-SEP-2003
DEFINITION  tigr-gss-dog-17000359883851 Dog Library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION   CE093997
VERSION     CE093997.1  GI:35160844
KEYWORDS    GSS.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 700)
  AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
            Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
            Venter,J.C.
  TITLE     The dog genome: survey sequencing and comparative analysis
  JOURNAL   Science 301 (5641), 1898-1903 (2003)
   PUBMED   14512627
COMMENT     Contact: Kirkness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirknes@tigr.org
            Class: shotgun.
FEATURES             Location/Qualifiers
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                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /strain="Standard Poodle"
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                     /db_xref="taxon:9615"
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                     peripheral blood"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 3.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        531 CTGCCC 536
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Db        420 CTGCCC 425


RESULT 2
CD559454/c
LOCUS       CD559454                725 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14497089 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971868 5', mRNA sequence.
ACCESSION   CD559454
VERSION     CD559454.2  GI:38453478
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 725)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585522.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: g  column: 11
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            High quality sequence stop: 573.
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971868"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             4.8%;  Score 44;  DB 5;  Length 725;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        426 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 383


RESULT 3
CD559605
LOCUS       CD559605                735 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496534 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971870 5', mRNA sequence.
ACCESSION   CD559605
VERSION     CD559605.2  GI:38558937
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 735)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585673.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 01
            High quality sequence stop: 709.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971870"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
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a Note: this is a NIH_MGC Library."
ORIGIN

Query Match 4.8%; Score 44; DB 5; Length 735;
Best Local Similarity 100.0%; Pred. No. 5.1e-12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
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Db 677 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 720

RESULT 4
CD559453/c
LOCUS CD559453 736 bp mRNA linear EST 19-NOV-2003
DEFINITION AGENCOURT_14497154 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971869 5', mRNA sequence.
ACCESSION CD559453
VERSION CD559453.2 GI:38453475
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 736)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585521.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: g column: 12
High quality sequence stop: 683.
FEATURES Location/Qualifiers
source 1. .736
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971869"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."
ORIGIN

Query Match 4.8%; Score 44; DB 5; Length 736;
Best Local Similarity 100.0%; Pred. No. 5.1e-12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
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Db 401 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 358

RESULT 5
CD559451/c
LOCUS CD559451 762 bp mRNA linear EST 19-NOV-2003
DEFINITION AGENCOURT_14496580 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971871 5', mRNA sequence.
ACCESSION CD559451
VERSION CD559451.2 GI:38453471
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 762)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585519.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: h column: 02
High quality sequence start: 38
High quality sequence stop: 761.
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/organism="Homo sapiens"
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/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."
ORIGIN

Query Match 4.8%; Score 44; DB 5; Length 762;
Best Local Similarity 100.0%; Pred. No. 5.1e-12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        422 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 379


RESULT 6
CD559449/c
LOCUS       CD559449                766 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496649 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971873 5', mRNA sequence.
ACCESSION   CD559449
VERSION     CD559449.2  GI:38453467
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 766)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585517.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 04
            High quality sequence stop: 641.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971873"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
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                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             4.8%;  Score 44;  DB 5;  Length 766;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
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Db        414 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 371


RESULT 7
CD559450/c
LOCUS       CD559450                772 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496612 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971872 5', mRNA sequence.
ACCESSION   CD559450
VERSION     CD559450.2  GI:38453469
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 772)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585518.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 03
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FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
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                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             4.8%;  Score 44;  DB 5;  Length 772;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
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Db        425 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 382


RESULT 8
CD559448/c
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LOCUS       CD559448                785 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496712 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971874 5', mRNA sequence.
ACCESSION   CD559448
VERSION     CD559448.2  GI:38453466
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 785)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585516.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 05
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FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
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                     /clone="IMAGE:6971874"
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                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             4.8%;  Score 44;  DB 5;  Length 785;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
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Db        416 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 373


RESULT 9
CD559604
LOCUS       CD559604                772 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496598 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971872 5', mRNA sequence.
ACCESSION   CD559604
VERSION     CD559604.2  GI:38558934
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 772)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585672.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 03
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                     /clone="IMAGE:6971872"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             4.5%;  Score 41;  DB 5;  Length 772;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-10;
  Matches   41;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAA 638
              |||||||||||||||||||||||||||||||||||||||||
Db        698 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAA 738


RESULT 10
CD559603
LOCUS       CD559603                724 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496630 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971873 5', mRNA sequence.
ACCESSION   CD559603
VERSION     CD559603.2  GI:38558932
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
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```
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 724)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585671.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 04
            High quality sequence stop: 525.
FEATURES              Location/Qualifiers
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                      /clone_lib="NIH_MGC_195"
                      /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                      loxP-HindIII; Clones from this library have been
                      PCR-amplified using gene-specific primers to contain the
                      complete open reading frame (based on known gene sequences
                      available from NCBI's RefSeq). Template for PCR is cDNA
                      derived from either pooled cytoplasmic polyA RNA from 30
                      cells lines or pooled total RNA from 10 different tissues
                      (from BD Biosciences/Clontech and Washington University).
                      PCR products are directionally cloned into the loxP sites
                      of the pDNR-Dual vector. Library constructed by Dr.
                      Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                      Expression Laboratory, Research Technology Program, SAIC
                      Frederick, NCI-Frederick, Frederick, MD 21702). For
                      information on which gene each clone represents, please
                      visit our anonymous ftp site at
                      ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                      a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             4.2%;  Score 39;  DB 5;  Length 724;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-09;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        334 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 372
              |||||||||||||||||||||||||||||||||||||||
Db        413 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 451


RESULT 11
CD559602
LOCUS       CD559602                745 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496684 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971874 5', mRNA sequence.
ACCESSION   CD559602
VERSION     CD559602.2  GI:38558930
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 745)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585670.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 05
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            High quality sequence stop: 644.
FEATURES              Location/Qualifiers
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                      /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
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                      PCR-amplified using gene-specific primers to contain the
                      complete open reading frame (based on known gene sequences
                      available from NCBI's RefSeq). Template for PCR is cDNA
                      derived from either pooled cytoplasmic polyA RNA from 30
                      cells lines or pooled total RNA from 10 different tissues
                      (from BD Biosciences/Clontech and Washington University).
                      PCR products are directionally cloned into the loxP sites
                      of the pDNR-Dual vector. Library constructed by Dr.
                      Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                      Expression Laboratory, Research Technology Program, SAIC
                      Frederick, NCI-Frederick, Frederick, MD 21702). For
                      information on which gene each clone represents, please
                      visit our anonymous ftp site at
                      ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                      a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             4.2%;  Score 39;  DB 5;  Length 745;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-09;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        334 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 372
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Db        405 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 443


RESULT 12
CD559607
LOCUS       CD559607                747 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14497061 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971868 5', mRNA sequence.
ACCESSION   CD559607
VERSION     CD559607.2  GI:38558941
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 747)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
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  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585675.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: g  column: 11
            High quality sequence start: 14
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                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             4.2%;  Score 39;  DB 5;  Length 747;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-09;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        334 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 372
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Db        428 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 466


RESULT 13
CD559452/c
LOCUS       CD559452                754 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496548 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971870 5', mRNA sequence.
ACCESSION   CD559452
VERSION     CD559452.2  GI:38453473
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 754)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585520.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 01
            High quality sequence start: 130
            High quality sequence stop: 572.
FEATURES             Location/Qualifiers
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                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             4.2%;  Score 39;  DB 5;  Length 754;
  Best Local Similarity   100.0%;  Pred. No. 3e-09;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        334 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 372
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Db        682 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 644


RESULT 14
CK130264
LOCUS       CK130264                756 bp    mRNA    linear   EST 02-DEC-2003
DEFINITION  AGENCOURT_14496566 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971871 5', mRNA sequence.
ACCESSION   CK130264
VERSION     CK130264.1  GI:38622200
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 756)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
```

```
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 02
            High quality sequence start: 5
            High quality sequence stop: 731.
FEATURES              Location/Qualifiers
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                      /db_xref="taxon:9606"
                      /clone="IMAGE:6971871"
                      /tissue_type="mixed"
                      /lab_host="DH5A (T1 phage-resistant)"
                      /clone_lib="NIH_MGC_195"
                      /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                      loxP-HindIII; Clones from this library have been
                      PCR-amplified using gene-specific primers to contain the
                      complete open reading frame (based on known gene sequences
                      available from NCBI's RefSeq). Template for PCR is cDNA
                      derived from either pooled cytoplasmic polyA RNA from 30
                      cells lines or pooled total RNA from 10 different tissues
                      (from BD Biosciences/Clontech and Washington University).
                      PCR products are directionally cloned into the loxP sites
                      of the pDNR-Dual vector. Library constructed by Dr.
                      Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                      Expression Laboratory, Research Technology Program, SAIC
                      Frederick, NCI-Frederick, Frederick, MD 21702). For
                      information on which gene each clone represents, please
                      visit our anonymous ftp site at
                      ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                      a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             4.2%;  Score 39;  DB 5;  Length 756;
  Best Local Similarity   100.0%;  Pred. No. 3e-09;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        334 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 372
              |||||||||||||||||||||||||||||||||||||||
Db        433 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 471


RESULT 15
CD559606
LOCUS       CD559606                1042 bp    mRNA    linear   EST 11-JUN-2003
DEFINITION  AGENCOURT_14497125 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971869 5', mRNA sequence.
ACCESSION   CD559606
VERSION     CD559606.1  GI:31585674
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1042)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: g  column: 12
            High quality sequence stop: 386.
FEATURES              Location/Qualifiers
     source           1. .1042
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:6971869"
                      /tissue_type="mixed"
                      /lab_host="DH5A (T1 phage-resistant)"
                      /clone_lib="NIH_MGC_195"
                      /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                      loxP-HindIII; Clones from this library have been
                      PCR-amplified using gene-specific primers to contain the
                      complete open reading frame (based on known gene sequences
                      available from NCBI's RefSeq). Template for PCR is cDNA
                      derived from either pooled cytoplasmic polyA RNA from 30
                      cells lines or pooled total RNA from 10 different tissues
                      (from BD Biosciences/Clontech and Washington University).
                      PCR products are directionally cloned into the loxP sites
                      of the pDNR-Dual vector. Library constructed by Dr.
                      Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                      Expression Laboratory, Research Technology Program, SAIC
                      Frederick, NCI-Frederick, Frederick, MD 21702). For
                      information on which gene each clone represents, please
                      visit our anonymous ftp site at
                      ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                      a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             4.2%;  Score 39;  DB 5;  Length 1042;
  Best Local Similarity   100.0%;  Pred. No. 3e-09;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        334 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 372
              |||||||||||||||||||||||||||||||||||||||
Db        403 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 441


RESULT 16
DV799576
LOCUS       DV799576                252 bp    mRNA    linear   EST 23-NOV-2005
DEFINITION  est_t_truncatus2262 HML_TuTr_IL-2_PBL Tursiops truncatus cDNA, mRNA
            sequence.
ACCESSION   DV799576
VERSION     DV799576.1  GI:82652485
KEYWORDS    EST.
SOURCE      Tursiops truncatus (bottlenosed dolphin)
  ORGANISM  Tursiops truncatus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
            Odontoceti; Delphinidae; Tursiops.
REFERENCE   1  (bases 1 to 252)
  AUTHORS   Mancia,A., Gefroh,H.A., Lundqvist,M.L., Romano,T.A., Almeida,J.S.,
            Chen,Y., McKillen,D.J., Trent,H.F., Wu,S. and Warr,G.W.
  TITLE     Construction and validation of T. truncatus immunospecific cDNA
            microarray at marinegenomics.org
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Annalaura Mancia
            Hollings Marine Lab
            Medical University of South Carolina
            Hollings Marine Lab, 331 Ft. Johnson Rd., Charleston, SC 29412, USA
            Tel: (843) 762 8962
            Fax: (843) 762 8737
            Email: mancia@musc.edu.
FEATURES              Location/Qualifiers
     source           1. .252
                      /organism="Tursiops truncatus"
                      /mol_type="mRNA"
                      /db_xref="taxon:9739"
```

/tissue_type="PBL"
/cell_type="PBL"
/clone_lib="HML_TuTr_IL-2_PBL"
/note="Vector: pCR2.1TOPO; Site_1: GAATTC"
ORIGIN

Query Match 3.6%; Score 33; DB 10; Length 252;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 254 AGGAAGATGGAATTTGGTCCACTGATATCTTAA 286
||||||||||||||||||||||||||||||||
Db 1 AGGAAGATGGAATTTGGTCCACTGATATCTTAA 33

RESULT 17
AK162981
LOCUS AK162981 1839 bp mRNA linear HTC 21-SEP-2005
DEFINITION Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430014H12 product:interleukin 12b, full insert sequence.
ACCESSION AK162981
VERSION AK162981.1 GI:74188061
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
CONSRTM RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
PUBMED 11217851
REFERENCE 5
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
CONSRTM FANTOM Consortium
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420 (6915), 563-573 (2002)
PUBMED 12466851
REFERENCE 6
AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M.,

```
            Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M.,
            Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K.,
            Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.
  CONSRTM   FANTOM Consortium
  TITLE     The transcriptional landscape of the mammalian genome
  JOURNAL   Science 309 (5740), 1559-1563 (2005)
   PUBMED   16141072
REFERENCE   7
  AUTHORS   Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M.,
            Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H.,
            Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T.,
            Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L.,
            Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A.,
            Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and
            Wahlestedt,C.
  CONSRTM   RIKEN Genome Exploration Research Group
  TITLE     Antisense transcription in the mammalian transcriptome
  JOURNAL   Science 309 (5740), 1564-1566 (2005)
   PUBMED   16141073
REFERENCE   8  (bases 1 to 1839)
  AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K.,
            Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S.,
            Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N.,
            Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D.,
            Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
     source          1. .1839
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM_DB:A430014H12"
                     /db_xref="taxon:10090"
                     /clone="A430014H12"
                     /tissue_type="thymus"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="0 day neonate"
     CDS             58. .1065
                     /note="unnamed protein product; interleukin 12b
                     (MGD|MGI:96540 GB|M86671, evidence: BLASTN, 100%,
                     match=1816)
                     putative"
                     /codon_start=1
                     /protein_id="BAE37146.1"
                     /db_xref="GI:74188062"
                     /translation="MCPQKLTISWFAIVLLVSPLMAMWELEKDVYVVEVDWTPDAPGE
                     TVNLTCDTPEEDDITWTSDQRHGVIGSGKTLTITVKEFLDAGQYTCHKGGETLSHSHL
                     LLHKKENGIWSTEILKNFKNKTFLKCEAPNYSGRFTCSWLVQRNMDLKFNIKSSSSSP
                     DSRAVTCGMASLSAEKVTLDQRDYEKYSVSCQEDVTCPTAEETLPIELALEARQQNKY
                     ENYSTSFFIRDIIKPDPPKNLQMKPLKNSQVEVSWEYPDSWSTPHSYFSLKFFVRIQR
                     KKEKMKETEEGCNQKGAFLVEKTSTEVQCKGGNVCVQAQDRYYNSSCSKWACVPCRVR
                     S"
ORIGIN

  Query Match             3.3%;  Score 30;  DB 6;  Length 1839;
  Best Local Similarity   100.0%;  Pred. No. 0.0003;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        612 CAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||
Db        726 CAGCTTCTTCATCAGGGACATCATCAAACC 755


RESULT 18
AK155593
LOCUS       AK155593               2908 bp    mRNA    linear   HTC 21-SEP-2005
DEFINITION  Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN
            full-length enriched library, clone:F730005O03 product:interleukin
            12b, full insert sequence.
ACCESSION   AK155593
VERSION     AK155593.1  GI:74212721
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
            Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
            Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
            Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
            Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
            Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
            Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
            Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
            Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  CONSRTM   RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
   PUBMED   11217851
REFERENCE   5
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
```

Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420 (6915), 563-573 (2002)

PUBMED 12466851

REFERENCE 6

AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE The transcriptional landscape of the mammalian genome

JOURNAL Science 309 (5740), 1559-1563 (2005)

PUBMED 16141072

REFERENCE 7

AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.

CONSRTM RIKEN Genome Exploration Research Group

TITLE Antisense transcription in the mammalian transcriptome

JOURNAL Science 309 (5740), 1564-1566 (2005)

PUBMED 16141073

REFERENCE 8 (bases 1 to 2908)

AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

source 1. .2908
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:F730005O03"
/db_xref="taxon:10090"
/clone="F730005O03"
/cell_type="B6-derived CD11 +ve dendritic cells"
/clone_lib="RIKEN full-length enriched mouse cDNA library"

misc_feature 1. .2908
/note="interleukin 12b (MGD|MGI:96540 GB|M86671, evidence: BLASTN, 99%, match=1807)
putative"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 612 CAGCTTCTTCATCAGGGACATCATCAAACC 641
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Db 1130 CAGCTTCTTCATCAGGGACATCATCAAACC 1159

RESULT 19
BY164658
LOCUS BY164658 346 bp mRNA linear EST 10-DEC-2002
DEFINITION BY164658 RIKEN full-length enriched, bone marrow macrophage Mus musculus cDNA clone I830052P21 5', mRNA sequence.
ACCESSION BY164658
VERSION BY164658.1 GI:26301304
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 346)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
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Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by David A. Hume (Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane,Q 4072 Australia) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
FEATURES Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.00092;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 91 CCTGAAGAAGATGACATCACCTGGACCTC 119
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Db 214 CCTGAAGAAGATGACATCACCTGGACCTC 242

RESULT 20
BY221814
LOCUS BY221814 355 bp mRNA linear EST 10-DEC-2002
DEFINITION BY221814 RIKEN full-length enriched, activated spleen Mus musculus cDNA clone F830223O08 5', mRNA sequence.
ACCESSION BY221814
VERSION BY221814.1 GI:26402917
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 355)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
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Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,

Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

```
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             3.1%;  Score 29;  DB 4;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 0.00092;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         91 CCTGAAGAAGATGACATCACCTGGACCTC 119
              ||||||||||||||||||||||||||||
Db        213 CCTGAAGAAGATGACATCACCTGGACCTC 241


RESULT 21
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LOCUS       BY222535                375 bp    mRNA    linear   EST 10-DEC-2002
DEFINITION  BY222535 RIKEN full-length enriched, activated spleen Mus musculus
            cDNA clone F830228K06 5', mRNA sequence.
ACCESSION   BY222535
VERSION     BY222535.1  GI:26403638
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 375)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
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            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
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            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
            Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
            Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
            Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
            Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
            Hayashizaki,Y. Direct Submission
            Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
            Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
            RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
            Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
            Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
            Trust/MRC building Addenbrookes Hospital Cambridge) whose
            assistance we gratefully acknowledge.
            Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .375
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                     /clone_lib="RIKEN full-length enriched, activated spleen"
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  Query Match             3.1%;  Score 29;  DB 4;  Length 375;
  Best Local Similarity   100.0%;  Pred. No. 0.00093;
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Qy         91 CCTGAAGAAGATGACATCACCTGGACCTC 119
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Db        213 CCTGAAGAAGATGACATCACCTGGACCTC 241
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RESULT 22
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DEFINITION BY167742 RIKEN full-length enriched, bone marrow macrophage Mus musculus cDNA clone I830068I17 5', mRNA sequence.
ACCESSION BY167742
VERSION BY167742.1 GI:26304388
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 387)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by David A. Hume (Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane,Q 4072 Australia) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
FEATURES Location/Qualifiers
source 1. .387
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="I830068I17"
/tissue_type="bone marrow"
/cell_type="macrophage"
/clone_lib="RIKEN full-length enriched, bone marrow macrophage"
ORIGIN

Query Match 3.1%; Score 29; DB 4; Length 387;
Best Local Similarity 100.0%; Pred. No. 0.00093;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 91 CCTGAAGAAGATGACATCACCTGGACCTC 119
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RESULT 23
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LOCUS CO949904 417 bp mRNA linear EST 09-SEP-2004
DEFINITION UMC-pd12cl-003-b07 Day 12 Corpus Luteum pd12cl Sus scrofa cDNA 3', mRNA sequence.
ACCESSION CO949904
VERSION CO949904.1 GI:51326849
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 417)
AUTHORS Jiang,H., Whitworth,K.M., Bivens,N.J., Ries,J.E., Woods,R.J., Forrester,L.J., Springer,G.K., Mathialagan,N., Agca,C., Prather,R.S. and Lucy,M.C.
TITLE Large-scale Generation and Analysis of Expressed Sequence Tags from Porcine Ovary
JOURNAL Unpublished (2004)
COMMENT Contact: DNA Core Facility (Swine Project)
Animal Science - RS Prather
University of Missouri-Columbia
M616 Medical Sciences Bldg., Columbia, MO 65212, USA
Tel: (573)882-0428
Fax: (573)884-5552
Email: porcine@rnet.missouri.edu
POLYA=No.
FEATURES Location/Qualifiers
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/note="Vector: T3T7PAC; Funding: A grant from the Monsanto Company to the University of Missouri. Genetic Source: Ovarian tissue (whole ovary, dissected follicles, or corpora lutea) was collected from crossbred pigs (Sus scrofa domestica), frozen in liquid nitrogen shortly after collection, and stored at -80 degrees Celsius until RNA

extraction. The tissue from several individual pigs was pooled for the purpose of RNA extraction. The specific tissues collected were fetal whole ovary; neonatal whole ovary; prepubutal whole ovary; 2, 4, 6 and 8 mm growing follicles; Day 0 follicles; Day 5 small antral follicles and corpora lutea; Day 12 corpora lutea and Day 12 follicles. More information regarding the methods can be found at:
http://genome.rnet.missouri.edu/Swine/Methods.html.
Library Construction (Standard Protocol): All procedures discussed in this section have been described in detail elsewhere (Soares et al., 1994; Bonaldo et al., 1996; Jiang et al., 2001). Total cellular RNA from each sample was isolated by using STAT-60 reagent (Tel-Test, Friendswood, TX) and the poly(A)+ RNA was obtained by two rounds of purification with the Oligotex mRNA isolation kit (Qiagen) according to the manufacturer's instructions. The libraries were constructed essentially as described by the manufacturer's instructions provided with the SuperScript Plasmid System (Invitrogen, cat. no. 18248-013). Briefly, 1mg of poly(A)+ RNA will be annealed at 37 degrees Celsius with 10mg of NotI-tag-dT18 oligonucleotide (GCTGCTCGCGGCCGC-tag-T18) and reverse transcribed at 37 degrees Celsius with SuperScript II (Invitrogen) reverse transcriptase (Jiang et al., 2001). The 'tag' represents a tissue/stage-specific ten-base sequence identifier (http://genome.uiowa.edu/pubsoft/software.html) present in the oligonucleotide used to prime first-strand synthesis. Second strand synthesis was performed with T4 DNA polymerase in the presence of DNA ligase and RNase H. After second strand synthesis, the double-stranded cDNAs was ligated to SalI adapters (Invitrogen-Life Technologies) and digested with NotI. The cDNAs will be size selected by passage through cDNA size fractionation columns (Invitrogen-Life technologies). The cDNAs derived from each developmental stage of a particular tissue were mixed on an equimolar basis and ligated directionally into the NotI and SalI sites of the pSPORT1 vector (Invitrogen). After ligation of the inserts, the plasmids will be electroporated into DH10B bacteria. Preliminary Library Characterization: Randomly chosen clones from each library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (~4 96-well plates) to confirm library quality [e.g. the presence of short polyA+ tails, genomic DNA contamination (must be <1%), ribosomal RNA clones (must be <1%), etc.] and to provide a sequence database representing the predominant clones in each library. The clones were sequenced at the University of Missouri-Columbia DNA Core Facility. Bioinformatics work was performed by GK Springer's bioinformatics group (WG Spollen, JE Ries, A Guillen, AA Khambati, RV Patel, CM Topinka, SB Bhuiyan) in Computer Science and Health Management and Informatics Departments at the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri DNA Core facility at: porcine@rnet.missouri.edu. Citations: 1. Bonaldo MF, Lennon G, Soares MB. Normalization and Subtraction: Two approaches to facilitate gene discovery. Genome Res, 1996; 6:791-806. 2. Jiang H, Bivens NJ, Ries JE, Whitworth KM, Green JA, Forrester LJ, Springer GK, Didion BA, Mathialagan N, Prather RS, Lucy MC (2001) Constructing cDNA libraries with fewer clones that contain long poly(dA) tails. Biotechniques 31:38-42. 3. Soares MB, MF Banaldo, P Jelene, L Su, L Lawton, A Efstrantiadis. 1994. Construction and characterization of a normalized cDNA library. Proc Natl Acad Sci, 91:9228-9232.
TAG_TISSUE=Day 12 Corpus Luteum
TAG_SEQ=Not found"

ORIGIN

Query Match 3.1%; Score 29; DB 8; Length 417;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         91 CCTGAAGAAGATGACATCACCTGGACCTC 119
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Db        201 CCTGAAGAAGATGACATCACCTGGACCTC 229
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RESULT 24
BY218447
LOCUS BY218447 423 bp mRNA linear EST 10-DEC-2002
DEFINITION BY218447 RIKEN full-length enriched, activated spleen Mus musculus cDNA clone F830107N16 5', mRNA sequence.
ACCESSION BY218447
VERSION BY218447.1 GI:26399344
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 423)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

```
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /tissue_type="activated spleen"
                     /clone_lib="RIKEN full-length enriched, activated spleen"
ORIGIN

  Query Match             3.1%;  Score 29;  DB 4;  Length 423;
  Best Local Similarity   100.0%;  Pred. No. 0.00094;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         91 CCTGAAGAAGATGACATCACCTGGACCTC 119
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Db        213 CCTGAAGAAGATGACATCACCTGGACCTC 241


RESULT 25
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ACCESSION   BY154173
VERSION     BY154173.1  GI:26290747
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
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            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 432)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
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            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
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            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
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            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
    TITLE   Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
            Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
            Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
            Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
            Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
            Hayashizaki,Y. Direct Submission
            Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
            Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
            RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
            Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
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            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Tissues were provided by David A. Hume ( Depts. of Biochemistry
            and Microbiology/Parasitology Institute for Molecular Bioscience
            University of Queensland Brisbane,Q 4072 Australia ) whose
            assistance we gratefully acknowledge.
            Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
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                     /clone_lib="RIKEN full-length enriched, bone marrow
                     macrophage"
ORIGIN

  Query Match             3.1%;  Score 29;  DB 4;  Length 432;
  Best Local Similarity   100.0%;  Pred. No. 0.00094;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         91 CCTGAAGAAGATGACATCACCTGGACCTC 119
              ||||||||||||||||||||||||||||||
Db        214 CCTGAAGAAGATGACATCACCTGGACCTC 242


RESULT 26
BF704417
LOCUS       BF704417                 475 bp    mRNA    linear   EST 22-DEC-2000
DEFINITION  MI-P-E6-acc-g-09-1-UM.s1 MI-P-E6 Sus scrofa cDNA clone
            MI-P-E6-acc-g-09-1-UM 3', mRNA sequence.
ACCESSION   BF704417
```

```
VERSION     BF704417.1  GI:11989825
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 475)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
   PUBMED   8889548
COMMENT     Contact: Tuggle CK
            Molecular Genetics Laboratory, Department of Animal Science
            Iowa State University
            201 Kildee Hall, Ames, IA 50011-3150, USA
            Tel: 5152944252
            Fax: 5152942401
            Email: cktuggle@iastate.edu
            Oligo-dT track not found, Not I site shown in beginning of sequence
            is likely internal to the message. cDNA Library Preparation: RJ
            Woods, JA Green, RS Prather S142 Animal Science Research Center,
            Department of Animal Science, University of Missouri-Columbia,
            65211 Clone distribution: clones will be available through Research
            Genetics (www.resgen.com)
            Seq primer: M13 Forward
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .475
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /strain="crossbreed"
                     /db_xref="taxon:9823"
                     /clone="MI-P-E6-acc-g-09-1-UM"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="MI-P-E6"
                     /note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: EcoRI;
                     The MI-P-E6 library is derived from fetus at gestational
                     day 20.  For a detailed description of the  library from
                     which this clone was derived, please visit our web site at
                     http://pigest.genome.iastate.edu/.
                     TAG_SEQ=None found"
ORIGIN

  Query Match             3.1%;  Score 29;  DB 7;  Length 475;
  Best Local Similarity   100.0%;  Pred. No. 0.00095;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         91 CCTGAAGAAGATGACATCACCTGGACCTC 119
              ||||||||||||||||||||||||||||
Db        202 CCTGAAGAAGATGACATCACCTGGACCTC 230


RESULT 27
AZ853726/c
LOCUS       AZ853726                569 bp    DNA     linear   GSS 21-FEB-2001
DEFINITION  2M0157M01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0157M01 F, genomic survey sequence.
ACCESSION   AZ853726
VERSION     AZ853726.1  GI:13042136
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 569)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0157  row: M  column: 01
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 569.
FEATURES             Location/Qualifiers
     source          1. .569
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0157M01"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             3.1%;  Score 29;  DB 11;  Length 569;
  Best Local Similarity   100.0%;  Pred. No. 0.00096;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         91 CCTGAAGAAGATGACATCACCTGGACCTC 119
              ||||||||||||||||||||||||||||
Db        214 CCTGAAGAAGATGACATCACCTGGACCTC 186


RESULT 28
CJ134671
LOCUS       CJ134671                649 bp    mRNA    linear   EST 23-SEP-2005
DEFINITION  CJ134671 RIKEN full-length enriched mouse cDNA library, C57BL/6J
            bone marrow macrophage Mus musculus cDNA clone G530135F14 5', mRNA
            sequence.
ACCESSION   CJ134671
VERSION     CJ134671.1  GI:76234999
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 649)
  AUTHORS   The FANTOM Consortium and RIKEN Genome Exploration Research Group
            and Genome Science Group (Genome Network Project Core Group).
  TITLE     The transcriptional landscape of the mammalian genome
```

```
  JOURNAL   Science 309 (5740), 1559-1563 (2005)
   PUBMED   16141072
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. Tissues were provided by David A. Hume (
            Depts. of Biochemistry and Microbiology/Parasitology Institute for
            Molecular Bioscience University of Queensland Brisbane,Q 4072
            Australia ) whose assistance we gratefully acknowledge.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/.
FEATURES             Location/Qualifiers
     source          1. .649
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="G530135F14"
                     /tissue_type="bone marrow"
                     /cell_type="macrophage"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library,
                     C57BL/6J bone marrow macrophage"
ORIGIN

  Query Match             3.1%;  Score 29;  DB 5;  Length 649;
  Best Local Similarity   100.0%;  Pred. No. 0.00098;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         91 CCTGAAGAAGATGACATCACCTGGACCTC 119
              ||||||||||||||||||||||||||||||
Db        214 CCTGAAGAAGATGACATCACCTGGACCTC 242


RESULT 29
BY749553
LOCUS       BY749553                 666 bp    mRNA    linear   EST 17-DEC-2002
DEFINITION  BY749553 RIKEN full-length enriched, B6-derived CD11 +ve dendritic
            cells Mus musculus cDNA clone F730005O03 5', mRNA sequence.
ACCESSION   BY749553
VERSION     BY749553.1  GI:27179008
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
            Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
            Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
            Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
            Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
            Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
            Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
            Direct Submission
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
             cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
             Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
            Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
            Trust/MRC building Addenbrookes Hospital Cambridge) whose
            assistance we gratefully acknowledge.
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="F730005O03"
                     /cell_type="B6-derived CD11 +ve dendritic cells"
                     /clone_lib="RIKEN full-length enriched, B6-derived CD11
                     +ve dendritic cells"
ORIGIN

  Query Match             3.1%;  Score 29;  DB 4;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 0.00098;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         91 CCTGAAGAAGATGACATCACCTGGACCTC 119
              ||||||||||||||||||||||||||||||
Db        614 CCTGAAGAAGATGACATCACCTGGACCTC 642
```

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RESULT 30
AZ441303
LOCUS       AZ441303                 535 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0232M24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0232M24 R, genomic survey sequence.
ACCESSION   AZ441303
VERSION     AZ441303.1  GI:10565316
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 535)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0232  row: M  column: 24
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 535.
FEATURES             Location/Qualifiers
     source          1. .535
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0232M24"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             3.0%;  Score 28;  DB 11;  Length 535;
  Best Local Similarity   100.0%;  Pred. No. 0.0034;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         92 CTGAAGAAGATGACATCACCTGGACCTC 119
              ||||||||||||||||||||||||||||
Db        157 CTGAAGAAGATGACATCACCTGGACCTC 184
```

```
RESULT 31
AG079702/c
LOCUS       AG079702                 668 bp    DNA     linear   GSS 03-NOV-2001
DEFINITION  Pan troglodytes DNA, clone: PTB-075I07.R, genomic survey sequence.
ACCESSION   AG079702
VERSION     AG079702.1  GI:16631504
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     BAC end sequences of Library PTB
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 668)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the chimpanzee BAC library PTB This BAC end
            was generated during the R&D process and may have higher chance of
            clone tracking errors.
             PRIMERS
                 Sequencing: M13Rev
             LIBRARY
                 Vector    : pKS145
                 R.Site 1  : SacI
                 R.Site 2  : SacI.
FEATURES             Location/Qualifiers
     source          1. .668
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
                     /clone="PTB-075I07.R"
                     /sex="male"
                     /cell_type="lymphoblast"
                     /clone_lib="PTB Chimpanzee Male BAC Library"
ORIGIN

  Query Match             2.9%;  Score 27;  DB 14;  Length 668;
  Best Local Similarity   100.0%;  Pred. No. 0.012;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        346 GGACGTTTCACCTGCTGGTGGCTGACG 372
              |||||||||||||||||||||||||||
Db        494 GGACGTTTCACCTGCTGGTGGCTGACG 468
```

```
RESULT 32
CW885638/c
LOCUS       CW885638                 414 bp    DNA     linear   GSS 08-DEC-2004
DEFINITION  RPCI42_102G16.TV RPCI-42 Bos taurus genomic clone RPCI42_102G16,
            genomic survey sequence.
ACCESSION   CW885638
VERSION     CW885638.1  GI:56424578
KEYWORDS    GSS.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 414)
  AUTHORS   Larkin,D.M., Donthu,K., LeDuc,R., Ryan,K., Liu,L., de Jong,P.J. and
            Lewin,H.A.
  TITLE     End sequencing of Holstein BAC library RPCI-42
```

```
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Harris Lewin
            Department of Animal Sciences
            University of Illinois at Urbana Champaign
            1201 W. Gregory Dr., Urbana, IL 61801, USA
            Tel: 217 333 5998
            Fax: 217 244 5617
            Email: h-lewin@uiuc.edu
            Clones are derived from the bovine BAC library RPCI-42
            (http://bacpac.chori.org/mbovine42.htm). For BAC library
            availability, please contact Pieter de Jong
            (pdejong@mail.cho.org).Clones may be purchased from BACPAC
            Resources (http://www.chori.org/bacpac/ordering_information.htm).
            Funding was provided in part by grant no. AG2004-34480-14417 from
            USDA-CSREES (Livestock Genome Sequencing Initiative) and
            AG58-5438-2-313 from USDA-ARS
            Plate: 102  row: G  column: 16
            Seq primer: T7
            Class: BAC ends.
FEATURES              Location/Qualifiers
     source           1. .414
                      /organism="Bos taurus"
                      /mol_type="genomic DNA"
                      /strain="Holstein"
                      /db_xref="taxon:9913"
                      /clone="RPCI42_102G16"
                      /sex="male"
                      /cell_type="blood"
                      /clone_lib="RPCI-42"
                      /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                      RPCI-42 Bovine BAC library (Male) produced by Pieter de
                      Jong"
ORIGIN

  Query Match             2.6%;  Score 24;  DB 13;  Length 414;
  Best Local Similarity   100.0%;  Pred. No. 0.54;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        643 GACCCACCCAAGAACCTGCAACTG 666
              ||||||||||||||||||||||||
Db         24 GACCCACCCAAGAACCTGCAACTG 1


RESULT 33
CW047416/c
LOCUS       CW047416                330 bp    DNA     linear   GSS 28-OCT-2004
DEFINITION  104_285_10512716_115_30217 Sorghum methylation filtered library
            (LibID: 104) Sorghum bicolor genomic clone 10512716, genomic survey
            sequence.
ACCESSION   CW047416
VERSION     CW047416.1  GI:54724146
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 330)
  AUTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
            Martienssen,R.A.
  TITLE     Sorghum genome sequencing by methylation filtration
  JOURNAL   PLoS Biol. 3 (1), e13 (2005)
   PUBMED   15660154
COMMENT     Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: 285  row: e  column: 18
            Seq primer: M13/pUC Reverse
            Class: methylation filtered
            High quality sequence stop: 330.
FEATURES              Location/Qualifiers
     source           1. .330
                      /organism="Sorghum bicolor"
                      /mol_type="genomic DNA"
                      /cultivar="ATx623"
                      /db_xref="taxon:4558"
                      /clone="10512716"
                      /clone_lib="Sorghum methylation filtered library (LibID:
                      104)"
                      /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                      prepared from purified nuclei was randomly sheared,
                      end-repaired, size fractionated to enrich for the 0.5 to 5
                      kb fraction, ligated into HincII-digested pBCSK(-) vector
                      and electroporated into E. coli cells. This is a
                      methylation filtered library."
ORIGIN

  Query Match             2.3%;  Score 21;  DB 13;  Length 330;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        375 AATCAGTACCGATTTGAAATT 395
              |||||||||||||||||||||
Db        100 AATCAGTACCGATTTGAAATT 80


RESULT 34
T99581/c
LOCUS       T99581                  374 bp    mRNA    linear   EST 31-MAR-1995
DEFINITION  ye65d08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone
            IMAGE:122607 5', mRNA sequence.
ACCESSION   T99581
VERSION     T99581.1  GI:749318
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 374)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 954
            High qality sequence stops: 243 Source: IMAGE Consortium, LLNL This
            clone is available royalty-free through LLNL ; contact the IMAGE
            Consortium (info@image.llnl.gov) for further information.
            Insert Length: 954   Std Error: 0.00
            Seq primer: M13RP1
            High quality sequence stop: 243.
FEATURES              Location/Qualifiers
     source           1. .374
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="GDB:475152"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:122607"
                      /sex="male"
                      /dev_stage="20 week-post conception fetus"
                      /lab_host="DH10B (ampicillin resistant)"
```

```
                     /clone_lib="Soares fetal liver spleen 1NFLS"
                     /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                     with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                     1st strand cDNA was primed with a Pac I - oligo(dT) primer
                     [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Pac I and cloned into the Pac I
                     and Eco RI sites of the modified pT7T3 vector.  Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
ORIGIN

  Query Match             2.3%;  Score 21;  DB 10;  Length 374;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        321 AAAATGTGAGGCAAAGAATTA 341
              |||||||||||||||||||||
Db         84 AAAATGTGAGGCAAAGAATTA 64


RESULT 35
CN071927/c
LOCUS       CN071927                508 bp    mRNA    linear   EST 30-MAR-2004
DEFINITION  1021022B08.x2 1021 - Unigene II from Maize Genome Project Zea mays
            cDNA, mRNA sequence.
ACCESSION   CN071927
VERSION     CN071927.1  GI:45847984
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 508)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 1021022  row: B  column: 08.
FEATURES             Location/Qualifiers
     source          1. .508
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /db_xref="dbEST:949071E08.x1"
                     /db_xref="taxon:4577"
                     /clone_lib="1021 - Unigene II from Maize Genome Project"
                     /note="This library represents the unique genes found in
                     the second round of EST sequencing at Stanford University
                     for the maize genome project. Sequences are present from
                     library 949. Contigs were assembled using ZmDBAssembler
                     and 2 representatives from each contig were selected for
                     the Unigene set. All singlets were also selected. Library
                     947, also part of Unigene II, was submitted under NAME
                     '1020 - Unigene II from Maize Genome Project'."
ORIGIN

  Query Match             2.3%;  Score 21;  DB 8;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         87 TACTCCTGAAGAAGATGACAT 107
              |||||||||||||||||||||
Db        314 TACTCCTGAAGAAGATGACAT 294


RESULT 36
CF059708/c
LOCUS       CF059708                509 bp    mRNA    linear   EST 21-JUL-2003
DEFINITION  QCS15g07.yg QCS Zea mays cDNA clone QCS15g07, mRNA sequence.
ACCESSION   CF059708
VERSION     CF059708.1  GI:33099748
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 509)
  AUTHORS   Genoplante.
  TITLE     Genoplante, a major partnership french program in plant genomics
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Genoplante
            Genoplante
            93, rue Henri Rochefort 91025 EVRY CEDEX France
            Tel: 33 1 69 47 54 00
            Fax: 33 1 69 47 54 10
            This sequence has been generated in the framework of the french
            plant genomics programme 'Genoplante' (http://www.genoplante.com
            and http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .509
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="F2"
                     /db_xref="taxon:4577"
                     /clone="QCS15g07"
                     /tissue_type="whole plant"
                     /clone_lib="QCS"
ORIGIN

  Query Match             2.3%;  Score 21;  DB 5;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         87 TACTCCTGAAGAAGATGACAT 107
              |||||||||||||||||||||
Db        362 TACTCCTGAAGAAGATGACAT 342


RESULT 37
CF060247/c
LOCUS       CF060247                509 bp    mRNA    linear   EST 21-JUL-2003
DEFINITION  QCS5b05.yg QCS Zea mays cDNA clone QCS5b05, mRNA sequence.
ACCESSION   CF060247
VERSION     CF060247.1  GI:33100287
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 509)
  AUTHORS   Genoplante.
  TITLE     Genoplante, a major partnership french program in plant genomics
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Genoplante
            Genoplante
            93, rue Henri Rochefort 91025 EVRY CEDEX France
            Tel: 33 1 69 47 54 00
            Fax: 33 1 69 47 54 10
            This sequence has been generated in the framework of the french
            plant genomics programme 'Genoplante' (http://www.genoplante.com
            and http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .509
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="F2"
```

```
                     /db_xref="taxon:4577"
                     /clone="QCS5b05"
                     /tissue_type="whole plant"
                     /clone_lib="QCS"
ORIGIN

  Query Match             2.3%;  Score 21;  DB 5;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         87 TACTCCTGAAGAAGATGACAT 107
              |||||||||||||||||||||
Db        362 TACTCCTGAAGAAGATGACAT 342


RESULT 38
CF059885/c
LOCUS       CF059885                510 bp    mRNA    linear   EST 21-JUL-2003
DEFINITION  QCS18b04.yg QCS Zea mays cDNA clone QCS18b04, mRNA sequence.
ACCESSION   CF059885
VERSION     CF059885.1  GI:33099925
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 510)
  AUTHORS   Genoplante.
  TITLE     Genoplante, a major partnership french program in plant genomics
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Genoplante
            Genoplante
            93, rue Henri Rochefort 91025 EVRY CEDEX France
            Tel: 33 1 69 47 54 00
            Fax: 33 1 69 47 54 10
            This sequence has been generated in the framework of the french
            plant genomics programme 'Genoplante' (http://www.genoplante.com
            and http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .510
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="F2"
                     /db_xref="taxon:4577"
                     /clone="QCS18b04"
                     /tissue_type="whole plant"
                     /clone_lib="QCS"
ORIGIN

  Query Match             2.3%;  Score 21;  DB 5;  Length 510;
  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         87 TACTCCTGAAGAAGATGACAT 107
              |||||||||||||||||||||
Db        363 TACTCCTGAAGAAGATGACAT 343


RESULT 39
BI431328/c
LOCUS       BI431328                521 bp    mRNA    linear   EST 20-AUG-2001
DEFINITION  949071E08.x1 949 - Juvenile leaf and shoot cDNA from Steve Moose
            Zea mays cDNA, mRNA sequence.
ACCESSION   BI431328
VERSION     BI431328.1  GI:15215523
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 521)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 949071  row: E  column: 08.
FEATURES             Location/Qualifiers
     source          1. .521
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="W64A"
                     /db_xref="taxon:4577"
                     /tissue_type="immature leaf primordium and vegetative
                     meristem"
                     /dev_stage="4 stages from 3-13 days after imbibing"
                     /lab_host="E. coli XLOLR"
                     /clone_lib="949 - Juvenile leaf and shoot cDNA from Steve
                     Moose"
                     /note="Organ: juvenile vegetative shoots; Vector:
                     pAD-GAL4-2.1; Site_1: EcoRI; Site_2: XhoI; Equal amounts
                     of total RNA by weight from 4 tissue sources (see below)
                     were pooled, polyA+ RNA isolated, and cDNA synthesized for
                     EcoRI (5') and XhoI (3') directional cloning into lambda
                     Hybrizap vector from Stratagene. Tissue Sources: 1. Whole
                     shoots 3 days after sowing/imbibing in wet soil. 2. Basal
                     1.5 cm shoots 6 days after sowing - includes yellow
                     portions of developing leaves 1-5, primordia from 6-8, and
                     the vegetative apex. 3. Non-green portions of developing
                     leaves 4-5 and the vegetative apex,  including adult leaf
                     primordia, 9 days after sowing. 4. Partially expanded and
                     greening leaves 4-5 at 13 days after sowing."
ORIGIN

  Query Match             2.3%;  Score 21;  DB 2;  Length 521;
  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         87 TACTCCTGAAGAAGATGACAT 107
              |||||||||||||||||||||
Db        351 TACTCCTGAAGAAGATGACAT 331


RESULT 40
AI491671/c
LOCUS       AI491671                523 bp    mRNA    linear   EST 22-APR-1999
DEFINITION  486020E06.x2 486 - leaf primordia cDNA library from Hake lab Zea
            mays cDNA, mRNA sequence.
ACCESSION   AI491671
VERSION     AI491671.2  GI:4646526
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 523)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     On Mar 8, 1999 this sequence version replaced gi:4388499.
            Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
```

```
           Email: walbot@stanford.edu
           Plate: 486020  row: E  column: 06.
FEATURES             Location/Qualifiers
     source          1. .523
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="B73"
                     /db_xref="taxon:4577"
                     /tissue_type="leaf primordia"
                     /dev_stage="P7-P11 leaf"
                     /lab_host="E.coli XL1-Blue MFR'"
                     /clone_lib="486 - leaf primordia cDNA library from Hake
                     lab"
                     /note="Organ: shoot; Vector: Lambda zap; Hake lab cDNA
                     library."
ORIGIN

  Query Match             2.3%;  Score 21;  DB 1;  Length 523;
  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         87 TACTCCTGAAGAAGATGACAT 107
              |||||||||||||||||||||
Db        408 TACTCCTGAAGAAGATGACAT 388


RESULT 41
AW566435/c
LOCUS       AW566435                553 bp    mRNA    linear   EST 10-MAR-2000
DEFINITION  660074D12.x1 660 - Mixed stages of anther and pollen Zea mays cDNA,
            mRNA sequence.
ACCESSION   AW566435
VERSION     AW566435.1  GI:7227794
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 553)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 660074  row: D  column: 12.
FEATURES             Location/Qualifiers
     source          1. .553
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="Ohio43"
                     /db_xref="taxon:4577"
                     /tissue_type="whole premieotic anthers to pollen shed"
                     /dev_stage="premieotic anthers to pollen shed"
                     /lab_host="XLOLR"
                     /clone_lib="660 - Mixed stages of anther and pollen"
                     /note="Organ: anthers; Vector: Lambda Zap; Site_1: EcoRI;
                     Site_2: XhoI; Anther and pollen cDNA library.
                     Directionally sequenced with 5' end at the EcoRI site.
                     Created by Amie Franklin."
ORIGIN

  Query Match             2.3%;  Score 21;  DB 7;  Length 553;
  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         87 TACTCCTGAAGAAGATGACAT 107
              |||||||||||||||||||||
Db        324 TACTCCTGAAGAAGATGACAT 304


RESULT 42
BQ294193
LOCUS       BQ294193                566 bp    mRNA    linear   EST 15-MAY-2002
DEFINITION  1091026G08.y2 1091 - Immature ear with common ESTs screened by
            Schmidt lab Zea mays cDNA, mRNA sequence.
ACCESSION   BQ294193
VERSION     BQ294193.1  GI:20803143
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 566)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 1091026  row: G  column: 08.
FEATURES             Location/Qualifiers
     source          1. .566
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="OH43"
                     /db_xref="taxon:4577"
                     /tissue_type="Inflorescence meristem - floral organ
                     primordia"
                     /dev_stage="0.5 cm to 2 cm"
                     /lab_host="Stratagene XLOLR"
                     /clone_lib="1091 - Immature ear with common ESTs screened
                     by Schmidt lab"
                     /note="Organ: Immature ear; Vector: pAD-GAL4; Site_1:
                     EcoRI; Site_2: XhoI; RNA from library 606 was filtered for
                     common ESTs found in 606."
ORIGIN

  Query Match             2.3%;  Score 21;  DB 3;  Length 566;
  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         87 TACTCCTGAAGAAGATGACAT 107
              |||||||||||||||||||||
Db        500 TACTCCTGAAGAAGATGACAT 520


RESULT 43
CA627255/c
LOCUS       CA627255                588 bp    mRNA    linear   EST 23-NOV-2002
DEFINITION  wl1n.pk154.e4 wl1n Triticum aestivum cDNA clone wl1n.pk154.e4 5'
            end, mRNA sequence.
ACCESSION   CA627255
VERSION     CA627255.1  GI:25205551
KEYWORDS    EST.
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 588)
  AUTHORS   Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,
            Miao,G., Caraher,N. and Hanafey,M.K.
  TITLE     DuPont Wheat cDNA Sequence
```

```
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Scott V. Tingey
            Crop Genetics
            E. I. DuPont de Nemours and Company
            1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
            Tel: 302-631-2602
            Fax: 302-631-2607
            Email: Scott.V.Tingey@USA.dupont.com
            Seq primer: M13.
FEATURES             Location/Qualifiers
     source          1. .588
                     /organism="Triticum aestivum"
                     /mol_type="mRNA"
                     /db_xref="taxon:4565"
                     /clone="wl1n.pk154.e4"
                     /tissue_type="leaf"
                     /clone_lib="wl1n"
                     /note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
                     XhoI; Wheat (Triticum aestivum L.) leaf 7 day old
                     seedling, light grown (normalized)"
ORIGIN

  Query Match             2.3%;  Score 21;  DB 4;  Length 588;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         87 TACTCCTGAAGAAGATGACAT 107
              |||||||||||||||||||||
Db        357 TACTCCTGAAGAAGATGACAT 337


RESULT 44
AW573354
LOCUS       AW573354                 594 bp    mRNA    linear   EST 13-MAR-2000
DEFINITION  660074D12.y1 660 - Mixed stages of anther and pollen Zea mays cDNA,
            mRNA sequence.
ACCESSION   AW573354
VERSION     AW573354.1  GI:7238132
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 594)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 660074  row: D  column: 12.
FEATURES             Location/Qualifiers
     source          1. .594
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="Ohio43"
                     /db_xref="taxon:4577"
                     /tissue_type="whole premieotic anthers to pollen shed"
                     /dev_stage="premieotic anthers to pollen shed"
                     /lab_host="XLOLR"
                     /clone_lib="660 - Mixed stages of anther and pollen"
                     /note="Organ: anthers; Vector: Lambda Zap; Site_1: EcoRI;
                     Site_2: XhoI; Anther and pollen cDNA library.
                     Directionally sequenced with 5' end at the EcoRI site.
                     Created by Amie Franklin."
ORIGIN

  Query Match             2.3%;  Score 21;  DB 7;  Length 594;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         87 TACTCCTGAAGAAGATGACAT 107
              |||||||||||||||||||||
Db        336 TACTCCTGAAGAAGATGACAT 356


RESULT 45
BI478972
LOCUS       BI478972                 599 bp    mRNA    linear   EST 27-AUG-2001
DEFINITION  949071E08.y1 949 - Juvenile leaf and shoot cDNA from Steve Moose
            Zea mays cDNA, mRNA sequence.
ACCESSION   BI478972
VERSION     BI478972.1  GI:15313824
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 599)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 949071  row: E  column: 08.
FEATURES             Location/Qualifiers
     source          1. .599
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="W64A"
                     /db_xref="taxon:4577"
                     /tissue_type="immature leaf primordium and vegetative
                     meristem"
                     /dev_stage="4 stages from 3-13 days after imbibing"
                     /lab_host="E. coli XLOLR"
                     /clone_lib="949 - Juvenile leaf and shoot cDNA from Steve
                     Moose"
                     /note="Organ: juvenile vegetative shoots; Vector:
                     pAD-GAL4-2.1; Site_1: EcoRI; Site_2: XhoI; Equal amounts
                     of total RNA by weight from 4 tissue sources (see below)
                     were pooled, polyA+ RNA isolated, and cDNA synthesized for
                     EcoRI (5') and XhoI (3') directional cloning into lambda
                     Hybrizap vector from Stratagene. Tissue Sources: 1. Whole
                     shoots 3 days after sowing/imbibing in wet soil. 2. Basal
                     1.5 cm shoots 6 days after sowing - includes yellow
                     portions of developing leaves 1-5, primordia from 6-8, and
                     the vegetative apex. 3. Non-green portions of developing
                     leaves 4-5 and the vegetative apex,  including adult leaf
                     primordia, 9 days after sowing. 4. Partially expanded and
                     greening leaves 4-5 at 13 days after sowing."
ORIGIN

  Query Match             2.3%;  Score 21;  DB 2;  Length 599;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         87 TACTCCTGAAGAAGATGACAT 107
              |||||||||||||||||||||
Db        471 TACTCCTGAAGAAGATGACAT 491


RESULT 46
CA293522/c
```

```
LOCUS       CA293522                632 bp    mRNA    linear   EST 26-SEP-2003
DEFINITION  SCSGLV1005G05.g LV1 Saccharum officinarum cDNA clone SCSGLV1005G05
            5', mRNA sequence.
ACCESSION   CA293522
VERSION     CA293522.1  GI:36054204
KEYWORDS    EST.
SOURCE      Saccharum officinarum
  ORGANISM  Saccharum officinarum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
            complex.
REFERENCE   1  (bases 1 to 632)
  AUTHORS   Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
  TITLE     The libraries that made SUCEST
  JOURNAL   Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT     Contact: Arruda P
            Centro de Biologia Molecular e Engenharia Genetica
            Universidade Estadual de Campinas
            Caixa Postal 6010, 13083-970, Campinas SP, Brazil
            Tel: 55 19 3788 1137
            Fax: 55 19 3788 1089
            Email: parruda@unicamp.br
            Clone distribution: clone distribution information can be found
            through the Brazilian Clone Collection Center (BCCC) at
            http://www.bcccenter.fcav.unesp.br
            Plate: 005  row: G  column: 05
            Seq primer: T7 Promoter Primer.
FEATURES             Location/Qualifiers
     source          1. .632
                     /organism="Saccharum officinarum"
                     /mol_type="mRNA"
                     /db_xref="taxon:4547"
                     /clone="SCSGLV1005G05"
                     /lab_host="DH10B"
                     /clone_lib="LV1"
                     /note="Organ: Etiolated leaves from in vitro grown
                     sedlings; Vector: pSport1; Site_1: SalI; Site_2: NotI; An
                     unidirectional cDNA library generated from [Etiolated
                     leaves from in  vitro grown sedlings]. cDNA was prepared
                     from polyA+ mRNA using  SuperScript Plasmid System Kit
                     (Invitrogen). The double-strand cDNAs were  fractionated
                     in a sepharose CL-2B 40cm-columns and fragments sizing
                     between 0.8 and 1.5 Kb were directionally cloned into the
                     vector. Details  of each source of RNA and library
                     construction can be obtained at
                     http://sucest.lad.ic.unicamp.br/public"
ORIGIN

  Query Match             2.3%;  Score 21;  DB 4;  Length 632;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        375 AATCAGTACCGATTTGAAATT 395
              |||||||||||||||||||||
Db        620 AATCAGTACCGATTTGAAATT 600


RESULT 47
DN207344/c
LOCUS       DN207344                633 bp    mRNA    linear   EST 28-FEB-2005
DEFINITION  MEST847_H05.T7-1 UGA-ZmSAM-XZ2 Zea mays cDNA, mRNA sequence.
ACCESSION   DN207344
VERSION     DN207344.1  GI:60340371
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 633)
  AUTHORS   Chen,H.D., Zhang,X., Zhou,R.L., Arias L,A.C., Shendelman,J.M.,
            Zazubovits,N., Borsuk,L.A., Emrich,S.J., Ashlock,D.A., Scanlon,M.J.
            and Schnable,P.S.
  TITLE     Expressed Sequence Tags from B73 Maize Shoot Apical Meristems
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Patrick S. Schnable
            Schnable Laboratory
            Iowa State University
            2035B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA
            Tel: 515-294-0975
            Fax: 515-294-5256
            Email: schnable@iastate.edu.
FEATURES             Location/Qualifiers
     source          1. .633
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="inbred B73"
                     /db_xref="taxon:4577"
                     /tissue_type="Vegetative Shoot Apical Meristem (SAM) and
                     leaf primordia staged P1-P4"
                     /lab_host="XL1-Blue"
                     /clone_lib="UGA-ZmSAM-XZ2"
                     /note="Organ: Shoot apex; Vector: Uni-Zap XR; Site_1:
                     EcoRI; Site_2: XhoI; This library was constructed by
                     Xiaolan Zhang. Vegetative Shoot Apical Meristem (SAM) and
                     leaf primordia staged P1-P4 from 14-17 day-after
                     germination seedlings were quickly dissected into dry ice
                     under a light microscope. Total RNA was isolated using
                     Trizol and mRNA was purified with Dynal Oligo-DT25.
                     ds-cDNA molecules were generated as follows.  First-strand
                     cDNA was prepared from oligo-dT selected mRNA by priming
                     with an XhoI oligo-dT primer
                     (5'-GAGAGAGAGAGAGAGAGAACTAGTCTCGAGTTTTTTTTTTTTTTTTT).
                     The resulting DNA:RNA hybrid was treated with RNase H and
                     used as a template for DNA PolI-catalyzed second strand
                     synthesis. After the addition of EcoRI adaptors, the
                     ds-cDNAs were digested with XhoI and size-selected to be
                     >600 bp. The resulting molecules were directionally cloned
                     into the EcoRI and XhoI sites of the Uni-Zap XR vector.
                     The lambda library was packaged with Gigapack III Gold
                     packaging extract and was mass excised by XL1-Blue cells
                     and ExAssist helper phage. Excised phagemids were titered
                     in SOLR cells and plated onto LB-ampicillin agar plates.
                     Base calling was conducted using Phred. Trimming was
                     performed using Lucy with the following criteria:
                     (-minimum 200 -error 0.01 0.01 -bracket 10 0.01). A low
                     complexity filter was applied and additional trimming was
                     conducted to remove E. coli, vector, and organelle
                     contamination. After processing ~30% of the sequences
                     contained a minimum of 10 Ts at the beginning of the
                     sequence.  For reasons that are not understood many of the
                     clones in this library lack an XhoI site at their 3'
                     ends."
ORIGIN

  Query Match             2.3%;  Score 21;  DB 9;  Length 633;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         87 TACTCCTGAAGAAGATGACAT 107
              |||||||||||||||||||||
Db        456 TACTCCTGAAGAAGATGACAT 436


RESULT 48
BQ294192/c
LOCUS       BQ294192                637 bp    mRNA    linear   EST 15-MAY-2002
DEFINITION  1091026G08.x2 1091 - Immature ear with common ESTs screened by
            Schmidt lab Zea mays cDNA, mRNA sequence.
ACCESSION   BQ294192
VERSION     BQ294192.1  GI:20803142
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
```

```
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 637)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 1091026  row: G  column: 08.
FEATURES             Location/Qualifiers
     source          1. .637
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="OH43"
                     /db_xref="taxon:4577"
                     /tissue_type="Inflorescence meristem - floral organ
                     primordia"
                     /dev_stage="0.5 cm to 2 cm"
                     /lab_host="Stratagene XLOLR"
                     /clone_lib="1091 - Immature ear with common ESTs screened
                     by Schmidt lab"
                     /note="Organ: Immature ear; Vector: pAD-GAL4; Site_1:
                     EcoRI; Site_2: XhoI; RNA from library 606 was filtered for
                     common ESTs found in 606."
ORIGIN

  Query Match             2.3%;  Score 21;  DB 3;  Length 637;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         87 TACTCCTGAAGAAGATGACAT 107
              |||||||||||||||||||||
Db        359 TACTCCTGAAGAAGATGACAT 339


RESULT 49
DN222336/c
LOCUS       DN222336                692 bp    mRNA    linear   EST 28-FEB-2005
DEFINITION  MEST1126_F09.T7-1 UGA-ZmSAM-XZ2 Zea mays cDNA, mRNA sequence.
ACCESSION   DN222336
VERSION     DN222336.1  GI:60355363
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 692)
  AUTHORS   Chen,H.D., Zhang,X., Zhou,R.L., Arias L,A.C., Shendelman,J.M.,
            Zazubovits,N., Borsuk,L.A., Emrich,S.J., Ashlock,D.A., Scanlon,M.J.
            and Schnable,P.S.
  TITLE     Expressed Sequence Tags from B73 Maize Shoot Apical Meristems
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Patrick S. Schnable
            Schnable Laboratory
            Iowa State University
            2035B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA
            Tel: 515-294-0975
            Fax: 515-294-5256
            Email: schnable@iastate.edu.
FEATURES             Location/Qualifiers
     source          1. .692
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="inbred B73"
                     /db_xref="taxon:4577"
                     /tissue_type="Vegetative Shoot Apical Meristem (SAM) and
                     leaf primordia staged P1-P4"
                     /lab_host="XL1-Blue"
                     /clone_lib="UGA-ZmSAM-XZ2"
                     /note="Organ: Shoot apex; Vector: Uni-Zap XR; Site_1:
                     EcoRI; Site_2: XhoI; This library was constructed by
                     Xiaolan Zhang. Vegetative Shoot Apical Meristem (SAM) and
                     leaf primordia staged P1-P4 from 14-17 day-after
                     germination seedlings were quickly dissected into dry ice
                     under a light microscope. Total RNA was isolated using
                     Trizol and mRNA was purified with Dynal Oligo-DT25.
                     ds-cDNA molecules were generated as follows.  First-strand
                     cDNA was prepared from oligo-dT selected mRNA by priming
                     with an XhoI oligo-dT primer
                     (5'-GAGAGAGAGAGAGAGAGAGAACTAGTCTCGAGTTTTTTTTTTTTTTTT).
                     The resulting DNA:RNA hybrid was treated with RNase H and
                     used as a template for DNA PolI-catalyzed second strand
                     synthesis. After the addition of EcoRI adaptors, the
                     ds-cDNAs were digested with XhoI and size-selected to be
                     >600 bp. The resulting molecules were directionally cloned
                     into the EcoRI and XhoI sites of the Uni-Zap XR vector.
                     The lambda library was packaged with Gigapack III Gold
                     packaging extract and was mass excised by XL1-Blue cells
                     and ExAssist helper phage. Excised phagemids were titered
                     in SOLR cells and plated onto LB-ampicillin agar plates.
                     Base calling was conducted using Phred. Trimming was
                     performed using Lucy with the following criteria:
                     (-minimum 200 -error 0.01 0.01 -bracket 10 0.01). A low
                     complexity filter was applied and additional trimming was
                     conducted to remove E. coli, vector, and organelle
                     contamination. After processing ~30% of the sequences
                     contained a minimum of 10 Ts at the beginning of the
                     sequence.  For reasons that are not understood many of the
                     clones in this library lack an XhoI site at their 3'
                     ends."
ORIGIN

  Query Match             2.3%;  Score 21;  DB 9;  Length 692;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         87 TACTCCTGAAGAAGATGACAT 107
              |||||||||||||||||||||
Db        388 TACTCCTGAAGAAGATGACAT 368


RESULT 50
DN220924/c
LOCUS       DN220924                693 bp    mRNA    linear   EST 28-FEB-2005
DEFINITION  MEST1104_C12.T7-1 UGA-ZmSAM-XZ2 Zea mays cDNA, mRNA sequence.
ACCESSION   DN220924
VERSION     DN220924.1  GI:60353951
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 693)
  AUTHORS   Chen,H.D., Zhang,X., Zhou,R.L., Arias L,A.C., Shendelman,J.M.,
            Zazubovits,N., Borsuk,L.A., Emrich,S.J., Ashlock,D.A., Scanlon,M.J.
            and Schnable,P.S.
  TITLE     Expressed Sequence Tags from B73 Maize Shoot Apical Meristems
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Patrick S. Schnable
            Schnable Laboratory
            Iowa State University
            2035B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA
            Tel: 515-294-0975
            Fax: 515-294-5256
            Email: schnable@iastate.edu.
FEATURES             Location/Qualifiers
     source          1. .693
                     /organism="Zea mays"
```

/mol_type="mRNA"
/cultivar="inbred B73"
/db_xref="taxon:4577"
/tissue_type="Vegetative Shoot Apical Meristem (SAM) and leaf primordia staged P1-P4"
/lab_host="XL1-Blue"
/clone_lib="UGA-ZmSAM-XZ2"
/note="Organ: Shoot apex; Vector: Uni-Zap XR; Site_1: EcoRI; Site_2: XhoI; This library was constructed by Xiaolan Zhang. Vegetative Shoot Apical Meristem (SAM) and leaf primordia staged P1-P4 from 14-17 day-after germination seedlings were quickly dissected into dry ice under a light microscope. Total RNA was isolated using Trizol and mRNA was purified with Dynal Oligo-DT25. ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with an XhoI oligo-dT primer (5'-GAGAGAGAGAGAGAGAGAGAACTAGTCTCGAGTTTTTTTTTTTTTTTTT). The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with XhoI and size-selected to be >600 bp. The resulting molecules were directionally cloned into the EcoRI and XhoI sites of the Uni-Zap XR vector. The lambda library was packaged with Gigapack III Gold packaging extract and was mass excised by XL1-Blue cells and ExAssist helper phage. Excised phagemids were titered in SOLR cells and plated onto LB-ampicillin agar plates. Base calling was conducted using Phred. Trimming was performed using Lucy with the following criteria: (-minimum 200 -error 0.01 0.01 -bracket 10 0.01). A low complexity filter was applied and additional trimming was conducted to remove E. coli, vector, and organelle contamination. After processing ~30% of the sequences contained a minimum of 10 Ts at the beginning of the sequence. For reasons that are not understood many of the clones in this library lack an XhoI site at their 3' ends."
ORIGIN

Query Match 2.3%; Score 21; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         87 TACTCCTGAAGAAGATGACAT 107
              |||||||||||||||||||||
Db        359 TACTCCTGAAGAAGATGACAT 339
```

RESULT 51
DN219584/c
LOCUS DN219584 694 bp mRNA linear EST 28-FEB-2005
DEFINITION MEST1083_C10.T7-1 UGA-ZmSAM-XZ2 Zea mays cDNA, mRNA sequence.
ACCESSION DN219584
VERSION DN219584.1 GI:60352611
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 694)
AUTHORS Chen,H.D., Zhang,X., Zhou,R.L., Arias L,A.C., Shendelman,J.M., Zazubovits,N., Borsuk,L.A., Emrich,S.J., Ashlock,D.A., Scanlon,M.J. and Schnable,P.S.
TITLE Expressed Sequence Tags from B73 Maize Shoot Apical Meristems
JOURNAL Unpublished (2004)
COMMENT Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
2035B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA
Tel: 515-294-0975
Fax: 515-294-5256
Email: schnable@iastate.edu.
FEATURES Location/Qualifiers
source 1. .694
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="inbred B73"
/db_xref="taxon:4577"
/tissue_type="Vegetative Shoot Apical Meristem (SAM) and leaf primordia staged P1-P4"
/lab_host="XL1-Blue"
/clone_lib="UGA-ZmSAM-XZ2"
/note="Organ: Shoot apex; Vector: Uni-Zap XR; Site_1: EcoRI; Site_2: XhoI; This library was constructed by Xiaolan Zhang. Vegetative Shoot Apical Meristem (SAM) and leaf primordia staged P1-P4 from 14-17 day-after germination seedlings were quickly dissected into dry ice under a light microscope. Total RNA was isolated using Trizol and mRNA was purified with Dynal Oligo-DT25. ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with an XhoI oligo-dT primer (5'-GAGAGAGAGAGAGAGAGAGAACTAGTCTCGAGTTTTTTTTTTTTTTTT). The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with XhoI and size-selected to be >600 bp. The resulting molecules were directionally cloned into the EcoRI and XhoI sites of the Uni-Zap XR vector. The lambda library was packaged with Gigapack III Gold packaging extract and was mass excised by XL1-Blue cells and ExAssist helper phage. Excised phagemids were titered in SOLR cells and plated onto LB-ampicillin agar plates. Base calling was conducted using Phred. Trimming was performed using Lucy with the following criteria: (-minimum 200 -error 0.01 0.01 -bracket 10 0.01). A low complexity filter was applied and additional trimming was conducted to remove E. coli, vector, and organelle contamination. After processing ~30% of the sequences contained a minimum of 10 Ts at the beginning of the sequence. For reasons that are not understood many of the clones in this library lack an XhoI site at their 3' ends."
ORIGIN

Query Match 2.3%; Score 21; DB 9; Length 694;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         87 TACTCCTGAAGAAGATGACAT 107
              |||||||||||||||||||||
Db        456 TACTCCTGAAGAAGATGACAT 436
```

RESULT 52
DV622355/c
LOCUS DV622355 716 bp mRNA linear EST 01-NOV-2005
DEFINITION IV-1091-403D-A11.T7-1 UGIV-1091-Reseq Zea mays cDNA, mRNA sequence.
ACCESSION DV622355
VERSION DV622355.1 GI:78544857
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 716)
AUTHORS Zhou,R.L., Shendelman,J.M., Borsuk,L.A., Chen,H.D., Chen,Y.R. and Schnable,P.S.
TITLE Resequencing Unigene IV-1091 EST set
JOURNAL Unpublished (2005)
COMMENT Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University

```
           2035B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA
           Tel: 515-294-0975
           Fax: 515-294-5256
           Email: schnable@iastate.edu.
FEATURES             Location/Qualifiers
     source          1. .716
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /db_xref="taxon:4577"
                     /clone_lib="UGIV-1091-Reseq"
ORIGIN

  Query Match             2.3%;  Score 21;  DB 10;  Length 716;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         87 TACTCCTGAAGAAGATGACAT 107
              |||||||||||||||||||||
Db        409 TACTCCTGAAGAAGATGACAT 389


RESULT 53
AY112414/c
LOCUS       AY112414                724 bp    mRNA    linear   HTC 01-MAR-2005
DEFINITION  Zea mays CL8984_1 mRNA sequence.
ACCESSION   AY112414
VERSION     AY112414.1  GI:21217004
KEYWORDS    HTC.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 724)
  AUTHORS   Gardiner,J., Schroeder,S., Polacco,M.L., Sanchez-Villeda,H.,
            Fang,Z., Morgante,M., Landewe,T., Fengler,K., Useche,F.,
            Hanafey,M., Tingey,S., Chou,H., Wing,R., Soderlund,C. and Coe,E.H.
            Jr.
  TITLE     Anchoring 9,371 maize expressed sequence tagged unigenes to the
            bacterial artificial chromosome contig map by two-dimensional
            overgo hybridization
  JOURNAL   Plant Physiol. 134 (4), 1317-1326 (2004)
   PUBMED   15020742
REFERENCE   2  (bases 1 to 724)
  AUTHORS   Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
            Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
  TITLE     Maize Mapping Project/DuPont Consensus Sequences for Design of
            Overgo Probes
  JOURNAL   Unpublished (2002)
REFERENCE   3  (bases 1 to 724)
  AUTHORS   Coe,E.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-APR-2002) Maize Mapping Project, University of
            Missouri, Columbia, MO 65211, USA
COMMENT     If you are interested in getting corresponding physical clones,
            these are publicly available from ZmDB and may be found by BLAST
            searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
            www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
            maize cDNA sequences is either Virginia Walbot, Stanford or Pat
            Schnable, Iowa State, then clones may be requested from ZmDB:
            www.zmdb.iastate.edu.
FEATURES             Location/Qualifiers
     source          1. .724
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /db_xref="MaizeGDB:633032"
                     /db_xref="taxon:4577"
                     /clone_lib="Maize Mapping Project/DuPont Cornsensus
                     Library"
                     /note="this sequence is part of a project of EST
                     assemblies resulting from the application of public
                     contigs to seed DuPont contigs; this resource was
                     assembled by DuPont as part of a collaboration for the
                     overgo addressing of BACs in conjunction with the Maize
                     Mapping Project"
ORIGIN

  Query Match             2.3%;  Score 21;  DB 6;  Length 724;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         87 TACTCCTGAAGAAGATGACAT 107
              |||||||||||||||||||||
Db        391 TACTCCTGAAGAAGATGACAT 371


RESULT 54
CL163765/c
LOCUS       CL163765                743 bp    DNA     linear   GSS 06-JAN-2004
DEFINITION  104_357_10807387_116_31813_139 Sorghum methylation-filtered library
            (LibID: 104) Sorghum bicolor genomic clone 10807387, genomic survey
            sequence.
ACCESSION   CL163765
VERSION     CL163765.1  GI:40671650
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 743)
  AUTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
            Martienssen,R.A.
  TITLE     Sorghum genome sequencing by methylation filtration
  JOURNAL   PLoS Biol. 3 (1), e13 (2005)
   PUBMED   15660154
COMMENT     Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: 357  row: f  column: 19
            Seq primer: T3 Reverse
            Class: methylation filtered
            High quality sequence stop: 743.
FEATURES             Location/Qualifiers
     source          1. .743
                     /organism="Sorghum bicolor"
                     /mol_type="genomic DNA"
                     /cultivar="ATx623"
                     /db_xref="taxon:4558"
                     /clone="10807387"
                     /clone_lib="Sorghum methylation-filtered library (LibID:
                     104)"
                     /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                     prepared from purified nuclei was randomly sheared,
                     end-repaired, size fractionated to enrich for the 0.5 to 5
                     kb fraction, ligated into HincII-digested pBCSK(-) vector
                     and electroporated into E. coli cells. This is a
                     methylation-filtered library."
ORIGIN

  Query Match             2.3%;  Score 21;  DB 12;  Length 743;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        375 AATCAGTACCGATTTGAAATT 395
              |||||||||||||||||||||
Db         77 AATCAGTACCGATTTGAAATT 57


RESULT 55
```

```
AG462380
LOCUS       AG462380                755 bp    DNA     linear   GSS 22-DEC-2004
DEFINITION  Mus musculus molossinus DNA, clone:MSMg01-350N23.T7, genomic survey
            sequence.
ACCESSION   AG462380
VERSION     AG462380.1  GI:48159636
KEYWORDS    GSS.
SOURCE      Mus musculus molossinus (Japanese wild mouse)
  ORGANISM  Mus musculus molossinus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T.,
            Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and
            Shiroishi,T.
  TITLE     Contribution of Asian mouse subspecies Mus musculus molossinus to
            genomic constitution of strain C57BL/6J, as defined by BAC-end
            sequence-SNP analysis
  JOURNAL   Genome Res. 14 (12), 2439-2447 (2004)
   PUBMED   15574823
REFERENCE   2  (bases 1 to 755)
  AUTHORS   Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
            (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the mouse BAC library MSMg01. For BAC
            library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
            Tsukuba Institude, Bio Resource Center,
            The Institute of Physical and Chemical Research (RIKEN) 3-1-1
            Koyadai, Tsukuba, 305-0074 Japan
            phone: 81-298-36-9189, fax: 81-298-36-9199
            e-mail: abe@rtc.riken.jp
            PRIMERS
            Sequencing : T7
            LIBRARY
            Vector     : pBACe3.6
            R.Site 1   : EcoRI
            R.Site 2   : EcoRI.
FEATURES             Location/Qualifiers
     source          1. .755
                     /organism="Mus musculus molossinus"
                     /mol_type="genomic DNA"
                     /sub_species="molossinus"
                     /db_xref="taxon:57486"
                     /clone="MSMg01-350N23.T7"
                     /sex="male"
                     /tissue_type="mixture of kidney and spleen"
                     /clone_lib="MSMg01 Mouse Male BAC Library"
ORIGIN

  Query Match             2.3%;  Score 21;  DB 14;  Length 755;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        280 ATCTTAAGGGAACAGAAAGAA 300
              |||||||||||||||||||||
Db        102 ATCTTAAGGGAACAGAAAGAA 122


RESULT 56
CC698019/c
LOCUS       CC698019                762 bp    DNA     linear   GSS 19-JUN-2003
DEFINITION  OGWBY19TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0532D13,
            genomic survey sequence.
ACCESSION   CC698019
VERSION     CC698019.1  GI:32102795
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
            Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
  TITLE     Consortium for Maize Genomics
  JOURNAL   Unpublished (2002)
COMMENT     Other_GSSs: OGWBY19TV
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TR
            Class: methylation filtered.
FEATURES             Location/Qualifiers
     source          1. .762
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBMa0532D13"
                     /clone_lib="ZM_0.7_1.5_KB"
                     /note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
                     methylation filtered genomic DNA library"
ORIGIN

  Query Match             2.3%;  Score 21;  DB 12;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         87 TACTCCTGAAGAAGATGACAT 107
              |||||||||||||||||||||
Db        308 TACTCCTGAAGAAGATGACAT 288


RESULT 57
CG122646
LOCUS       CG122646                803 bp    DNA     linear   GSS 20-AUG-2003
DEFINITION  PUIMH25TB ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0615F02,
            genomic survey sequence.
ACCESSION   CG122646
VERSION     CG122646.1  GI:34006083
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 803)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
  TITLE     Maize Genomics Consortium
  JOURNAL   Unpublished (2003)
COMMENT     Other_GSSs: PUIMH25TD
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TR
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .803
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
```

```
                     /clone="ZMMBTa0615F02"
                     /clone_lib="ZM_0.6_1.0_KB"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
                     CoT selected genomic DNA library"
ORIGIN

  Query Match             2.3%;  Score 21;  DB 12;  Length 803;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         87 TACTCCTGAAGAAGATGACAT 107
              |||||||||||||||||||||
Db        252 TACTCCTGAAGAAGATGACAT 272


RESULT 58
CG134486/c
LOCUS       CG134486                837 bp    DNA     linear   GSS 21-AUG-2003
DEFINITION  PUFSJ61TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0722K02,
            genomic survey sequence.
ACCESSION   CG134486
VERSION     CG134486.1  GI:34021933
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 837)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
  TITLE     Maize Genomics Consortium
  JOURNAL   Unpublished (2003)
COMMENT     Other_GSSs: PUFSJ61TB
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .837
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBTa0722K02"
                     /clone_lib="ZM_0.6_1.0_KB"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
                     CoT selected genomic DNA library"
ORIGIN

  Query Match             2.3%;  Score 21;  DB 12;  Length 837;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        375 AATCAGTACCGATTTGAAATT 395
              |||||||||||||||||||||
Db        401 AATCAGTACCGATTTGAAATT 381


RESULT 59
CC927699/c
LOCUS       CC927699                853 bp    DNA     linear   GSS 11-AUG-2003
DEFINITION  ZMMBBc0532M21r ZMMBBc Zea mays genomic clone ZMMBBc0532M21 3',
            genomic survey sequence.
ACCESSION   CC927699
VERSION     CC927699.1  GI:33578797
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 853)
  AUTHORS   Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
            Rouzard,K., Fuks,G., Yu,Y., Wing,R. and Messing,J.
  TITLE     Sequencing of the maize genome at PGIR (2003b)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Bharti,A.K.
            Dr.Joachim Messing's lab
            The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
            University
            190 Frelinghuysen Road, Piscataway, NJ 08854, USA
            Tel: 732 445 3801
            Fax: 732 445 5735
            Email: bharti@waksman.rutgers.edu
            Seq primer: SP6
            Class: BAC ends
            High quality sequence start: 431.
FEATURES             Location/Qualifiers
     source          1. .853
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /cultivar="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBBc0532M21"
                     /lab_host="E. coli DH10B"
                     /clone_lib="ZMMBBc"
                     /note="Vector: pTARBAC1.3; Site_1: BamHI; Site_2: BamHI"
ORIGIN

  Query Match             2.3%;  Score 21;  DB 12;  Length 853;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        642 GGACCCACCCAAGAACCTGCA 662
              |||||||||||||||||||||
Db         86 GGACCCACCCAAGAACCTGCA 66


RESULT 60
BF241716/c
LOCUS       BF241716                895 bp    mRNA    linear   EST 14-NOV-2000
DEFINITION  601879850F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108381 5',
            mRNA sequence.
ACCESSION   BF241716
VERSION     BF241716.1  GI:11155642
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 895)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: CLONETECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM991  row: d  column: 14
            High quality sequence stop: 588.
FEATURES             Location/Qualifiers
     source          1. .895
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
```

```
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4108381"
                     /tissue_type="from acute myelogenous leukemia"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_55"
                     /note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
                     Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI
                     (ggccattatggcc); Double-stranded cDNA was prepared from
                     cell line RNA.  5' and 3' adaptors were used in cloning as
                     follows: 5' adaptor sequence:  5'-CACGGCCATTATGGCC-3' and
                     3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).   Average insert size
                     1.65 kb (range 0.9-4.0 kb).  14/15 colonies contained
                     inserts by PCR. This library was enriched for full-length
                     clones and was constructed by Clontech  Laboratories (Palo
                     Alto, CA)."
ORIGIN

  Query Match             2.3%;  Score 21;  DB 7;  Length 895;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        527 GTGCCTGCCCGGCTGCCGAGG 547
              |||||||||||||||||||||
Db        813 GTGCCTGCCCGGCTGCCGAGG 793


RESULT 61
CG033595/c
LOCUS       CG033595                983 bp    DNA     linear   GSS 19-AUG-2003
DEFINITION  PUKDR51TB ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0795J06,
            genomic survey sequence.
ACCESSION   CG033595
VERSION     CG033595.1  GI:33905751
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 983)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
  TITLE     Maize Genomics Consortium
  JOURNAL   Unpublished (2003)
COMMENT     Other_GSSs: PUKDR51TD
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TR
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .983
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBTa0795J06"
                     /clone_lib="ZM_0.6_1.0_KB"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
                     CoT selected genomic DNA library"
ORIGIN

  Query Match             2.3%;  Score 21;  DB 12;  Length 983;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         87 TACTCCTGAAGAAGATGACAT 107
              |||||||||||||||||||||
Db        267 TACTCCTGAAGAAGATGACAT 247


RESULT 62
BZ782656
LOCUS       BZ782656                987 bp    DNA     linear   GSS 17-MAR-2003
DEFINITION  PUFDX77TB ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa297M10,
            genomic survey sequence.
ACCESSION   BZ782656
VERSION     BZ782656.1  GI:28976253
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
  TITLE     Maize Genomics Consortium
  JOURNAL   Unpublished (2003)
COMMENT     Other_GSSs: PUFDX77TD
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TR
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBTa297M10"
                     /clone_lib="ZM_0.6_1.0_KB"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
                     CoT selected genomic DNA library"
ORIGIN

  Query Match             2.3%;  Score 21;  DB 12;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         87 TACTCCTGAAGAAGATGACAT 107
              |||||||||||||||||||||
Db        463 TACTCCTGAAGAAGATGACAT 483


RESULT 63
BZ782662/c
LOCUS       BZ782662                999 bp    DNA     linear   GSS 17-MAR-2003
DEFINITION  PUFDX77TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa297M10,
            genomic survey sequence.
ACCESSION   BZ782662
VERSION     BZ782662.1  GI:28976259
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 999)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
  TITLE     Maize Genomics Consortium
  JOURNAL   Unpublished (2003)
COMMENT     Other_GSSs: PUFDX77TB
```

```
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TF
            Class: sheared ends.
FEATURES              Location/Qualifiers
     source           1. .999
                      /organism="Zea mays"
                      /mol_type="genomic DNA"
                      /strain="B73"
                      /db_xref="taxon:4577"
                      /clone="ZMMBTa297M10"
                      /clone_lib="ZM_0.6_1.0_KB"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
                      CoT selected genomic DNA library"
ORIGIN

  Query Match             2.3%;  Score 21;  DB 12;  Length 999;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         87 TACTCCTGAAGAAGATGACAT 107
              |||||||||||||||||||||
Db        686 TACTCCTGAAGAAGATGACAT 666


RESULT 64
CE034167
LOCUS       CE034167                366 bp    DNA     linear   GSS 24-SEP-2003
DEFINITION  tigr-gss-dog-17000348379744 Dog Library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION   CE034167
VERSION     CE034167.1  GI:35059603
KEYWORDS    GSS.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 366)
  AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
            Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
            Venter,J.C.
  TITLE     The dog genome: survey sequencing and comparative analysis
  JOURNAL   Science 301 (5641), 1898-1903 (2003)
   PUBMED   14512627
COMMENT     Contact: Kirkness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirknes@tigr.org
            Class: shotgun.
FEATURES              Location/Qualifiers
     source           1. .366
                      /organism="Canis familiaris"
                      /mol_type="genomic DNA"
                      /strain="Standard Poodle"
                      /db_xref="taxon:9615"
                      /clone_lib="Dog Library"
                      /note="Site_1: BstXI; Libraries were prepared from
                      peripheral blood"
ORIGIN

  Query Match             2.2%;  Score 20;  DB 12;  Length 366;
  Best Local Similarity   100.0%;  Pred. No. 87;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        248 ACAAAAAGGAAGATGGAATT 267
              ||||||||||||||||||||
Db         58 ACAAAAAGGAAGATGGAATT 77


RESULT 65
DN901347
LOCUS       DN901347                376 bp    mRNA    linear   EST 25-APR-2005
DEFINITION  naq18f07.y1 Zebrafish retina. Unnormalized (naq) Danio rerio cDNA
            clone naq18f07 5', mRNA sequence.
ACCESSION   DN901347
VERSION     DN901347.1  GI:62886110
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 376)
  AUTHORS   Wistow,G.
  TITLE     NEIBank analysis of Zebrafish retina
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Wistow G
            Section on Molecular Structure and Function
            National Eye Institute
            6/331, NIH, Bethesda, MD 20892-2740, USA
            Tel: 301 402 3452
            Fax: 301 496 0078
            Email: graeme@helix.nih.gov
            Plate: 18  row: f  column: 07
            Seq primer: Universal M13 Reverse.
FEATURES              Location/Qualifiers
     source           1. .376
                      /organism="Danio rerio"
                      /mol_type="mRNA"
                      /db_xref="taxon:7955"
                      /clone="naq18f07"
                      /tissue_type="Retina"
                      /dev_stage="Adult"
                      /lab_host="EMDH10B"
                      /clone_lib="Zebrafish retina. Unnormalized (naq)"
                      /note="Organ: Eye; Vector: pCMVSport6; RNA was extracted
                      from Zebrafish retina tissue. A directionally cloned cDNA
                      library in the pCMVSPORT6 vector (Invitrogen) was
                      constructed at Bioserve Biotechnology (Laurel MD)
                      essentially following the protocols of the SuperScript
                      Plasmid System, full details of which are contained in the
                      manufacturer's Instruction manual
                      (http://www.lifetech.com/). First strand synthesis was
                      carried out using a Not I primer-adapter
                      [5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)15-3']. cDNA was
                      cloned in Not I/Sal I sites. EST analysis was performed at
                      the NIH Intramural Sequencing Center (NISC). Analyzed data
                      available through http://neibank.nei.nih.gov."
ORIGIN

  Query Match             2.2%;  Score 20;  DB 9;  Length 376;
  Best Local Similarity   100.0%;  Pred. No. 87;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        776 AGAACAACAGAGAAAAGAAA 795
              ||||||||||||||||||||
Db         72 AGAACAACAGAGAAAAGAAA 91


RESULT 66
BH772784
LOCUS       BH772784                454 bp    DNA     linear   GSS 01-AUG-2002
DEFINITION  4CTF CTSSR-PCRlibrary Biomphalaria glabrata genomic clone 4-CTF,
            genomic survey sequence.
ACCESSION   BH772784
VERSION     BH772784.1  GI:22038714
KEYWORDS    GSS.
SOURCE      Biomphalaria glabrata
```

```
  ORGANISM  Biomphalaria glabrata
            Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata;
            Basommatophora; Lymnaeoidea; Planorbidae; Biomphalaria.
REFERENCE   1  (bases 1 to 454)
  AUTHORS   Caldeira,R.L., Carvalho,O.S., Lage,R.C.G., Cardoso,P.C.M. and
            Oliveira,G.C.
  TITLE     Sequence Characterization of Biomphalaria glabrata Simple Sequence
            Repeat Anchored Polymerase Chain Reaction Amplification Products
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Oliveira GC
            Laboratorio de Parasitologia Celular e Molecular
            Centro de Pesquisas Rene Rachou - FIOCRUZ
            Av. Augusto de Lima 1715, Barro Preto, Belo Horizonte, MG,
            30190-002, Brazil
            Tel: 55 31 32953566
            Fax: 55 31 32953115
            Email: oliveira@cpqrr.fiocruz.br
            PCR fragment amplified with CAA(CT)6.
            Seq primer: M13-Forward Universal
            Class: Random amplified microsatellites.
FEATURES             Location/Qualifiers
     source          1. .454
                     /organism="Biomphalaria glabrata"
                     /mol_type="genomic DNA"
                     /strain="Rene Rachou"
                     /db_xref="taxon:6526"
                     /clone="4-CTF"
                     /sex="hermaphrodite"
                     /dev_stage="Adult"
                     /clone_lib="CTSSR-PCRlibrary"
                     /note="The sequence was obtained by SSR-PCR amplification
                     using primer CAA(CT)6 for CT named clones or (CA)8RY for
                     CA named clones. The PCR products were cloned into the pCR
                     II vector (Invitrogen), selected on LB/amp plates and
                     sequenced in an ALF automated sequencer using the Thermo
                     Sequenase Kit (Amersham) using the universal reverse
                     primer."
ORIGIN

  Query Match             2.2%;  Score 20;  DB 11;  Length 454;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        782 ACAGAGAAAAGAAAGACAGA 801
              ||||||||||||||||||||
Db        404 ACAGAGAAAAGAAAGACAGA 423


RESULT 67
BM849607
LOCUS       BM849607                460 bp    mRNA    linear   EST 06-MAR-2002
DEFINITION  K-EST0129703 S21SNU520 Homo sapiens cDNA clone S21SNU520-38-F05 5',
            mRNA sequence.
ACCESSION   BM849607
VERSION     BM849607.1  GI:19206006
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 460)
  AUTHORS   Oh,J.H., Yang,J.O., Hahn,Y., Kim,M.R., Byun,S.S., Jeon,Y.J.,
            Kim,J.M., Song,K.S., Noh,S.M., Kim,S., Yoo,H.S., Kim,Y.S. and
            Kim,N.S.
  TITLE     Transcriptome analysis of human gastric cancer
  JOURNAL   Mamm. Genome 16 (12), 942-954 (2005)
   PUBMED   16341674
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 38  row: F  column: 05
            High quality sequence stop: 460.
FEATURES             Location/Qualifiers
     source          1. .460
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="S21SNU520-38-F05"
                     /sex="F"
                     /tissue_type="Stomach"
                     /cell_type="Floating aggregates"
                     /cell_line="SNU-520"
                     /lab_host="Top10F'"
                     /clone_lib="S21SNU520"
                     /note="Organ: Stomach; Vector: pTZ18RP1; Site_1: EcoRI;
                     Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tabacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including EcoR
                     I site by treatment of T4 RNA ligase and the first strand
                     cDNA was synthesized from oligo dT-selected mRNA by
                     priming with dT-tailed vector. The dT-tailed vector was
                     adjusted to have about 60nt. The cDNA vector was
                     circularized with E. coli DNA ligase after digestion of
                     EcoRI which site is also included in vector. An RNA strand
                     converted to a DNA strand by Okayama-Berg method. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library."
ORIGIN

  Query Match             2.2%;  Score 20;  DB 3;  Length 460;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        776 AGAACAACAGAGAAAAGAAA 795
              ||||||||||||||||||||
Db         65 AGAACAACAGAGAAAAGAAA 84


RESULT 68
DN504486/c
LOCUS       DN504486                467 bp    mRNA    linear   EST 10-MAR-2005
DEFINITION  HL010009000_F09_70_075 Equine lymphocyte cDNA Library Equus
            caballus cDNA clone HL010009000_F09_70_075, mRNA sequence.
ACCESSION   DN504486
VERSION     DN504486.1  GI:60714676
KEYWORDS    EST.
SOURCE      Equus caballus (horse)
  ORGANISM  Equus caballus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
REFERENCE   1  (bases 1 to 467)
  AUTHORS   Antczak,D.F.
  TITLE     Expressed sequence tags from a normalized equine lymphocyte cDNA
            library
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Antczak DF
            Baker Institute for Animal Health, College of Veterinary Medicine
            Cornell University
            Hungerford Hill Rd., Ithaca, NY 14853, USA
            Tel: 607.256.5633
            Fax: 607.256.5608
            Email: dfa1@cornell.edu
            High quality sequence stop: 467.
FEATURES             Location/Qualifiers
     source          1. .467
                     /organism="Equus caballus"
                     /mol_type="mRNA"
                     /strain="Thoroughbred & Standardbred breeds"
```

```
                     /db_xref="taxon:9796"
                     /clone="HL010009000_F09_70_075"
                     /tissue_type="Lymphocytes"
                     /dev_stage="Unstimulated [Tag-(polyA)TCGGA] & stimulated
                     in vitro with PWM [Tag-(polyA)TGCGA]"
                     /lab_host="DH12S E. coli cells (Invitrogen)"
                     /clone_lib="Equine lymphocyte cDNA Library"
                     /note="Vector: pGEM11Zf(+) (Promega); Site_1: EcoR1;
                     Site_2: Not1"
ORIGIN

  Query Match             2.2%;  Score 20;  DB 9;  Length 467;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        290 AACAGAAAGAATCCAAAAAT 309
              ||||||||||||||||||||
Db         79 AACAGAAAGAATCCAAAAAT 60


RESULT 69
BI983815
LOCUS       BI983815                479 bp    mRNA    linear   EST 24-OCT-2001
DEFINITION  fu08a02.x3 Campbell zebrafish ovary Danio rerio cDNA clone
            IMAGE:5304482 3', mRNA sequence.
ACCESSION   BI983815
VERSION     BI983815.1  GI:16374696
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 479)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
            Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library constructed by Library constructed by Invitrogen and
            donated by R. Campbell (Marine Biology Laboratory, Woods Hole, MA).
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: the I.M.A.G.E. Consortium/LLNL, send email to:
            info@image.llnl.gov
            Seq primer: T7 from Gibco
            High quality sequence stop: 417.
FEATURES             Location/Qualifiers
     source          1. .479
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:5304482"
                     /sex="female"
                     /dev_stage="4-5 months, 1 year and 2 years"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="Campbell zebrafish ovary"
                     /note="Organ: ovary(pooled); Vector: pCMV-SPORT6; Site_1:
                     NotI; Site_2: SalI; Whole ovaries collected from zebrafish
                     aged 4-5 months, 1 year and 2 years.  Oligo-dT primed,
                     directionally cloned.  Average insert size 2 kb.  Library
                     constructed by Invitrogen and donated by R. Campbell
                     (Marine Biology Laboratory, Woods Hole, MA)."
ORIGIN

  Query Match             2.2%;  Score 20;  DB 2;  Length 479;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        776 AGAACAACAGAGAAAAGAAA 795
              ||||||||||||||||||||
Db        188 AGAACAACAGAGAAAAGAAA 207


RESULT 70
BH772785/c
LOCUS       BH772785                486 bp    DNA     linear   GSS 01-AUG-2002
DEFINITION  4CTr CTSSR-PCRlibrary Biomphalaria glabrata genomic clone 4-CTr,
            genomic survey sequence.
ACCESSION   BH772785
VERSION     BH772785.1  GI:22038715
KEYWORDS    GSS.
SOURCE      Biomphalaria glabrata
  ORGANISM  Biomphalaria glabrata
            Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata;
            Basommatophora; Lymnaeoidea; Planorbidae; Biomphalaria.
REFERENCE   1  (bases 1 to 486)
  AUTHORS   Caldeira,R.L., Carvalho,O.S., Lage,R.C.G., Cardoso,P.C.M. and
            Oliveira,G.C.
  TITLE     Sequence Characterization of Biomphalaria glabrata Simple Sequence
            Repeat Anchored Polymerase Chain Reaction Amplification Products
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Oliveira GC
            Laboratorio de Parasitologia Celular e Molecular
            Centro de Pesquisas Rene Rachou - FIOCRUZ
            Av. Augusto de Lima 1715, Barro Preto, Belo Horizonte, MG,
            30190-002, Brazil
            Tel: 55 31 32953566
            Fax: 55 31 32953115
            Email: oliveira@cpqrr.fiocruz.br
            PCR fragment amplified with CAA(CT)6.
            Seq primer: M13-Forward Universal
            Class: Random amplified microsatellites.
FEATURES             Location/Qualifiers
     source          1. .486
                     /organism="Biomphalaria glabrata"
                     /mol_type="genomic DNA"
                     /strain="Rene Rachou"
                     /db_xref="taxon:6526"
                     /clone="4-CTr"
                     /sex="hermaphrodite"
                     /dev_stage="Adult"
                     /clone_lib="CTSSR-PCRlibrary"
                     /note="The sequence was obtained by SSR-PCR amplification
                     using primer CAA(CT)6 for CT named clones or (CA)8RY for
                     CA named clones. The PCR products were cloned into the pCR
                     II vector (Invitrogen), selected on LB/amp plates and
                     sequenced in an ALF automated sequencer using the Thermo
                     Sequenase Kit (Amersham) using the universal reverse
                     primer."
ORIGIN

  Query Match             2.2%;  Score 20;  DB 11;  Length 486;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        782 ACAGAGAAAAGAAAGACAGA 801
              ||||||||||||||||||||
Db        201 ACAGAGAAAAGAAAGACAGA 182


RESULT 71
AI292392
LOCUS       AI292392                488 bp    mRNA    linear   EST 01-DEC-1998
DEFINITION  NYZ036 Appel-Eisen zebrafish embryo 15-19 hr Danio rerio cDNA clone
            ZAE24 3', mRNA sequence.
ACCESSION   AI292392
VERSION     AI292392.1  GI:3941779
```

```
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 488)
  AUTHORS   Gates,M.A., Cardozo,T., Tobin,T., Egan,E., Sirotkin,H., Schier,A.F.
            and Talbot,W.S.
  TITLE     NYU zebrafish embryo EST project
  JOURNAL   Unpublished (1998)
COMMENT     Contact: William S. Talbot
            Skirball Institute, New York University School of Medicine
            540 First Avenue, New York, NY 10016, USA
            Fax: 212 263 7760
            Email: talbot@saturn.med.nyu.edu
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .488
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="ZAE24"
                     /sex="mixed"
                     /tissue_type="pooled 15-19 hr zebrafish embryos"
                     /clone_lib="Appel-Eisen zebrafish embryo 15-19 hr"
                     /note="Vector: pBluescript SK (-); Site_1: EcoRI; Site_2:
                     XhoI; Library was constructed by Bruce Appel and Judith
                     Eisen in Stratagene Uni-Zap XR lambda vector with Zap-cDNA
                     synthesis kit: EcoRI linkers were added to 5' ends and
                     XhoI linkers were added to 3' ends and resulting cDNAs
                     were ligated into Uni-Zap XR lambda vector. In vivo mass
                     excision was used to generate cDNAs in pBluescript SK."
ORIGIN

  Query Match             2.2%;  Score 20;  DB 1;  Length 488;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        776 AGAACAACAGAGAAAAGAAA 795
              ||||||||||||||||||||
Db        149 AGAACAACAGAGAAAAGAAA 168


RESULT 72
BI476340
LOCUS       BI476340                 496 bp    mRNA    linear   EST 26-JUL-2002
DEFINITION  fq26h04.x3 zebrafish adult brain Danio rerio cDNA clone
            IMAGE:4832862 3', mRNA sequence.
ACCESSION   BI476340
VERSION     BI476340.1  GI:15309207
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 496)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
            Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library Preparation: John Ngai. cDNA Library Arrayed by:
            Matthew Clark. DNA Sequencing by: Washington University Genome
            Sequencing Center Clone distribution: Genome Systems, St. Louis,
            Missouri (web address: www.genomesystems.com) (email contact:
            info@genomesystems.com) and Research Genetics, Huntsville, Alabama
            (web address: www.resgen.com) (email contact: info@resgen.com) and
            RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
            www.rzpd.de)
            Seq primer: -40UP
            High quality sequence stop: 447.
FEATURES             Location/Qualifiers
     source          1. .496
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:4832862"
                     /sex="mixed male and female"
                     /tissue_type="brain"
                     /dev_stage="adult"
                     /lab_host="E. coli DH10B"
                     /clone_lib="zebrafish adult brain"
                     /note="Vector: pZIPLOX; Site_1: NotI; Site_2: SalI;
                     Original library was constructed in lambdaZIPLOX.  Mass
                     excision of the cDNA library was performed to yield
                     pZIPLOX plasmids. Insert check was done in original
                     library."
ORIGIN

  Query Match             2.2%;  Score 20;  DB 2;  Length 496;
  Best Local Similarity   100.0%;  Pred. No. 90;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        776 AGAACAACAGAGAAAAGAAA 795
              ||||||||||||||||||||
Db         84 AGAACAACAGAGAAAAGAAA 103


RESULT 73
BI981239
LOCUS       BI981239                 504 bp    mRNA    linear   EST 26-JUL-2002
DEFINITION  fu41h06.x1 zebrafish adult brain Danio rerio cDNA clone
            IMAGE:5332091 3', mRNA sequence.
ACCESSION   BI981239
VERSION     BI981239.1  GI:16369655
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 504)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
            Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library Preparation: John Ngai. cDNA Library Arrayed by:
            Matthew Clark. DNA Sequencing by: Washington University Genome
            Sequencing Center Clone distribution: Genome Systems, St. Louis,
            Missouri (web address: www.genomesystems.com) (email contact:
            info@genomesystems.com) and Research Genetics, Huntsville, Alabama
            (web address: www.resgen.com) (email contact: info@resgen.com) and
            RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
            www.rzpd.de)
            Seq primer: -40UP
```

```
            High quality sequence stop: 444.
FEATURES             Location/Qualifiers
     source          1. .504
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:5332091"
                     /sex="mixed male and female"
                     /tissue_type="brain"
                     /dev_stage="adult"
                     /lab_host="E. coli DH10B"
                     /clone_lib="zebrafish adult brain"
                     /note="Vector: pZIPLOX; Site_1: NotI; Site_2: SalI;
                     Original library was constructed in lambdaZIPLOX.  Mass
                     excision of the cDNA library was performed to yield
                     pZIPLOX plasmids. Insert check was done in original
                     library."
ORIGIN

  Query Match             2.2%;  Score 20;  DB 2;  Length 504;
  Best Local Similarity   100.0%;  Pred. No. 90;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        776 AGAACAACAGAGAAAAGAAA 795
              ||||||||||||||||||||
Db         83 AGAACAACAGAGAAAAGAAA 102


RESULT 74
CB179502
LOCUS       CB179502                 515 bp    mRNA    linear   EST 31-JAN-2003
DEFINITION  EST0595 Zea mays sperm cell cDNA library Zea mays cDNA clone
            Zmsp3098 5' similar to putative polyprotein, mRNA sequence.
ACCESSION   CB179502
VERSION     CB179502.1  GI:28187892
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 515)
  AUTHORS   Engel,M.L., Chaboud,A., Dumas,C. and McCormick,S.
  TITLE     Sperm cells of Zea mays have a complex complement of mRNAs
  JOURNAL   Plant J. 34 (5), 697-707 (2003)
   PUBMED   12787250
COMMENT     Contact: McCormick, S.
            Plant Gene Expression Center
            USDA/ARS
            800 Buchanan St. Albany, CA 94710, USA
            Tel: 510 559 5906
            Fax: 510 559 5678
            Email: sheilamc@nature.berkeley.edu.
FEATURES             Location/Qualifiers
     source          1. .515
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="A188"
                     /db_xref="taxon:4577"
                     /clone="Zmsp3098"
                     /cell_type="sperm"
                     /clone_lib="Zea mays sperm cell cDNA library"
                     /note="Vector: Clontech Triplex2; RNA was isolated from
                     fluorescent-activated cell sorted sperm cells. A cDNA
                     library was constructed by oligo dT priming using the
                     Clontech SMART cDNA synthesis kit. The cDNAs were
                     directionally cloned."
ORIGIN

  Query Match             2.2%;  Score 20;  DB 4;  Length 515;
  Best Local Similarity   100.0%;  Pred. No. 90;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        309 TAAGATCTTTCTAAAATGTG 328
              ||||||||||||||||||||
Db        182 TAAGATCTTTCTAAAATGTG 201


RESULT 75
BM270069
LOCUS       BM270069                 520 bp    mRNA    linear   EST 08-JUL-2004
DEFINITION  sak24b12.y1 Gm-c1075 Glycine max cDNA clone SOYBEAN CLONE ID:
            Gm-c1075-3912 5' similar to TR:O22892 O22892 T2P4.22 PROTEIN. ;,
            mRNA sequence.
ACCESSION   BM270069
VERSION     BM270069.1  GI:17963327
KEYWORDS    EST.
SOURCE      Glycine max (soybean)
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 520)
  AUTHORS   Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
            Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
            Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
            Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
            Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
            McCann,R., Waterston,R. and Wilson,R.
  TITLE     Public Soybean EST Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            When it has been determined, an EST from the other end of this
            clone is listed in the 'Other ESTs on clone' field. This clone is
            available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
            57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
            Seq primer: -40RP from Gibco
            High quality sequence stop: 435.
FEATURES             Location/Qualifiers
     source          1. .520
                     /organism="Glycine max"
                     /mol_type="mRNA"
                     /cultivar="Jack"
                     /db_xref="taxon:3847"
                     /clone="SOYBEAN CLONE ID: Gm-c1075-3912"
                     /tissue_type="differentiating somatic embryos cultered on
                     MSM6AC"
                     /lab_host="DH10B"
                     /clone_lib="Gm-c1075"
                     /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
                     XhoI; The cDNA library was constructed from mRNA isolated
                     from differentiating  somatic embryos cultered on MSM6AC.
                     The library was prepared using the  Stratagene pBluescript
                     II SK(+) library construction kit. Complementary  DNA was
                     synthesized from mRNA using a primer consisting of a
                     poly(dT)  sequence with an XhoI restriction site. EcoRI
                     adaptors were ligated to the  blunt-ended cDNA fragments
                     followed by XhoI digestion. The cDNA fragments  were
                     directionally cloned into the EcoRI-XhoI restriction site
                     of the  pBluescript vector. The ligated cDNA fragments
                     were transformed into E.coli ElectroMax DH10B host cells.
                     Tissue culture and library construction were performed by
                     Franooise Thibaud-Nissen and Anu Khana (Lila Vodkin lab,
                     University of Illinois)."
ORIGIN

  Query Match             2.2%;  Score 20;  DB 2;  Length 520;
  Best Local Similarity   100.0%;  Pred. No. 90;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy        775 AAGAACAACAGAGAAAAGAA 794
              ||||||||||||||||||||
Db         35 AAGAACAACAGAGAAAAGAA 54


RESULT 76
BQ777940
LOCUS       BQ777940                526 bp    mRNA    linear   EST 26-JUL-2002
DEFINITION  il39a02.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6032162 5',
            mRNA sequence.
ACCESSION   BQ777940
VERSION     BQ777940.1  GI:21986412
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 526)
  AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
            Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
            Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
            Williams,T., Jackson,Y. and Bowers,Y.
  TITLE     Endocrine Pancreas Consortium
  JOURNAL   Unpublished (2000)
COMMENT     Other_ESTs: il39a02.x1
            Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
            Washington University Genome Sequencing Center For information on
            obtaining a clone please contact: Dr. Hiroshi Inoue
            (hinoue@im.wustl.edu)
            Seq primer: -40RP from Gibco
            High quality sequence stop: 412.
FEATURES             Location/Qualifiers
     source          1. .526
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6032162"
                     /tissue_type="Purified pancreatic islet"
                     /lab_host="DH10B"
                     /clone_lib="HR85 islet"
                     /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
                     NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
                     Size-selected on agarose gel. Average insert size ~1kb. 5'
                     XhoI site was destroyed after directional cloning.
                     Amplified once. Contact information: Hiroshi Inoue, MD,
                     Metabolism Div. (Alan Permutt Lab), Washington University
                     School of Medicine, Box 8127, 660 South Euclid Ave., St.
                     Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
                     314-362-1916, Fax: 314-747-2692."
ORIGIN

  Query Match             2.2%;  Score 20;  DB 3;  Length 526;
  Best Local Similarity   100.0%;  Pred. No. 90;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        776 AGAACAACAGAGAAAAGAAA 795
              ||||||||||||||||||||
Db        109 AGAACAACAGAGAAAAGAAA 128


RESULT 77
CW070565/c
LOCUS       CW070565                528 bp    DNA     linear   GSS 28-OCT-2004
DEFINITION  104_321_10526839_5_30098 Sorghum methylation filtered library
            (LibID: 104) Sorghum bicolor genomic clone 10526839, genomic survey
            sequence.
ACCESSION   CW070565
VERSION     CW070565.1  GI:54747295
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 528)
  AUTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
            Martienssen,R.A.
  TITLE     Sorghum genome sequencing by methylation filtration
  JOURNAL   PLoS Biol. 3 (1), e13 (2005)
  PUBMED    15660154
COMMENT     Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: 321  row: n  column: 05
            Seq primer: SKPrimer Reverse
            Class: methylation filtered
            High quality sequence stop: 528.
FEATURES             Location/Qualifiers
     source          1. .528
                     /organism="Sorghum bicolor"
                     /mol_type="genomic DNA"
                     /cultivar="ATx623"
                     /db_xref="taxon:4558"
                     /clone="10526839"
                     /clone_lib="Sorghum methylation filtered library (LibID:
                     104)"
                     /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                     prepared from purified nuclei was randomly sheared,
                     end-repaired, size fractionated to enrich for the 0.5 to 5
                     kb fraction, ligated into HincII-digested pBCSK(-) vector
                     and electroporated into E. coli cells. This is a
                     methylation filtered library."
ORIGIN

  Query Match             2.2%;  Score 20;  DB 13;  Length 528;
  Best Local Similarity   100.0%;  Pred. No. 90;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        239 TCCTGATACACAAAAAGGAA 258
              ||||||||||||||||||||
Db        388 TCCTGATACACAAAAAGGAA 369


RESULT 78
CK902268
LOCUS       CK902268                535 bp    mRNA    linear   EST 11-MAR-2004
DEFINITION  il39a02.x5 HR85 islet Homo sapiens cDNA clone IMAGE:6032162 3',
            mRNA sequence.
ACCESSION   CK902268
VERSION     CK902268.1  GI:45363799
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 535)
  AUTHORS   Melton,D., Meadows,A., Clifton,S., Hillier,L., Marra,M., Pape,D.,
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            Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B.,
            Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M.,
            McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and
            Bowers,Y.
  TITLE     WashU-Harvard Pancreas EST Project
  JOURNAL   Unpublished (2000)
COMMENT     Other_ESTs: il39a02.y1
            Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            This read is a 3' RESEQUENCE of a previously sequenced pancreas
            clone
            Good hit to opposite strand read. . .wrong orientation BUT PASSED FOR
            MOUSE-PANCREAS VERIFICATION
            Seq primer: -40RP from Gibco
            High quality sequence stop: 535.
FEATURES             Location/Qualifiers
     source          1. .535
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6032162"
                     /tissue_type="Purified pancreatic islet"
                     /lab_host="DH10B"
                     /clone_lib="HR85 islet"
                     /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
                     NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
                     Size-selected on agarose gel. Average insert size ~1kb. 5'
                     XhoI site was destroyed after directional cloning.
                     Amplified once. Contact information: Hiroshi Inoue, MD,
                     Metabolism Div. (Alan Permutt Lab), Washington University
                     School of Medicine, Box 8127, 660 South Euclid Ave., St.
                     Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
                     314-362-1916, Fax: 314-747-2692."
ORIGIN

  Query Match             2.2%;  Score 20;  DB 5;  Length 535;
  Best Local Similarity   100.0%;  Pred. No. 90;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        776 AGAACAACAGAGAAAAGAAA 795
              ||||||||||||||||||||
Db        108 AGAACAACAGAGAAAAGAAA 127


RESULT 79
AG826456
LOCUS       AG826456                545 bp    DNA     linear   GSS 01-DEC-2004
DEFINITION  Sus scrofa DNA, BAC clone 0732F12, shotgun sequence of subclone
            0732F12S001E11, read with M13Reverse primer, genomic survey
            sequence.
ACCESSION   AG826456
VERSION     AG826456.1  GI:56372954
KEYWORDS    GSS.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1
  AUTHORS   Tanaka,M., Suzuki,K., Morozumi,T., Kobayashi,E., Matsumoto,T.,
            Domukai,M., Eguchi-Ogawa,T., Shinkai,H., Awata,T. and Uenishi,H.
  TITLE     Genomic structure of the distal extended-class II region in swine
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 545)
  AUTHORS   Uenishi,H., Tanaka,M. and Awata,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-OCT-2004) Hirohide Uenishi, National Institute of
            Agrobiological Sciences, Animal Genome Laboratory, Genome Research
            Department; 2 Ikenodai, Tsukuba, Ibaraki, 305-8602, Japan
            (E-mail:huenishi@affrc.go.jp, Tel:81-29-838-8627,
            Fax:81-29-838-8627)
COMMENT     Correspondence to:
            Hirohide Uenishi
            Animal Genome Laboratory, Genome Research Department, National
            Institute of Agrobiological Sciences
            2 Ikenodai, Tsukuba, Ibaraki 305-8602, JAPAN
            Tel: +81-29-838-8627
            Fax: +81-29-838-8627
            e-mail: huenishi@affrc.go.jp
            Sequencing was carried out in Animal Genome Research Program
            (Japan)
            by National Institute of Agrobiological Sciences
            and STAFF-Institute.
            Subclones of BAC clones were constructed with pUC18 vector.
            Basecalling was performed by Phred 0.020425.c.
            Vector sequences were eliminated by crossmatch version 0.990319.
            Low quality bases were trimmed based on the quality values with the
            aid of the trim_alt option of Phred.
FEATURES             Location/Qualifiers
     source          1. .545
                     /organism="Sus scrofa"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9823"
                     /clone="0732F12"
                     /sub_clone="0732F12S001E11"
                     /clone_lib="Sus scrofa shotgun BAC sequence"
ORIGIN

  Query Match             2.2%;  Score 20;  DB 14;  Length 545;
  Best Local Similarity   100.0%;  Pred. No. 90;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        429 CCAAGAGGTGACTTGTGGAG 448
              ||||||||||||||||||||
Db        447 CCAAGAGGTGACTTGTGGAG 466


RESULT 80
AG826409/c
LOCUS       AG826409                551 bp    DNA     linear   GSS 01-DEC-2004
DEFINITION  Sus scrofa DNA, BAC clone 0732F12, shotgun sequence of subclone
            0732F12S001E11, read with -21M13 primer, genomic survey sequence.
ACCESSION   AG826409
VERSION     AG826409.1  GI:56372907
KEYWORDS    GSS.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1
  AUTHORS   Tanaka,M., Suzuki,K., Morozumi,T., Kobayashi,E., Matsumoto,T.,
            Domukai,M., Eguchi-Ogawa,T., Shinkai,H., Awata,T. and Uenishi,H.
  TITLE     Genomic structure of the distal extended-class II region in swine
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 551)
  AUTHORS   Uenishi,H., Tanaka,M. and Awata,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-OCT-2004) Hirohide Uenishi, National Institute of
            Agrobiological Sciences, Animal Genome Laboratory, Genome Research
            Department; 2 Ikenodai, Tsukuba, Ibaraki, 305-8602, Japan
            (E-mail:huenishi@affrc.go.jp, Tel:81-29-838-8627,
            Fax:81-29-838-8627)
COMMENT     Correspondence to:
            Hirohide Uenishi
            Animal Genome Laboratory, Genome Research Department, National
            Institute of Agrobiological Sciences
            2 Ikenodai, Tsukuba, Ibaraki 305-8602, JAPAN
            Tel: +81-29-838-8627
            Fax: +81-29-838-8627
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            e-mail: huenishi@affrc.go.jp
            Sequencing was carried out in Animal Genome Research Program
            (Japan)
            by National Institute of Agrobiological Sciences
            and STAFF-Institute.
            Subclones of BAC clones were constructed with pUC18 vector.
            Basecalling was performed by Phred 0.020425.c.
            Vector sequences were eliminated by crossmatch version 0.990319.
            Low quality bases were trimmed based on the quality values with the
            aid of the trim_alt option of Phred.
FEATURES              Location/Qualifiers
     source           1. .551
                      /organism="Sus scrofa"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9823"
                      /clone="0732F12"
                      /sub_clone="0732F12S001E11"
                      /clone_lib="Sus scrofa shotgun BAC sequence"
ORIGIN

  Query Match             2.2%;  Score 20;  DB 14;  Length 551;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        429 CCAAGAGGTGACTTGTGGAG 448
              ||||||||||||||||||||
Db         99 CCAAGAGGTGACTTGTGGAG 80


RESULT 81
CO854235/c
LOCUS       CO854235                555 bp    mRNA    linear   EST 21-NOV-2004
DEFINITION  LM_SH5_004998 Locusta migratoria solitarious phase's head cDNA
            library Locusta migratoria cDNA, mRNA sequence.
ACCESSION   CO854235
VERSION     CO854235.1  GI:55914042
KEYWORDS    EST.
SOURCE      Locusta migratoria (migratory locust)
  ORGANISM  Locusta migratoria
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
            Acridoidea; Acrididae; Oedipodinae; Locusta.
REFERENCE   1  (bases 1 to 555)
  AUTHORS   Kang,L., Chen,X., Zhou,Y., Liu,B., Zheng,W., Li,R., Wang,J. and
            Yu,J.
  TITLE     The analysis of large-scale gene expression correlated to the phase
            changes of the migratory locust
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 101 (51), 17611-17615 (2004)
   PUBMED   15591108
COMMENT     Contact: Le Kang
            National Laboratory of Integrated Management of Insect Pests and
            Rodents
            Institute of zoology, Chinese Academy of Sciences
            25 Beisihuanxi Road, Haidian, Beijing, 100080, China
            Tel: 86-10-68597439
            Fax: 86-10-68597486
            Email: lkang@panda.ioz.ac.cn
            High quality sequence stop: 555.
FEATURES              Location/Qualifiers
     source           1. .555
                      /organism="Locusta migratoria"
                      /mol_type="mRNA"
                      /db_xref="taxon:7004"
                      /tissue_type="head"
                      /dev_stage="fifth-instar"
                      /clone_lib="Locusta migratoria solitarious phase's head
                      cDNA library"
ORIGIN

  Query Match             2.2%;  Score 20;  DB 8;  Length 555;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        608 CCAGCAGCTTCTTCATCAGG 627
              ||||||||||||||||||||
Db        362 CCAGCAGCTTCTTCATCAGG 343


RESULT 82
BI785024
LOCUS       BI785024                556 bp    mRNA    linear   EST 21-JUL-2004
DEFINITION  saf96h10.y3 Gm-c1079 Glycine max cDNA clone GENOME SYSTEMS CLONE
            ID: Gm-c1079-1915 5' similar to TR:O22892 O22892 T2P4.22 PROTEIN.
            ;, mRNA sequence.
ACCESSION   BI785024
VERSION     BI785024.1  GI:15812749
KEYWORDS    EST.
SOURCE      Glycine max (soybean)
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 556)
  AUTHORS   Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
            Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
            Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
            Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
            Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
            McCann,R., Waterston,R. and Wilson,R.
  TITLE     Public Soybean EST Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            When it has been determined, an EST from the other end of this
            clone is listed in the 'Other ESTs on clone' field. This clone is
            available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
            57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
            Seq primer: -40RP from Gibco
            High quality sequence stop: 421.
FEATURES              Location/Qualifiers
     source           1. .556
                      /organism="Glycine max"
                      /mol_type="mRNA"
                      /cultivar="Bragg"
                      /db_xref="taxon:3847"
                      /clone="GENOME SYSTEMS CLONE ID: Gm-c1079-1915"
                      /tissue_type="Roots of 8 day old 'Bragg' seedlings"
                      /dev_stage="8 days old"
                      /lab_host="DH10B"
                      /clone_lib="Gm-c1079"
                      /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
                      XhoI; The mRNA was isolated from roots of 8 day old
                      'Bragg' seedlings that were mock-infected 72 hours prior
                      to harvest. Dr. Gary Stacey generously donated the
                      tissue. The roots were flash-frozen in liquid nitrogen.
                      Stratagene's cDNA Synthesis Kit (catalog number 200401)
                      was used to synthesize the cDNA. First-strand synthesis
                      was performed with 5-methyl dCTP, hence the ligated cDNA
                      was hemimethylated. A modification of Stratagene's
                      first-strand synthesis primer was used. An 'anchor'
                      nucleotide (V=A, C, or G) was added to the 3' end of the
                      primer [GAGAGAGAGAGAGAGAGAGAACTAGTCTCGAG(T)18V] to anchor
                      the primer at the 5' end of the poly(A) tract. After
                      second-strand synthesis, the cDNA ends were filled in with
                      cloned Pfu DNA, ligated to EcoRI adapters and subsequently
                      phosphorylated. The cDNA was then precipitated and
                      redissolved in sterile, RNase-, DNase-free water. The XhoI
                      site within the first- strand synthesis primer was then
                      restricted by digestion with XhoI from Promega (40U/ul);
                      all XhoI sites in the cDNA would be protected by their
```

hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using Sephacryl S-500 High Resolution (Pharmacia Biotech) in a 2-mm diameter column and a bed volume of approximately 1ml. The column eluent was precipitated, redissolved, and ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+) vector that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene). This library was constucted in the laboratory of Dr. Paul Keim and Dr. Virginia H. Coryell at Northern Arizona University."
ORIGIN

Query Match 2.2%; Score 20; DB 2; Length 556;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 775 AAGAACAACAGAGAAAAGAA 794
||||||||||||||||||||
Db 160 AAGAACAACAGAGAAAAGAA 179

RESULT 83
AL956562
LOCUS AL956562 563 bp mRNA linear EST 04-DEC-2003
DEFINITION AL956562 XGC-gastrula Xenopus tropicalis cDNA clone TGas105e12 5', mRNA sequence.
ACCESSION AL956562
VERSION AL956562.2 GI:38706017
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 563)
AUTHORS Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
TITLE Sanger Xenopus tropicalis EST project 2001 (11_2003)
JOURNAL Unpublished (2003)
COMMENT On Nov 27, 2002 this sequence version replaced gi:25780157.
Contact: Taylor R
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TGas105e12.p1kSP6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
cDNA was oligo dT primed from 5ug of poly A+ RNA from stages 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end.
Vector: pCS107; Site_1: EcoRI; Site_2: NotI
Host: Escherichia coli XL1- blue.
FEATURES Location/Qualifiers
source 1. .563
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TGas105e12"
/dev_stage="gastrula (stages 10.5-12 mixed)"
/lab_host="Escherichia coli XL1-blue"
/clone_lib="XGC-gastrula"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from stages 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

Query Match 2.2%; Score 20; DB 1; Length 563;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 184 GATGCTGGCCAGTATACCTG 203
||||||||||||||||||||
Db 246 GATGCTGGCCAGTATACCTG 265

RESULT 84
BJ030774
LOCUS BJ030774 564 bp mRNA linear EST 26-SEP-2003
DEFINITION BJ030774 NIBB Mochii normalized Xenopus neurula library Xenopus laevis cDNA clone XL005c01 5', mRNA sequence.
ACCESSION BJ030774
VERSION BJ030774.1 GI:17377868
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Xenopus.
REFERENCE 1 (bases 1 to 564)
AUTHORS Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara,Y.
TITLE Expressed genes in X. laevis embryo
JOURNAL Unpublished (2001)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
The information of this clone is available through the following URL.
http://xenopus.nibb.ac.jp.
FEATURES Location/Qualifiers
source 1. .564
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL005c01"
/tissue_type="whole embryo"
/dev_stage="stage 15"
/clone_lib="NIBB Mochii normalized Xenopus neurula library"
ORIGIN

Query Match 2.2%; Score 20; DB 2; Length 564;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 184 GATGCTGGCCAGTATACCTG 203
||||||||||||||||||||
Db 178 GATGCTGGCCAGTATACCTG 197

RESULT 85
AI666909
LOCUS AI666909 570 bp mRNA linear EST 08-JUN-1999
DEFINITION fd16d08.x1 Sugano Kawakami zebrafish DRA Danio rerio cDNA clone IMAGE:2351727 3', mRNA sequence.
ACCESSION AI666909
VERSION AI666909.1 GI:4805265
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 570)
AUTHORS Sugano,S., Kawakami,K., Johnson,S., Li,F., Marra,M., Eddy,S., Hillier,L., Clifton,S., Allen,M., Gibbons,M., Jost,S., Kucaba,T., Martin,J., Pape,D., Steptoe,M., Underwood,K., Theising,B., Ritter,E., Bowers,Y., Wylie,T., Waterston,R. and Wilson,R.

```
  TITLE     WashU Zebrafish EST Project 1999
  JOURNAL   Unpublished (1999)
COMMENT     Contact: S.L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Library constructed by Dr. Sumio Sugano and D. Koichi Kawakami DNA
            Sequencing by: Washington University Genome Sequencing Center
            Seq primer: T7 ET from Amersham
            High quality sequence stop: 499.
FEATURES             Location/Qualifiers
     source          1. .570
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /strain="AB"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:2351727"
                     /sex="mixed (one male and one female, including
                     unfertilized eggs)"
                     /dev_stage="adult"
                     /lab_host="DH10B (phage resistant)"
                     /clone_lib="Sugano Kawakami zebrafish DRA"
                     /note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
                     Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
                     with an oligo(dT) primer  [ATGTGGCCTTTTTTTTTTTTTTTT];
                     double-stranded cDNA was ligated to a  DraIII adaptor
                     [TGTTGGCCTACTGG], digested and cloned into distinct DraIII
                     sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
                     CACCATGTG). XhoI should be used to isolate the cDNA
                     insert.  Size selection was performed to exclude fragments
                     <1.5kb.  Library constructed by Dr. Sumio Sugano
                     (University of Tokyo Institute of Medical Science) and
                     kindly donated by Dr. Koichi Kawakami.  Custom primers for
                     sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
                     primer CGACCTGCAGCTCGAGCACA.  "
ORIGIN

  Query Match             2.2%;  Score 20;  DB 1;  Length 570;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        776 AGAACAACAGAGAAAAGAAA 795
              ||||||||||||||||||||
Db         83 AGAACAACAGAGAAAAGAAA 102


RESULT 86
BJ032049
LOCUS       BJ032049                571 bp    mRNA    linear   EST 26-SEP-2003
DEFINITION  BJ032049 NIBB Mochii normalized Xenopus neurula library Xenopus
            laevis cDNA clone XL015h03 5', mRNA sequence.
ACCESSION   BJ032049
VERSION     BJ032049.1  GI:17375617
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Xenopus.
REFERENCE   1  (bases 1 to 571)
  AUTHORS   Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
            Kohara,Y.
  TITLE     Expressed genes in X. laevis embryo
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp
            The information of this clone is available through the following
            URL.
            http://xenopus.nibb.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .571
                     /organism="Xenopus laevis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8355"
                     /clone="XL015h03"
                     /tissue_type="whole embryo"
                     /dev_stage="stage 15"
                     /clone_lib="NIBB Mochii normalized Xenopus neurula
                     library"
ORIGIN

  Query Match             2.2%;  Score 20;  DB 2;  Length 571;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        184 GATGCTGGCCAGTATACCTG 203
              ||||||||||||||||||||
Db        140 GATGCTGGCCAGTATACCTG 159


RESULT 87
BJ627752
LOCUS       BJ627752                578 bp    mRNA    linear   EST 01-OCT-2003
DEFINITION  BJ627752 NIBB Mochii normalized Xenopus early gastrula library
            Xenopus laevis cDNA clone XL219d21 5', mRNA sequence.
ACCESSION   BJ627752
VERSION     BJ627752.1  GI:37274652
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Xenopus.
REFERENCE   1  (bases 1 to 578)
  AUTHORS   Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
            Kohara,Y.
  TITLE     Expressed genes in X. laevis embryo
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp
            The information of this clone is available through the following
            URL.
            http://xenopus.nibb.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .578
                     /organism="Xenopus laevis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8355"
                     /clone="XL219d21"
                     /tissue_type="whole embryo"
                     /dev_stage="stage 10.5"
                     /clone_lib="NIBB Mochii normalized Xenopus early gastrula
                     library"
ORIGIN

  Query Match             2.2%;  Score 20;  DB 2;  Length 578;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        184 GATGCTGGCCAGTATACCTG 203
              ||||||||||||||||||||
Db        417 GATGCTGGCCAGTATACCTG 436
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RESULT 88
CX600301/c
LOCUS       CX600301                621 bp    mRNA    linear   EST 13-JAN-2005
DEFINITION  CT020026A20C01 Equine Articular Cartilage cDNA Library Equus
            caballus cDNA clone CT020026A20C01, mRNA sequence.
ACCESSION   CX600301
VERSION     CX600301.1  GI:57713619
KEYWORDS    EST.
SOURCE      Equus caballus (horse)
  ORGANISM  Equus caballus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
REFERENCE   1  (bases 1 to 621)
  AUTHORS   MacLeod,J.N.
  TITLE     Expressed sequence tags from a normalized equine articular
            cartilage cDNA library
  JOURNAL   Unpublished (2005)
COMMENT     Contact: MacLeod JN
            Department of Veterinary Science
            University of Kentucky
            Gluck Equine Research Center, Lexington, KY 40546-0099, USA
            Tel: 859.257.4757
            Fax: 859.257.8542
            Email: jnmacleod@uky.edu
            High quality sequence stop: 621.
FEATURES             Location/Qualifiers
     source          1. .621
                     /organism="Equus caballus"
                     /mol_type="mRNA"
                     /strain="Thoroughbred"
                     /db_xref="taxon:9796"
                     /clone="CT020026A20C01"
                     /sex="male"
                     /tissue_type="articular cartilage"
                     /dev_stage="1.5 year old"
                     /lab_host="DH12S E. Coli cells (Invitrogen)"
                     /clone_lib="Equine Articular Cartilage cDNA Library"
                     /note="Vector: pGEM11Zf(+) (Promega); Site_1: EcoR1;
                     Site_2: Not1"
ORIGIN

  Query Match             2.2%;  Score 20;  DB 9;  Length 621;
  Best Local Similarity   100.0%;  Pred. No. 92;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        290 AACAGAAAGAATCCAAAAAT 309
              ||||||||||||||||||||
Db        569 AACAGAAAGAATCCAAAAAT 550


RESULT 89
AL900775
LOCUS       AL900775                633 bp    mRNA    linear   EST 04-DEC-2003
DEFINITION  AL900775 XGC-egg Xenopus tropicalis cDNA clone TEgg018m09 5', mRNA
            sequence.
ACCESSION   AL900775
VERSION     AL900775.2  GI:38699538
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 633)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     On Sep 16, 2002 this sequence version replaced gi:22953010.
            Contact: Taylor R
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TEgg018m09.p1kSP6
            Sequencing primer: SP6
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from egg.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
            5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli XL1-blue.
FEATURES             Location/Qualifiers
     source          1. .633
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TEgg018m09"
                     /dev_stage="egg"
                     /lab_host="Escherichia coli XL1-blue"
                     /clone_lib="XGC-egg"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from egg.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end"
ORIGIN

  Query Match             2.2%;  Score 20;  DB 1;  Length 633;
  Best Local Similarity   100.0%;  Pred. No. 92;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        184 GATGCTGGCCAGTATACCTG 203
              ||||||||||||||||||||
Db        183 GATGCTGGCCAGTATACCTG 202


RESULT 90
CE454520/c
LOCUS       CE454520                646 bp    DNA     linear   GSS 27-SEP-2003
DEFINITION  tigr-gss-dog-17000319465791 Dog Library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION   CE454520
VERSION     CE454520.1  GI:36748105
KEYWORDS    GSS.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 646)
  AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
            Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
            Venter,J.C.
  TITLE     The dog genome: survey sequencing and comparative analysis
  JOURNAL   Science 301 (5641), 1898-1903 (2003)
   PUBMED   14512627
COMMENT     Contact: Kirkness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirknes@tigr.org
            Class: shotgun.
FEATURES             Location/Qualifiers
     source          1. .646
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /strain="Standard Poodle"
                     /db_xref="taxon:9615"
                     /clone_lib="Dog Library"
                     /note="Site_1: BstXI; Libraries were prepared from
                     peripheral blood"
ORIGIN

  Query Match             2.2%;  Score 20;  DB 12;  Length 646;
```

```
  Best Local Similarity   100.0%;  Pred. No. 92;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        241 CTGATACACAAAAAGGAAGA 260
              ||||||||||||||||||||
Db        140 CTGATACACAAAAAGGAAGA 121


RESULT 91
CZ709509
LOCUS       CZ709509                649 bp    DNA     linear   GSS 25-JUL-2005
DEFINITION  OC__Ba0030E21.r OC__Ba Oryza coarctata genomic clone OC__Ba0030E21
            3', genomic survey sequence.
ACCESSION   CZ709509
VERSION     CZ709509.1  GI:71114283
KEYWORDS    GSS.
SOURCE      Oryza coarctata (Porteresia coarctata)
  ORGANISM  Oryza coarctata
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 649)
  AUTHORS   Kim,H., Collura,K., Wissotski,M., Byrne,M., Stum,D., Smart,D.,
            Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and
            Wing,R.
  TITLE     OMAP (Oryza Map Alignment Project)- Arizona Genomics Institute
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Rod A. Wing
            Arizona Genomics Institute
            University of Arizona
            Forbes Building Room 303, Tucson, AZ 85721-0036, USA
            Tel: 520 626 9595
            Fax: 520 621 1259
            Email: rwing@genome.arizona.edu
            PCR PRimers
            FORWARD: TAA TAC GAC TCA CTA TAG GG
            BACKWARD: CAC TCA TTA GGC ACC CCA
            Plate: 0030  row: E  column: 21
            Seq primer: CAC TCA TTA GGC ACC CCA
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .649
                     /organism="Oryza coarctata"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:77588"
                     /clone="OC__Ba0030E21"
                     /tissue_type="leaves"
                     /dev_stage="mature"
                     /lab_host="DH10B"
                     /clone_lib="OC__Ba"
                     /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
ORIGIN

  Query Match             2.2%;  Score 20;  DB 13;  Length 649;
  Best Local Similarity   100.0%;  Pred. No. 92;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        244 ATACACAAAAAGGAAGATGG 263
              ||||||||||||||||||||
Db         27 ATACACAAAAAGGAAGATGG 46


RESULT 92
BM096034
LOCUS       BM096034                654 bp    mRNA    linear   EST 20-NOV-2001
DEFINITION  fv29g12.x1 Sugano SJD adult male Danio rerio cDNA clone
            IMAGE:5410006 3', mRNA sequence.
ACCESSION   BM096034
VERSION     BM096034.1  GI:17025000
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 654)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
            Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution information can be found through the I.M.A.G.E.
            Consortium/LLNL, send email to: info@image.llnl.gov
            High quality sequence stop: 525.
FEATURES             Location/Qualifiers
     source          1. .654
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:5410006"
                     /sex="male"
                     /tissue_type="whole body"
                     /dev_stage="adult"
                     /lab_host="DH10B (phage resistant)"
                     /clone_lib="Sugano SJD adult male"
                     /note="Vector: pME18S-FL3; Site_1: DraIII (CACCATGTG);
                     Site_2: DraIII (CACTGTGTG); 1st strand cDNA was primed
                     with an oligo(dT) primer  [ATGTGGCCTTTTTTTTTTTTTTTT];
                     double-stranded cDNA was ligated to a  DraIII adaptor
                     [TGTTGGCCTACTGG], digested and cloned into distinct DraIII
                     sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
                     CACCATGTG). XhoI should be used to isolate the cDNA
                     insert. Size selection was performed to exclude fragments
                     <1.5kb. Library constructed and donated by Dr. Sumio
                     Sugano (University of Tokyo Institute of Medical Science).
                     Custom primers for sequencing: 5' end primer
                     CTTCTGCTCTAAAAGCTGCG and 3' end primer
                     CGACCTGCAGCTCGAGCACA. "
ORIGIN

  Query Match             2.2%;  Score 20;  DB 2;  Length 654;
  Best Local Similarity   100.0%;  Pred. No. 92;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        776 AGAACAACAGAGAAAAGAAA 795
              ||||||||||||||||||||
Db         95 AGAACAACAGAGAAAAGAAA 114


RESULT 93
BJ042592
LOCUS       BJ042592                667 bp    mRNA    linear   EST 29-SEP-2003
DEFINITION  BJ042592 NIBB Mochii normalized Xenopus neurula library Xenopus
            laevis cDNA clone XL032c23 5', mRNA sequence.
ACCESSION   BJ042592
VERSION     BJ042592.1  GI:17392768
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Xenopus.
REFERENCE   1  (bases 1 to 667)
  AUTHORS   Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
            Kohara,Y.
```

```
  TITLE     Expressed genes in X. laevis embryo
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp
            The information of this clone is available through the following
            URL.
            http://xenopus.nibb.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .667
                     /organism="Xenopus laevis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8355"
                     /clone="XL032c23"
                     /tissue_type="whole embryo"
                     /dev_stage="stage 15"
                     /clone_lib="NIBB Mochii normalized Xenopus neurula
                     library"
ORIGIN

  Query Match             2.2%;  Score 20;  DB 2;  Length 667;
  Best Local Similarity   100.0%;  Pred. No. 92;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        184 GATGCTGGCCAGTATACCTG 203
              ||||||||||||||||||||
Db        281 GATGCTGGCCAGTATACCTG 300


RESULT 94
CT167835
LOCUS       CT167835                667 bp    DNA     linear   GSS 02-NOV-2005
DEFINITION  Sus scrofa genomic clone CH242-122N13, genomic survey sequence.
ACCESSION   CT167835
VERSION     CT167835.1  GI:79683824
KEYWORDS    GSS.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 667)
  AUTHORS   Humphray,S.J., Plumb,R.W. and Durham,J.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Unpublished
COMMENT     This sequence was generated from the SP6 end of BAC 122N13. 122N13
            is part of the CHORI-242 BAC Library created by P. de Jong. Further
            details: http://www.sanger.ac.uk/Projects/S_scrofa/.
FEATURES             Location/Qualifiers
     source          1. .667
                     /organism="Sus scrofa"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9823"
                     /clone="CH242-122N13"
                     /tissue_type="White blood cells"
                     /note="vector pTARBAC1.3_BamHI
                     sex female"
ORIGIN

  Query Match             2.2%;  Score 20;  DB 14;  Length 667;
  Best Local Similarity   100.0%;  Pred. No. 92;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        776 AGAACAACAGAGAAAAGAAA 795
              ||||||||||||||||||||
Db        164 AGAACAACAGAGAAAAGAAA 183


RESULT 95
DU179885
LOCUS       DU179885                672 bp    DNA     linear   GSS 03-OCT-2005
DEFINITION  1098553497457 CHORI-243 Ovis aries genomic clone CH243-410B4,
            genomic survey sequence.
ACCESSION   DU179885
VERSION     DU179885.1  GI:76820406
KEYWORDS    GSS.
SOURCE      Ovis aries (sheep)
  ORGANISM  Ovis aries
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Caprinae; Ovis.
REFERENCE   1  (bases 1 to 672)
  AUTHORS   Kirkness,E., Shetty,J., de Jong,P., McEwan,J.C., Oddy,H. and
            Cockett,N.
  TITLE     Ovine BAC End Sequences from Library CHORI-243
  JOURNAL   Unpublished (2004)
COMMENT     Other_GSSs: 1098553723711
            Contact: Ewen Kirkness
            The Institute for Genomic Research (TIGR; www.tigr.org)
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-795-7536
            Email: ekirknes@tigr.org
            Sequences generated at the J. Craig Venter Institute Joint
            Technology Center (JCVIJTC; http://www.venterinstitute.org/).
            Original Trace: 1098553497457 Trace TI: gnl|ti|918706746
            Insert Length: 184000   Std Error: 0.00  row: B  column: 4
            Seq primer: SP6
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .672
                     /organism="Ovis aries"
                     /mol_type="genomic DNA"
                     /strain="Texel breed"
                     /db_xref="taxon:9940"
                     /clone="CH243-410B4"
                     /sex="Male"
                     /cell_type="Blood"
                     /clone_lib="CHORI-243"
                     /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
                     The CHORI-243 sheep (M) (Ovis aries) BAC library produced
                     by Pieter de Jong's lab at CHORI
                     http://bacpac.chori.org/library.php?id=162"
ORIGIN

  Query Match             2.2%;  Score 20;  DB 13;  Length 672;
  Best Local Similarity   100.0%;  Pred. No. 92;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAA 20
              ||||||||||||||||||||
Db        149 ATATGGGAACTGGAGAAAAA 168


RESULT 96
AG826544/c
LOCUS       AG826544                676 bp    DNA     linear   GSS 01-DEC-2004
DEFINITION  Sus scrofa DNA, BAC clone 0732F12, shotgun sequence of subclone
            0732F12S002B02, read with M13Reverse primer, genomic survey
            sequence.
ACCESSION   AG826544
VERSION     AG826544.1  GI:56373042
KEYWORDS    GSS.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1
  AUTHORS   Tanaka,M., Suzuki,K., Morozumi,T., Kobayashi,E., Matsumoto,T.,
            Domukai,M., Eguchi-Ogawa,T., Shinkai,H., Awata,T. and Uenishi,H.
```

```
  TITLE     Genomic structure of the distal extended-class II region in swine
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 676)
  AUTHORS   Uenishi,H., Tanaka,M. and Awata,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-OCT-2004) Hirohide Uenishi, National Institute of
            Agrobiological Sciences, Animal Genome Laboratory, Genome Research
            Department; 2 Ikenodai, Tsukuba, Ibaraki, 305-8602, Japan
            (E-mail:huenishi@affrc.go.jp, Tel:81-29-838-8627,
            Fax:81-29-838-8627)
COMMENT     Correspondence to:
            Hirohide Uenishi
            Animal Genome Laboratory, Genome Research Department, National
            Institute of Agrobiological Sciences
            2 Ikenodai, Tsukuba, Ibaraki 305-8602, JAPAN
            Tel: +81-29-838-8627
            Fax: +81-29-838-8627
            e-mail: huenishi@affrc.go.jp
            Sequencing was carried out in Animal Genome Research Program
            (Japan)
            by National Institute of Agrobiological Sciences
            and STAFF-Institute.
            Subclones of BAC clones were constructed with pUC18 vector.
            Basecalling was performed by Phred 0.020425.c.
            Vector sequences were eliminated by crossmatch version 0.990319.
            Low quality bases were trimmed based on the quality values with the
            aid of the trim_alt option of Phred.
FEATURES             Location/Qualifiers
     source          1. .676
                     /organism="Sus scrofa"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9823"
                     /clone="0732F12"
                     /sub_clone="0732F12S002B02"
                     /clone_lib="Sus scrofa shotgun BAC sequence"
ORIGIN

  Query Match             2.2%;  Score 20;  DB 14;  Length 676;
  Best Local Similarity   100.0%;  Pred. No. 92;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        429 CCAAGAGGTGACTTGTGGAG 448
              ||||||||||||||||||||
Db        249 CCAAGAGGTGACTTGTGGAG 230


RESULT 97
CC008436/c
LOCUS       CC008436                681 bp    DNA     linear   GSS 31-MAR-2003
DEFINITION  PUDHR12TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa213B24,
            genomic survey sequence.
ACCESSION   CC008436
VERSION     CC008436.1  GI:29387056
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 681)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
  TITLE     Maize Genomics Consortium
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .681
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBTa213B24"
                     /clone_lib="ZM_0.6_1.0_KB"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
                     CoT selected genomic DNA library"
ORIGIN

  Query Match             2.2%;  Score 20;  DB 12;  Length 681;
  Best Local Similarity   100.0%;  Pred. No. 92;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        309 TAAGATCTTTCTAAAATGTG 328
              ||||||||||||||||||||
Db        677 TAAGATCTTTCTAAAATGTG 658


RESULT 98
AZ424475/c
LOCUS       AZ424475                690 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0204A12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0204A12 F, genomic survey sequence.
ACCESSION   AZ424475
VERSION     AZ424475.1  GI:10548488
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 690)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0204  row: A  column: 12
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 690.
FEATURES             Location/Qualifiers
     source          1. .690
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0204A12"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
```

ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 2.2%; Score 20; DB 11; Length 690;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        485 ACAGGGATTATAAGAAGTAC 504
              ||||||||||||||||||||
Db        250 ACAGGGATTATAAGAAGTAC 231
```

RESULT 99
BZ240832/c
LOCUS BZ240832 696 bp DNA linear GSS 12-OCT-2002
DEFINITION CH230-272O10.TJB CHORI-230 Segment 2 Rattus norvegicus genomic clone CH230-272O10, genomic survey sequence.
ACCESSION BZ240832
VERSION BZ240832.1 GI:23901096
KEYWORDS GSS.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 696)
AUTHORS Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de Jong,P. and Fraser,C.M.
TITLE Rat BAC End Sequences from Library CHORI-230 MboI segment
JOURNAL Unpublished (1999)
COMMENT Other_GSSs: CH230-272O10.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 272 row: O column: 10
Seq primer: SP6
Class: BAC ends.

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FEATURES             Location/Qualifiers
     source          1. .696
                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /strain="BN/SsNHsd/MCW"
                     /db_xref="taxon:10116"
                     /clone="CH230-272O10"
                     /sex="Female"
                     /cell_type="Brain"
                     /clone_lib="CHORI-230 Segment 2"
                     /note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
                     CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
                     Pieter de Jong"
```

ORIGIN

Query Match 2.2%; Score 20; DB 11; Length 696;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         89 CTCCTGAAGAAGATGACATC 108
              ||||||||||||||||||||
Db        105 CTCCTGAAGAAGATGACATC 86
```

RESULT 100
BG740695
LOCUS BG740695 698 bp mRNA linear EST 15-MAY-2001
DEFINITION 602631544F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4776634 5', mRNA sequence.
ACCESSION BG740695
VERSION BG740695.1 GI:14051348
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 698)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10629 row: h column: 11
High quality sequence stop: 694.

```
FEATURES             Location/Qualifiers
     source          1. .698
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4776634"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Skn3"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.5kb. Library constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
```

ORIGIN

Query Match 2.2%; Score 20; DB 2; Length 698;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        776 AGAACAACAGAGAAAAGAAA 795
              ||||||||||||||||||||
Db        281 AGAACAACAGAGAAAAGAAA 300
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Search completed: June 10, 2006, 14:54:02
Job time : 5645.93 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2006, 22:44:33 ; Search time 209.38 Seconds
(without alignments)
8230.433 Million cell updates/sec

Title: US-10-821-670A-26
Perfect score: 921
Sequence: 1 atatgggaactggagaaaaa.....gggcatccgtgtcctgcagt 921

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1403666 seqs, 935554401 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2806514

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 200 summaries

Database : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	921	100.0	921	3	US-09-917-265A-26	Sequence 26, Appl
c	2	921	100.0	921	3	US-09-917-265A-28	Sequence 28, Appl
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ALIGNMENTS

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RESULT 1
US-09-917-265A-26
; Sequence 26, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
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US-09-917-265A-26

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Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 2
US-09-917-265A-28/c
; Sequence 28, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2

; SEQ ID NO 28
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-28

  Query Match             100.0%;  Score 921;  DB 3;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
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Db         21 TGGGCATCCGTGTCCTGCAGT 1
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RESULT 3
US-09-917-265A-43
; Sequence 43, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-09-917-265A-43

  Query Match             100.0%;  Score 921;  DB 3;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 4
US-09-917-265A-45/c
; Sequence 45, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-45

  Query Match             100.0%;  Score 921;  DB 3;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174
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Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613
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RESULT 5
US-09-917-265A-38
; Sequence 38, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1599)
US-09-917-265A-38

Query Match 100.0%; Score 921; DB 3; Length 1599;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
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Db        967 TGGGCATCCGTGTCCTGCAGT 987
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RESULT 6
US-09-917-265A-40/c
; Sequence 40, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A

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;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-40

  Query Match             100.0%;  Score 921;  DB 3;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613


RESULT 7
US-09-011-143-6
; Sequence 6, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  921 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-6

  Query Match             94.5%;  Score 870;  DB 3;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
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Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 8
US-09-302-495-6
; Sequence 6, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-302-495-6

  Query Match            94.5%;  Score 870;  DB 3;  Length 921;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
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Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
                |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 9
US-10-079-616-6
; Sequence 6, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-079-616-6

  Query Match             94.5%;  Score 870;  DB 3;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
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Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
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Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
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Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 10
US-09-917-265A-29
; Sequence 29, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
US-09-917-265A-29

  Query Match             94.5%;  Score 870;  DB 3;  Length 987;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              ||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987


RESULT 11
US-09-917-265A-31/c
; Sequence 31, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-31

  Query Match             94.5%;  Score 870;  DB 3;  Length 987;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562
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Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCAGT 1


RESULT 12
US-09-011-143-5
; Sequence 5, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2193 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-5

  Query Match             94.5%;  Score 870;  DB 3;  Length 2193;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 189

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 249

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 309

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 369

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 429

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 489

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 549

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        550 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 609

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 669

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 729

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 789

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 849

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        850 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 909

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 969

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 1029

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db       1030 TGGGCATCCGTGTCCTGCAGT 1050


RESULT 13
US-09-302-495-5
; Sequence 5, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2193 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-302-495-5

  Query Match             94.5%;  Score 870;  DB 3;  Length 2193;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        130 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 189

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 249

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 309

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 369

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 429

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 489

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 549

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 609

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 669

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 729

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 789

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 849

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 909

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 969

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 1029

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db       1030 TGGGCATCCGTGTCCTGCAGT 1050


RESULT 14
US-10-079-616-5
; Sequence 5, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
```

```
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 5:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 2193 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-079-616-5

  Query Match             94.5%;  Score 870;  DB 3;  Length 2193;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 189

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 249

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 309

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 369

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 429

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 489

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 549

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 609

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 669

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 729

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 789

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 849

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 909

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 969

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 1029

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db       1030 TGGGCATCCGTGTCCTGCAGT 1050


RESULT 15
US-09-917-265A-55
; Sequence 55, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(984)
US-09-917-265A-55

  Query Match             94.2%;  Score 868;  DB 3;  Length 985;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCA 919
              ||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCA 985


RESULT 16
US-09-917-265A-57/c
; Sequence 57, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-57

  Query Match             94.2%;  Score 868;  DB 3;  Length 985;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 860

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 800

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 740

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 680

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 620

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 560

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 500

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        499 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 440

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 380

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 320

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 260

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 200

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 140

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 80

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 20

Qy        901 TGGGCATCCGTGTCCTGCA 919
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Db         19 TGGGCATCCGTGTCCTGCA 1


RESULT 17
US-09-011-143-7
; Sequence 7, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  921 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-7

  Query Match             88.9%;  Score 819;  DB 3;  Length 921;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches  919;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 18
US-09-302-495-7
; Sequence 7, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
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;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/302,495
;            FILING DATE: 30-Apr-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 7:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 921 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-302-495-7

  Query Match             88.9%;  Score 819;  DB 3;  Length 921;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches  919;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 19
US-10-079-616-7
; Sequence 7, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 7:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 921 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
```

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;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-079-616-7

  Query Match             88.9%;  Score 819;  DB 3;  Length 921;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches  919;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
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Db        901 TGGGCATCCGTGTCCTGCAGT 921
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RESULT 20
US-09-917-265A-52
; Sequence 52, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(921)
US-09-917-265A-52

  Query Match             7.2%;  Score 66;  DB 3;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 2e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy        531 CTGCCC 536
              ||||||
Db        531 CTGCCC 536


RESULT 21
US-09-917-265A-54/c
; Sequence 54, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-54

  Query Match             7.2%;  Score 66;  DB 3;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 2e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy        531 CTGCCC 536
              ||||||
Db        391 CTGCCC 386
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RESULT 22
US-09-917-265A-58
; Sequence 58, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
US-09-917-265A-58

  Query Match             7.2%;  Score 66;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        531 CTGCCC 536
              ||||||
Db        597 CTGCCC 602


RESULT 23
US-09-917-265A-60/c
; Sequence 60, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-60

  Query Match             7.2%;  Score 66;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy        531 CTGCCC 536
              ||||||
Db        391 CTGCCC 386


RESULT 24
US-09-079-984A-1
; Sequence 1, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,984A
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  990 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 987
;      IDENTIFICATION METHOD:  Similarity
US-09-079-984A-1

  Query Match             7.2%;  Score 66;  DB 3;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        531 CTGCCC 536
              ||||||
Db        597 CTGCCC 602


RESULT 25
US-09-079-984A-11
; Sequence 11, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
```

```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,984A
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  990 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 987
;      IDENTIFICATION METHOD:  Similarity
US-09-079-984A-11

  Query Match             7.2%;  Score 66;  DB 3;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        531 CTGCCC 536
              ||||||
Db        597 CTGCCC 602


RESULT 26
US-09-390-729-1
; Sequence 1, Application US/09390729
; Patent No. 6562334
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/390,729
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/079,984
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  990 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 987
;      IDENTIFICATION METHOD:  Similarity
US-09-390-729-1

  Query Match             7.2%;  Score 66;  DB 3;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        531 CTGCCC 536
              ||||||
Db        597 CTGCCC 602


RESULT 27
US-09-390-729-11
; Sequence 11, Application US/09390729
; Patent No. 6562334
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/390,729
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/079,984
;      FILING DATE:  15-MAY-1998
```

```
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Austin R. Miller
;       REGISTRATION NUMBER:  16,602
;       REFERENCE/DOCKET NUMBER:  1051-98
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (215) 563-1810
;       TELEFAX:  (215) 568-6946
;   INFORMATION FOR SEQ ID NO:  11:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  990 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA to mRNA
;     ORIGINAL SOURCE:
;       ORGANISM:  Canis familiaris
;     FEATURE:
;       NAME/KEY:  Canine IL12
;       LOCATION:  1 to 987
;       IDENTIFICATION METHOD:  Similarity
US-09-390-729-11

  Query Match             7.2%;  Score 66;  DB 3;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        531 CTGCCC 536
              ||||||
Db        597 CTGCCC 602


RESULT 28
US-09-917-265A-66
; Sequence 66, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-09-917-265A-66

  Query Match             7.2%;  Score 66;  DB 3;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 2e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy        531 CTGCCC 536
              ||||||
Db        531 CTGCCC 536


RESULT 29
US-09-917-265A-68/c
; Sequence 68, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-68

  Query Match             7.2%;  Score 66;  DB 3;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 2e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy        531 CTGCCC 536
              ||||||
Db       1003 CTGCCC 998


RESULT 30
US-09-917-265A-61
; Sequence 61, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-09-917-265A-61

  Query Match             7.2%;  Score 66;  DB 3;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 2e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        531 CTGCCC 536
              ||||||
Db        597 CTGCCC 602
```

RESULT 31
US-09-917-265A-63/c
; Sequence 63, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-917-265A-63

Query Match 7.2%; Score 66; DB 3; Length 1599;
Best Local Similarity 100.0%; Pred. No. 2e-23;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy        531 CTGCCC 536
              ||||||
Db       1003 CTGCCC 998
```

RESULT 32
US-09-917-265A-107
; Sequence 107, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 107
; LENGTH: 2267
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154)..(1140)
US-09-917-265A-107

Query Match 7.2%; Score 66; DB 3; Length 2267;
Best Local Similarity 100.0%; Pred. No. 2.1e-23;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 749

Qy        531 CTGCCC 536
              ||||||
Db        750 CTGCCC 755
```

RESULT 33
US-09-917-265A-109/c
; Sequence 109, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 109
; LENGTH: 2267
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-917-265A-109

Query Match 7.2%; Score 66; DB 3; Length 2267;
Best Local Similarity 100.0%; Pred. No. 2.1e-23;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1578 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1519

Qy        531 CTGCCC 536
              ||||||
Db       1518 CTGCCC 1513
```

RESULT 34
US-08-186-529-1
; Sequence 1, Application US/08186529
; Patent No. 5573764
; GENERAL INFORMATION:
; APPLICANT: Sykes, Megan
; APPLICANT: Wolf, Stanley F.
; TITLE OF INVENTION: USE OF INTERLEUKIN-12 TO PREVENT
; TITLE OF INVENTION: GRAFT-VERSUS-HOST DISEASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc., Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,529
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniels, Patricia A.
; REGISTRATION NUMBER: 33,194
; REFERENCE/DOCKET NUMBER: GI 5225
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-498-8401
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 987 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

```
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     ORIGINAL SOURCE:
;       ORGANISM:  Homo sapiens
;       CELL TYPE:  Lymphoblast
;       CELL LINE:  RPMI 8866
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..987
US-08-186-529-1

  Query Match             4.8%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 35
US-08-640-386A-1
; Sequence 1, Application US/08640386A
; Patent No. 5756085
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/640,386A
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;      REFERENCE/DOCKET NUMBER:  GI 5225A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8224
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  987 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Lymphoblast
;      CELL LINE:  RPMI 8866
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..987
US-08-640-386A-1

  Query Match             4.8%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 36
US-08-848-760B-24
; Sequence 24, Application US/08848760B
; Patent No. 6248721
;   GENERAL INFORMATION:
;       APPLICANT: Chang, Lung-Ji
;       TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
;       NUMBER OF SEQUENCES: 33
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
;            STREET: 2421 N.W. 41st Street, Suite A-1
;            CITY: Gainesville
;            STATE: Florida
;            COUNTRY: United States of America
;            ZIP: 32606
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/848,760B
;            FILING DATE: 25-Jan-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/838,702
;            FILING DATE: 09-APR-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: PACE, DORAN R.
;            REGISTRATION NUMBER: 38,261
;            REFERENCE/DOCKET NUMBER: CNG-100C1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (352) 375-8100
;            TELEFAX: (352) 372-5800
;   INFORMATION FOR SEQ ID NO: 24:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 987 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: other nucleic acid
;            DESCRIPTION: /desc = "DNA"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-08-848-760B-24

  Query Match             4.8%;  Score 44;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 37
US-09-826-025-24
; Sequence 24, Application US/09826025
; Patent No. 6730512
;   GENERAL INFORMATION:
;       APPLICANT: Chang, Lung-Ji
;       TITLE OF INVENTION: Combination Immunogene Therapy
;       NUMBER OF SEQUENCES: 25
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Medlen & Carroll, LLP
;            STREET: 220 Montgomery Street, Suite 2200
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: United States of America
```

```
;           ZIP: 94104
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/826,025
;           FILING DATE: 04-Apr-2001
;           CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: 08/838,702
;           FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;           NAME: Ingolia, Diane E.
;           REGISTRATION NUMBER: 40,027
;           REFERENCE/DOCKET NUMBER: CHANG-02687
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (415) 705-8410
;           TELEFAX: (415) 397-8338
;   INFORMATION FOR SEQ ID NO: 24:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 987 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: double
;           TOPOLOGY: linear
;       MOLECULE TYPE: other nucleic acid
;           DESCRIPTION: /desc = "DNA"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-826-025-24

  Query Match             4.8%;  Score 44;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 38
US-08-184-009-194
; Sequence 194, Application US/08184009
; Patent No. 5833975
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/184,009
;      FILING DATE:  19-JAN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  194:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1018 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-184-009-194

  Query Match             4.8%;  Score 44;  DB 2;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 39
US-08-458-356-194
; Sequence 194, Application US/08458356
; Patent No. 5942235
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,356
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  194:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1018 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-458-356-194

  Query Match             4.8%;  Score 44;  DB 2;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735
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RESULT 40
US-08-460-736-194
; Sequence 194, Application US/08460736
; Patent No. 6265189
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,736
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  194:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1018 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-460-736-194

  Query Match             4.8%;  Score 44;  DB 3;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 41
US-09-535-370-194
; Sequence 194, Application US/09535370
; Patent No. 6537594
;  GENERAL INFORMATION:
;       APPLICANT: Paoletti, Enzo
;                  Tartaglia, James
;                  Cox, William I.
;       TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
;       NUMBER OF SEQUENCES: 217
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Curtis, Morris & Safford
;            STREET: 530 Fifth Avenue
;            CITY: New York
;            STATE: NY
;            COUNTRY: USA
;            ZIP: 10036
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/535,370
;            FILING DATE: 24-Mar-2000
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/460,736
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Frommer, William S.
;            REGISTRATION NUMBER: 25,506
;            REFERENCE/DOCKET NUMBER: 454310-2530
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 840-3333
;            TELEFAX: (212) 840-0712
;            TELEX: 425066CURTMS
;  INFORMATION FOR SEQ ID NO: 194:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1018 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-09-535-370-194

  Query Match             4.8%;  Score 44;  DB 3;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 42
US-09-663-667-194
; Sequence 194, Application US/09663667
; Patent No. 6780407
;  GENERAL INFORMATION:
;       APPLICANT: Paoletti, Enzo
;                  Tartaglia, James
;                  Cox, William I.
;       TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
;       NUMBER OF SEQUENCES: 217
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Curtis, Morris & Safford
;            STREET: 530 Fifth Avenue
;            CITY: New York
;            STATE: NY
;            COUNTRY: USA
;            ZIP: 10036
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/663,667
;            FILING DATE: 15-Sep-2000
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/184,009
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Frommer, William S.
;            REGISTRATION NUMBER: 25,506
;            REFERENCE/DOCKET NUMBER: 454310-2530
;       TELECOMMUNICATION INFORMATION:
```

```
;             TELEPHONE: (212) 840-3333
;             TELEFAX: (212) 840-0712
;             TELEX: 425066CURTMS
;   INFORMATION FOR SEQ ID NO: 194:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1018 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-09-663-667-194

  Query Match             4.8%;  Score 44;  DB 3;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 43
US-09-634-368-4
; Sequence 4, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 1389
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: human
;   OTHER INFORMATION: p40-IL-2 fusion protein coding sequence
US-09-634-368-4

  Query Match             4.8%;  Score 44;  DB 3;  Length 1389;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 44
US-08-751-767A-3
; Sequence 3, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1399 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  43..1026
US-08-751-767A-3

  Query Match             4.8%;  Score 44;  DB 2;  Length 1399;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        703 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 746


RESULT 45
US-08-751-767A-11
; Sequence 11, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1560 base pairs
;      TYPE:  nucleic acid
```

```
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..1557
US-08-751-767A-11

  Query Match             4.8%;  Score 44;  DB 2;  Length 1560;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641


RESULT 46
US-08-751-767A-9
; Sequence 9, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1623 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1620
US-08-751-767A-9

  Query Match             4.8%;  Score 44;  DB 2;  Length 1623;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 47
US-09-310-842-4
; Sequence 4, Application US/09310842A
; Patent No. 6451593
; GENERAL INFORMATION:
;  APPLICANT: Wittig, Prof. Burghardt
;  APPLICANT: Junghans, Claas
;  TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
;  TITLE OF INVENTION: Therapy
;  FILE REFERENCE: XI 597/99
;  CURRENT APPLICATION NUMBER: US/09/310,842A
;  CURRENT FILING DATE: 1999-05-12
;  EARLIER APPLICATION NUMBER: DE 196 48 625.4
;  EARLIER FILING DATE: 1996-11-13
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 1870
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (1)..(1870)
;   OTHER INFORMATION: Interleukin-12 (IL-12, p40-subunit); Oligo DNA Dumbbell
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1)..(2)
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to
;   OTHER INFORMATION: 2  can be modified with amino or caroxy features
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1869)..(1870)
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1869
;   OTHER INFORMATION: to 1870  can be modified with amino or caroxy features
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Strandness: both;  nucleic
;   OTHER INFORMATION: acid (linear),  hypothetical: No. 6451593 anti-sense: No
US-09-310-842-4

  Query Match             4.8%;  Score 44;  DB 3;  Length 1870;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db       1293 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 1336


RESULT 48
US-09-949-016-5452
; Sequence 5452, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5452
;   LENGTH: 2307
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-5452

  Query Match             4.8%;  Score 44;  DB 3;  Length 2307;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-12;
```

```
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        663 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 706


RESULT 49
US-09-851-062-3
; Sequence 3, Application US/09851062
; Patent No. 6448081
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0247
;  CURRENT APPLICATION NUMBER: US/09/851,062
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 3
;   LENGTH: 2318
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (14)...(1000)
US-09-851-062-3

  Query Match             4.8%;  Score 44;  DB 3;  Length 2318;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        674 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 717


RESULT 50
US-09-949-016-315
; Sequence 315, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 315
;   LENGTH: 2318
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-315

  Query Match             4.8%;  Score 44;  DB 3;  Length 2318;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        674 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 717


RESULT 51
US-08-265-087-1
; Sequence 1, Application US/08265087
; Patent No. 5571515
; GENERAL INFORMATION:
;   APPLICANT:  Scott, Phillip
;   APPLICANT:  Trinchieri, Giorgio
;   TITLE OF INVENTION:  Compositions and Methods for Use of
;   TITLE OF INVENTION:  IL-12 as an Adjuvant
;   NUMBER OF SEQUENCES:  4
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Howson and Howson
;     STREET:  Spring House Corporate Center, PO Box 457
;     CITY:  Spring House
;     STATE:  Pennsylvania
;     COUNTRY:  USA
;     ZIP:  19477
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/265,087
;     FILING DATE:
;     CLASSIFICATION:  424
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/229,282
;     FILING DATE:  18-APR-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Bak, Mary E.
;     REGISTRATION NUMBER:  31,215
;     REFERENCE/DOCKET NUMBER:  WST51AUSA
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  215-540-9206
;     TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  2362 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  double
;     TOPOLOGY:  unknown
;   MOLECULE TYPE:  cDNA
;   FEATURE:
;     NAME/KEY:  CDS
;     LOCATION:  33..1016
US-08-265-087-1

  Query Match             4.8%;  Score 44;  DB 2;  Length 2362;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        693 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 736


RESULT 52
US-08-621-493-1
; Sequence 1, Application US/08621493
; Patent No. 5723127
; GENERAL INFORMATION:
;   APPLICANT:  Scott, Phillip
;   APPLICANT:  Trinchieri, Giorgio
;   TITLE OF INVENTION:  Compositions and Methods for Use of
;   TITLE OF INVENTION:  IL-12 as an Adjuvant
;   NUMBER OF SEQUENCES:  4
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Howson and Howson
;     STREET:  Spring House Corporate Center, PO Box 457
;     CITY:  Spring House
;     STATE:  Pennsylvania
;     COUNTRY:  USA
;     ZIP:  19477
;   COMPUTER READABLE FORM:
```

```
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/621,493
;       FILING DATE:  25-MAR-1996
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/265,087
;       FILING DATE:  17-JUN-1994
;       APPLICATION NUMBER:  US 08/229,282
;       FILING DATE:  18-APR-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Bak, Mary E.
;       REGISTRATION NUMBER:  31,215
;       REFERENCE/DOCKET NUMBER:  WST51AUSA
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  215-540-9206
;       TELEFAX:  215-540-5818
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2362 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  unknown
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  33..1016
US-08-621-493-1

  Query Match             4.8%;  Score 44;  DB 2;  Length 2362;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        693 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 736


RESULT 53
US-08-965-688-1
; Sequence 1, Application US/08965688
; Patent No. 5976539
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/965,688
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/621,493
;      FILING DATE:  25-MAR-1996
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2362 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  33..1016
US-08-965-688-1

  Query Match             4.8%;  Score 44;  DB 2;  Length 2362;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        693 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 736


RESULT 54
US-09-260-173-1
; Sequence 1, Application US/09260173
; Patent No. 6168923
;   GENERAL INFORMATION:
;       APPLICANT: Scott, Phillip
;                  Trinchieri, Giorgio
;       TITLE OF INVENTION: Compositions and Methods for Use of
;                           IL-12 as an Adjuvant
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Howson and Howson
;            STREET: Spring House Corporate Center, PO Box 457
;            CITY: Spring House
;            STATE: Pennsylvania
;            COUNTRY: USA
;            ZIP: 19477
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/260,173
;            FILING DATE: 01-Mar-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/965,688
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: 08/265,087
;            FILING DATE: 17-JUN-1994
;            APPLICATION NUMBER: US 08/229,282
;            FILING DATE: 18-APR-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Bak, Mary E.
;            REGISTRATION NUMBER: 31,215
;            REFERENCE/DOCKET NUMBER: WST51AUSA
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 215-540-9206
;            TELEFAX: 215-540-5818
;   INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
```

```
;             LENGTH: 2362 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: unknown
;          MOLECULE TYPE: cDNA
;          FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  33..1016
;          SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-260-173-1

  Query Match             4.8%;  Score 44;  DB 3;  Length 2362;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        693 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 736


RESULT 55
US-09-924-703-3
; Sequence 3, Application US/09924703
; Patent No. 6555658
; GENERAL INFORMATION:
;  APPLICANT: TRINCHIERI, GIORGIO
;  APPLICANT:  PERUSSIA, BICE
;  APPLICANT:  CLARK, STEVEN C.
;  APPLICANT:  WONG, GORDON G.
;  APPLICANT:  HEWICK, RODNEY
;  APPLICANT:  KOBAYASHI, MICHIKO
;  TITLE OF INVENTION: ANTIBODIES TO NATURAL KILLER STIMULATORY FACTOR
;  FILE REFERENCE: 01142.0142.0100
;  CURRENT APPLICATION NUMBER: US/09/924,703
;  CURRENT FILING DATE:  2001-08-09
;  PRIOR APPLICATION NUMBER: 09/325,958
;  PRIOR FILING DATE: 1999-06-04
;  PRIOR APPLICATION NUMBER: 08/858,000
;  PRIOR FILING DATE: 1997-05-16
;  PRIOR APPLICATION NUMBER: 08/403,013
;  PRIOR FILING DATE: 1995-03-13
;  PRIOR APPLICATION NUMBER: 07/584,941
;  PRIOR FILING DATE: 1990-09-18
;  PRIOR APPLICATION NUMBER: 07/307,817
;  PRIOR FILING DATE: 1989-02-07
;  PRIOR APPLICATION NUMBER: 07/269,945
;  PRIOR FILING DATE: 1988-11-10
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 2362
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
;   OTHER INFORMATION: sequence of the 40 kD subunit of NKSF
;   NAME/KEY: CDS
;   LOCATION: (33)..(1016)
US-09-924-703-3

  Query Match             4.8%;  Score 44;  DB 3;  Length 2362;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        693 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 736


RESULT 56
US-08-751-767A-7
; Sequence 7, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6139 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3222..4841
US-08-751-767A-7

  Query Match             4.8%;  Score 44;  DB 2;  Length 6139;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db       3882 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 3925


RESULT 57
US-09-949-016-12057
; Sequence 12057, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12057
;   LENGTH: 16002
;   TYPE: DNA
;   ORGANISM: Human
```

US-09-949-016-12057

Query Match 4.2%; Score 39; DB 3; Length 16002;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 334 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 372
||||||||||||||||||||||||||||||||||||||||
Db 6309 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 6347

RESULT 58
US-09-949-016-17194
; Sequence 17194, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17194
; LENGTH: 16003
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17194

Query Match 4.2%; Score 39; DB 3; Length 16003;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 334 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 372
||||||||||||||||||||||||||||||||||||||||
Db 6309 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 6347

RESULT 59
US-09-949-016-24253/c
; Sequence 24253, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24253
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-24253

Query Match 4.0%; Score 37; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCA 634
||||||||||||||||||||||||||||||||||||
Db 87 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCA 51

RESULT 60
US-09-949-016-190686/c
; Sequence 190686, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 190686
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-190686

Query Match 4.0%; Score 37; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCA 634
||||||||||||||||||||||||||||||||||||
Db 87 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCA 51

RESULT 61
US-09-823-549-77
; Sequence 77, Application US/09823549
; Patent No. 6664442
; GENERAL INFORMATION:
; APPLICANT: McConlogue, Lisa C
; APPLICANT: Games, Kate D.
; APPLICANT: Yednock, Theodore A.
; APPLICANT: Hua, Tan
; APPLICANT: Messersmith, Elizabeth
; APPLICANT: Bard, Frederique
; TITLE OF INVENTION: SCREENING MARKERS AND METHODS FOR NEURODEGENERATIVE DISORDERS
; FILE REFERENCE: 015270-009110US
; CURRENT APPLICATION NUMBER: US/09/823,549
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/193,847
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
; LENGTH: 73
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-12 p40, #1 marker
US-09-823-549-77

Query Match 3.3%; Score 30; DB 3; Length 73;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 612 CAGCTTCTTCATCAGGGACATCATCAAACC 641
||||||||||||||||||||||||||||||

```
Db          8 CAGCTTCTTCATCAGGGACATCATCAAACC 37


RESULT 62
US-08-385-335A-13
; Sequence 13, Application US/08385335A
; Patent No. 5891680
;  GENERAL INFORMATION:
;    APPLICANT:  Lieschke, Graham J.
;    APPLICANT:  Mulligan, Richard C.
;    TITLE OF INVENTION:  Bioactive Fusion Proteins
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/385,335A
;      FILING DATE:  08-FEB-1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  WHI95-01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-861-6240
;      TELEFAX:  617-861-9540
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1061 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-08-385-335A-13

  Query Match             3.3%;  Score 30;  DB 2;  Length 1061;
  Best Local Similarity   100.0%;  Pred. No. 5.3e-05;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        612 CAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||
Db        715 CAGCTTCTTCATCAGGGACATCATCAAACC 744


RESULT 63
US-09-634-368-3
; Sequence 3, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1409
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p40-GM-CSF fusion protein coding sequence
US-09-634-368-3

  Query Match             3.3%;  Score 30;  DB 3;  Length 1409;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-05;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        612 CAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||
Db        689 CAGCTTCTTCATCAGGGACATCATCAAACC 718


RESULT 64
US-09-634-368-2
; Sequence 2, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 1472
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p40-IL-2 fusion protein coding sequence
US-09-634-368-2

  Query Match             3.3%;  Score 30;  DB 3;  Length 1472;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-05;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        612 CAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||
Db        689 CAGCTTCTTCATCAGGGACATCATCAAACC 718


RESULT 65
US-09-634-368-12
; Sequence 12, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 1569
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p35-linker-p40 fusion protein coding sequence
US-09-634-368-12

  Query Match             3.3%;  Score 30;  DB 3;  Length 1569;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-05;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy        612 CAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||
Db       1230 CAGCTTCTTCATCAGGGACATCATCAAACC 1259


RESULT 66
US-09-634-368-11
; Sequence 11, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 2013
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p35-linker-p40-IL-2 fusion protein coding sequence
US-09-634-368-11

  Query Match             3.3%;  Score 30;  DB 3;  Length 2013;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-05;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        612 CAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||
Db       1230 CAGCTTCTTCATCAGGGACATCATCAAACC 1259


RESULT 67
US-09-634-368-13
; Sequence 13, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 13
;   LENGTH: 2709
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: Fc-p35-linker-p40-IL-2 fusion protein coding
;   OTHER INFORMATION: sequence
US-09-634-368-13

  Query Match             3.3%;  Score 30;  DB 3;  Length 2709;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-05;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        612 CAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||
Db       1926 CAGCTTCTTCATCAGGGACATCATCAAACC 1955


RESULT 68
US-08-659-206A-4
; Sequence 4, Application US/08659206A
; Patent No. 5922685
;  GENERAL INFORMATION:
;    APPLICANT:  Rakhmilevich, Alexander
;    TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/659,206A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  110229.91144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6295 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "plasmid pWRG3196"
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(955..1260, 1334..1675)
;      OTHER INFORMATION:  /product= "p35 gene product"
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2377..3384
;      OTHER INFORMATION:  /product= "p40 gene product"
US-08-659-206A-4

  Query Match             3.3%;  Score 30;  DB 2;  Length 6295;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-05;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        612 CAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||
Db       3045 CAGCTTCTTCATCAGGGACATCATCAAACC 3074


RESULT 69
US-08-659-206A-1
; Sequence 1, Application US/08659206A
; Patent No. 5922685
;  GENERAL INFORMATION:
;    APPLICANT:  Rakhmilevich, Alexander
;    TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53703
```

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;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/659,206A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  110229.91144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7287 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Plasmid DNA"
;    IMMEDIATE SOURCE:
;      CLONE:  pWRG3169
;    FEATURE:
;      NAME/KEY:  promoter
;      LOCATION:  1..628
;    FEATURE:
;      NAME/KEY:  iDNA
;      LOCATION:  629..810
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(953..1258, 1332..1673)
;      OTHER INFORMATION:  /product= "p35 gene product"
;    FEATURE:
;      NAME/KEY:  polyA_site
;      LOCATION:  1797..2024
;    FEATURE:
;      NAME/KEY:  promoter
;      LOCATION:  2110..2737
;    FEATURE:
;      NAME/KEY:  iDNA
;      LOCATION:  2738..2919
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2983..3990
;      OTHER INFORMATION:  /product= "p40 gene product"
;    FEATURE:
;      NAME/KEY:  polyA_site
;      LOCATION:  4075..4306
US-08-659-206A-1

  Query Match             3.3%;  Score 30;  DB 2;  Length 7287;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-05;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        612 CAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||
Db       3651 CAGCTTCTTCATCAGGGACATCATCAAACC 3680


RESULT 70
US-09-917-265A-86/c
; Sequence 86, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 86
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-917-265A-86

  Query Match             2.7%;  Score 25;  DB 3;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 0.016;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        895 AGCAACTGGGCATCCGTGTCCTGCA 919
              |||||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGCA 1


RESULT 71
US-09-949-016-24250/c
; Sequence 24250, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24250
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-24250

  Query Match             2.5%;  Score 23;  DB 3;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 0.2;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         61 GGAGAAATGGTGGTCCTCACCTG 83
              |||||||||||||||||||||||
Db         69 GGAGAAATGGTGGTCCTCACCTG 47


RESULT 72
US-09-949-016-24251/c
; Sequence 24251, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
```

```
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24251
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-24251

  Query Match             2.5%;  Score 23;  DB 3;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 0.2;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         61 GGAGAAATGGTGGTCCTCACCTG 83
              |||||||||||||||||||||||
Db         88 GGAGAAATGGTGGTCCTCACCTG 66


RESULT 73
US-09-949-016-190683/c
; Sequence 190683, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 190683
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-190683

  Query Match             2.5%;  Score 23;  DB 3;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 0.2;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         61 GGAGAAATGGTGGTCCTCACCTG 83
              |||||||||||||||||||||||
Db         69 GGAGAAATGGTGGTCCTCACCTG 47


RESULT 74
US-09-949-016-190684/c
; Sequence 190684, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 190684
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-190684

  Query Match             2.5%;  Score 23;  DB 3;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 0.2;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         61 GGAGAAATGGTGGTCCTCACCTG 83
              |||||||||||||||||||||||
Db         88 GGAGAAATGGTGGTCCTCACCTG 66


RESULT 75
US-09-917-265A-88/c
; Sequence 88, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 88
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-917-265A-88

  Query Match             2.4%;  Score 22;  DB 3;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 0.56;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        900 CTGGGCATCCGTGTCCTGCAGT 921
              ||||||||||||||||||||||
Db         25 CTGGGCATCCGTGTCCTGCAGT 4


RESULT 76
US-08-781-891-79/c
; Sequence 79, Application US/08781891
; Patent No. 6090620
;  GENERAL INFORMATION:
;    APPLICANT:  Fu, Ying-Hui
;    APPLICANT:  Yu, Chang-En
;    APPLICANT:  Oshima, Junko
;    APPLICANT:  Mulligan, John T.
;    APPLICANT:  Schellenberg, Gerald D.
;    TITLE OF INVENTION:  GENE AND GENE PRODUCTS RELATED TO
;    TITLE OF INVENTION:  WERNER'S SYNDROME
;    NUMBER OF SEQUENCES:  209
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/781,891
```

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;      FILING DATE:  27-DEC-1996
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 6090620tenburg Ph.D., Carol
;      REGISTRATION NUMBER:  39,317
;      REFERENCE/DOCKET NUMBER:  240052.419
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  79:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  87350 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-781-891-79

  Query Match             2.4%;  Score 22;  DB 3;  Length 87350;
  Best Local Similarity   100.0%;  Pred. No. 0.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        777 GAACAACAGAGAAAAGAAAGAC 798
              ||||||||||||||||||||||
Db      80388 GAACAACAGAGAAAAGAAAGAC 80367


RESULT 77
US-09-618-166-79/c
; Sequence 79, Application US/09618166
; Patent No. 6583112
;   GENERAL INFORMATION:
;       APPLICANT: Fu, Ying-Hui
;                  Yu, Chang-En
;                  Oshima, Junko
;                  Mulligan, John T.
;                  Schellenberg, Gerald D.
;       TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
;                           WERNER'S SYNDROME
;       NUMBER OF SEQUENCES: 209
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Seed Intellectual Property Law Group
;            STREET: 701 Fifth Avenue, Suite 6300
;            CITY: Seattle
;            STATE: Washington
;            COUNTRY: USA
;            ZIP: 98104-7092
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/618,166
;            FILING DATE: 17-Jul-2000
;            CLASSIFICATION: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: McMasters, David D.
;            REGISTRATION NUMBER: 33,963
;            REFERENCE/DOCKET NUMBER: 240052.419C1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (206) 622-4900
;            TELEFAX: (206) 682-6031
;   INFORMATION FOR SEQ ID NO: 79:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 87350 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-09-618-166-79

  Query Match             2.4%;  Score 22;  DB 3;  Length 87350;
  Best Local Similarity   100.0%;  Pred. No. 0.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        777 GAACAACAGAGAAAAGAAAGAC 798
              ||||||||||||||||||||||
Db      80388 GAACAACAGAGAAAAGAAAGAC 80367


RESULT 78
US-09-791-211-3/c
; Sequence 3, Application US/09791211
; Patent No. 6448080
; GENERAL INFORMATION:
;  APPLICANT:  Donna T. Ward
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION:  ANTISENSE MODULATION OF WRN EXPRESSION
;  FILE REFERENCE:  RTS-0205
;  CURRENT APPLICATION NUMBER: US/09/791,211
;  CURRENT FILING DATE:  2001-02-23
;  NUMBER OF SEQ ID NOS:  90
; SEQ ID NO 3
;   LENGTH: 87543
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 7421
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 7427
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 11609
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 12605
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 12742
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 29370
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 29422
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 29979
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 29980
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 29981
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 30136
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 30140
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 31205
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 31206
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 31592
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 33095
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
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; LOCATION: 33160
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 34066
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 34072
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 36816
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 39020
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 42164
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 42459
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 46808
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 46823
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 46826
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 47291
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 52786
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 52787
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 53384
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 54684
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 59215
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 59235
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 59242
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 63290
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 66614
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 68660
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 68697
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 68718
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 68733
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 68739
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 69785
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 79134
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 79198
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 86336
; OTHER INFORMATION: unknown
; OTHER INFORMATION:
US-09-791-211-3

Query Match 2.4%; Score 22; DB 3; Length 87543;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 777 GAACAACAGAGAAAAGAAAGAC 798
||||||||||||||||||||||
Db 80581 GAACAACAGAGAAAAGAAAGAC 80560

RESULT 79
US-09-011-143-14
; Sequence 14, Application US/09011143
; Patent No. 6472509
; GENERAL INFORMATION:
; APPLICANT: IMAMURA, Takayuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: FUJIYASU, Takeshi
; APPLICANT: IMAGAWA, Yoshitaka
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011,143
; FILING DATE: 04-FEB-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP97/01824
; FILING DATE: 29-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 165249/1996
; FILING DATE: 04-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: IMAMURA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

```
US-09-011-143-14

  Query Match             2.3%;  Score 21;  DB 3;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 1.9;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        481 GACAACAGGGATTATAAGAAG 501
              |||||||||||||||||||||
Db         24 GACAACAGGGATTATAAGAAG 44


RESULT 80
US-09-302-495-14
; Sequence 14, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 14:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 44 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-302-495-14

  Query Match             2.3%;  Score 21;  DB 3;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 1.9;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        481 GACAACAGGGATTATAAGAAG 501
              |||||||||||||||||||||
Db         24 GACAACAGGGATTATAAGAAG 44


RESULT 81
```

```
US-10-079-616-14
; Sequence 14, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 14:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 44 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-079-616-14

  Query Match             2.3%;  Score 21;  DB 3;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 1.9;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        481 GACAACAGGGATTATAAGAAG 501
              |||||||||||||||||||||
Db         24 GACAACAGGGATTATAAGAAG 44


RESULT 82
US-09-851-062-17/c
; Sequence 17, Application US/09851062
; Patent No. 6448081
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0247
;  CURRENT APPLICATION NUMBER: US/09/851,062
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 17
```

```
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-062-17

  Query Match             2.2%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.9;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        157 CTGACCATCCAAGTCAAAGA 176
              ||||||||||||||||||||
Db         20 CTGACCATCCAAGTCAAAGA 1


RESULT 83
US-09-851-062-22/c
; Sequence 22, Application US/09851062
; Patent No. 6448081
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0247
;  CURRENT APPLICATION NUMBER: US/09/851,062
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 22
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-062-22

  Query Match             2.2%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.9;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        254 AGGAAGATGGAATTTGGTCC 273
              ||||||||||||||||||||
Db         20 AGGAAGATGGAATTTGGTCC 1


RESULT 84
US-09-851-062-23/c
; Sequence 23, Application US/09851062
; Patent No. 6448081
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0247
;  CURRENT APPLICATION NUMBER: US/09/851,062
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 23
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-062-23

  Query Match             2.2%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.9;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        260 ATGGAATTTGGTCCACTGAT 279
              ||||||||||||||||||||
Db         20 ATGGAATTTGGTCCACTGAT 1


RESULT 85
US-09-851-062-26/c
; Sequence 26, Application US/09851062
; Patent No. 6448081
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0247
;  CURRENT APPLICATION NUMBER: US/09/851,062
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 26
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-062-26

  Query Match             2.2%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.9;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        352 TTCACCTGCTGGTGGCTGAC 371
              ||||||||||||||||||||
Db         20 TTCACCTGCTGGTGGCTGAC 1


RESULT 86
US-09-851-062-34/c
; Sequence 34, Application US/09851062
; Patent No. 6448081
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0247
;  CURRENT APPLICATION NUMBER: US/09/851,062
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 34
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-062-34

  Query Match             2.2%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.9;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        612 CAGCTTCTTCATCAGGGACA 631
              ||||||||||||||||||||
Db         20 CAGCTTCTTCATCAGGGACA 1


RESULT 87
US-09-851-062-35/c
; Sequence 35, Application US/09851062
; Patent No. 6448081
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0247
;  CURRENT APPLICATION NUMBER: US/09/851,062
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 35
;   LENGTH: 20
```

```
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-062-35

  Query Match             2.2%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.9;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        617 TCTTCATCAGGGACATCATC 636
              ||||||||||||||||||||
Db         20 TCTTCATCAGGGACATCATC 1


RESULT 88
US-09-851-062-36/c
; Sequence 36, Application US/09851062
; Patent No. 6448081
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0247
;  CURRENT APPLICATION NUMBER: US/09/851,062
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 36
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-062-36

  Query Match             2.2%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.9;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        622 ATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||
Db         20 ATCAGGGACATCATCAAACC 1


RESULT 89
US-09-011-143-13/c
; Sequence 13, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-13

  Query Match             2.2%;  Score 20;  DB 3;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        460 TCAGCAGAGAAGGTCAGAGT 479
              ||||||||||||||||||||
Db         32 TCAGCAGAGAAGGTCAGAGT 13


RESULT 90
US-09-302-495-13/c
; Sequence 13, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 13:
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;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 32 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-302-495-13

  Query Match             2.2%;  Score 20;  DB 3;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        460 TCAGCAGAGAAGGTCAGAGT 479
              ||||||||||||||||||||
Db         32 TCAGCAGAGAAGGTCAGAGT 13


RESULT 91
US-10-079-616-13/c
; Sequence 13, Application US/10079616
; Patent No. 6566097
;  GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 13:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 32 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-079-616-13

  Query Match             2.2%;  Score 20;  DB 3;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        460 TCAGCAGAGAAGGTCAGAGT 479
              ||||||||||||||||||||
Db         32 TCAGCAGAGAAGGTCAGAGT 13


RESULT 92
US-09-949-016-11844
; Sequence 11844, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11844
;   LENGTH: 119981
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-11844

  Query Match             2.2%;  Score 20;  DB 3;  Length 119981;
  Best Local Similarity   100.0%;  Pred. No. 8.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        305 AAAATAAGATCTTTCTAAAA 324
              ||||||||||||||||||||
Db      89012 AAAATAAGATCTTTCTAAAA 89031


RESULT 93
US-09-949-016-13606
; Sequence 13606, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13606
;   LENGTH: 119982
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-13606

  Query Match             2.2%;  Score 20;  DB 3;  Length 119982;
  Best Local Similarity   100.0%;  Pred. No. 8.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        305 AAAATAAGATCTTTCTAAAA 324
              ||||||||||||||||||||
Db      89012 AAAATAAGATCTTTCTAAAA 89031
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RESULT 94
US-09-851-062-33/c
; Sequence 33, Application US/09851062
; Patent No. 6448081
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0247
;  CURRENT APPLICATION NUMBER: US/09/851,062
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 33
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-062-33

  Query Match             2.1%;  Score 19;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCT 616
              |||||||||||||||||||
Db         19 GAAAACTACACCAGCAGCT 1


RESULT 95
US-08-359-850-3
; Sequence 3, Application US/08359850
; Patent No. 5951982
;  GENERAL INFORMATION:
;    APPLICANT:  Z ller, Margot
;    APPLICANT:  Herrlich, Peter
;    APPLICANT:  Ponta, Helmut
;    TITLE OF INVENTION:  Use of Antibody-Containing Preparations
;    TITLE OF INVENTION:  for Immunosuppression
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein and Fox
;      STREET:  1225 Connecticut Avenue
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/359,850
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/963,323
;      FILING DATE:
;      APPLICATION NUMBER:  DE P 41 34 982.2
;      FILING DATE:  23-OCT-1991
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 833-7533
;      TELEFAX:  (202) 833-8716
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1002 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
US-08-359-850-3

  Query Match             2.1%;  Score 19;  DB 2;  Length 1002;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        160 ACCATCCAAGTCAAAGAAT 178
              |||||||||||||||||||
Db        502 ACCATCCAAGTCAAAGAAT 520


RESULT 96
US-07-946-497-1
; Sequence 1, Application US/07946497
; Patent No. 5506119
;  GENERAL INFORMATION:
;    APPLICANT:  HERRLICH, Peter
;    APPLICANT:  PONTA, Helmut
;    APPLICANT:  GUENTHERT, Ursula
;    APPLICANT:  MATZKU, Siegfried
;    APPLICANT:  WENZL, Achim
;    TITLE OF INVENTION:  VARIANT CD44 SURFACE PROTEINS, DNA
;    TITLE OF INVENTION:  SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
;    TITLE OF INVENTION:  AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington, D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/946,497
;      FILING DATE:  19921109
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  16915/145
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3207 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  p-Meta-1
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  113..1624
US-07-946-497-1

  Query Match             2.1%;  Score 19;  DB 2;  Length 3207;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        160 ACCATCCAAGTCAAAGAAT 178
              |||||||||||||||||||
Db       1158 ACCATCCAAGTCAAAGAAT 1176


RESULT 97
US-08-483-322-1
; Sequence 1, Application US/08483322
; Patent No. 5760178
;  GENERAL INFORMATION:
```

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;     APPLICANT:  HERRLICH, Peter
;     APPLICANT:  PONTA, Helmut
;     APPLICANT:  GUENTHERT, Ursula
;     APPLICANT:  MATZKU, Siegfried
;     APPLICANT:  WENZL, Achim
;     TITLE OF INVENTION:  VARIANT CD44 SURFACE PROTEINS, DNA
;     TITLE OF INVENTION:  SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
;     TITLE OF INVENTION:  AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
;     NUMBER OF SEQUENCES:  8
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Foley & Lardner
;       STREET:  3000 K Street, N.W., Suite 500
;       CITY:  Washington, D.C.
;       COUNTRY:  USA
;       ZIP:  20007-5109
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/483,322
;       FILING DATE:  07-JUN-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/946,497
;       FILING DATE:  09-NOV-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  BENT, Stephen A.
;       REGISTRATION NUMBER:  29,768
;       REFERENCE/DOCKET NUMBER:  16915/145
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202)672-5300
;       TELEFAX:  (202)672-5399
;       TELEX:  904136
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  3207 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     IMMEDIATE SOURCE:
;       CLONE:  p-Meta-1
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  113..1624
US-08-483-322-1

  Query Match             2.1%;  Score 19;  DB 2;  Length 3207;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        160 ACCATCCAAGTCAAAGAAT 178
              ||||||||||||||||||
Db       1158 ACCATCCAAGTCAAAGAAT 1176


RESULT 98
US-08-478-882-1
; Sequence 1, Application US/08478882
; Patent No. 5885575
;  GENERAL INFORMATION:
;     APPLICANT:  HERRLICH, Peter
;     APPLICANT:  PONTA, Helmut
;     APPLICANT:  GUENTHERT, Ursula
;     APPLICANT:  MATZKU, Siegfried
;     APPLICANT:  WENZL, Achim
;     TITLE OF INVENTION:  VARIANT CD44 SURFACE PROTEINS, DNA
;     TITLE OF INVENTION:  SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
;     TITLE OF INVENTION:  AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
;     NUMBER OF SEQUENCES:  8
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Foley & Lardner
;       STREET:  3000 K Street, N.W., Suite 500
;       CITY:  Washington, D.C.
;       COUNTRY:  USA
;       ZIP:  20007-5109
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/478,882
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/946,497
;       FILING DATE:  19921109
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  BENT, Stephen A.
;       REGISTRATION NUMBER:  29,768
;       REFERENCE/DOCKET NUMBER:  16915/145
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202)672-5300
;       TELEFAX:  (202)672-5399
;       TELEX:  904136
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  3207 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     IMMEDIATE SOURCE:
;       CLONE:  p-Meta-1
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  113..1624
US-08-478-882-1

  Query Match             2.1%;  Score 19;  DB 2;  Length 3207;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        160 ACCATCCAAGTCAAAGAAT 178
              ||||||||||||||||||
Db       1158 ACCATCCAAGTCAAAGAAT 1176


RESULT 99
US-08-817-926-27
; Sequence 27, Application US/08817926
; Patent No. 6001590
;  GENERAL INFORMATION:
;     APPLICANT:  Komeda, Toshihiro
;     APPLICANT:  Suda, Hisako
;     APPLICANT:  Tamai, Yukio
;     APPLICANT:  Iwamatsu, Akihiro
;     APPLICANT:  Kato, No. 6001590uo
;     APPLICANT:  Sakai, Yasuyoshi
;     TITLE OF INVENTION:  PROMOTER/TERMINATOR FOR CANDIDA BOIDINII
;     TITLE OF INVENTION:  FORMATE DEHYDROGENASE GENE
;     NUMBER OF SEQUENCES:  51
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Foley & Lardner
;       STREET:  3000 K Street, N.W., Suite 500
;       CITY:  Washington
;       STATE:  D.C.
;       COUNTRY:  USA
;       ZIP:  20007-5109
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
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;       APPLICATION NUMBER:  US/08/817,926
;       FILING DATE:  09-MAY-1997
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/JP96/02597
;       FILING DATE:  12-SEP-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 234133/1995
;       FILING DATE:  12-SEP-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 42536/1996
;       FILING DATE:  29-FEB-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Bent, Stephen A.
;       REGISTRATION NUMBER:  29,768
;       REFERENCE/DOCKET NUMBER:  081356/0112
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202)672-5300
;       TELEFAX:  (202)672-5399
;       TELEX:  904136
;   INFORMATION FOR SEQ ID NO:  27:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  4818 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     ORIGINAL SOURCE:
;       ORGANISM:  Candida boidinii
US-08-817-926-27

  Query Match             2.1%;  Score 19;  DB 3;  Length 4818;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        775 AAGAACAACAGAGAAAAGA 793
              |||||||||||||||||||
Db       3169 AAGAACAACAGAGAAAAGA 3187


RESULT 100
US-09-949-016-12134
; Sequence 12134, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12134
;   LENGTH: 37838
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-12134

  Query Match             2.1%;  Score 19;  DB 3;  Length 37838;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        319 CTAAAATGTGAGGCAAAGA 337
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Db       6811 CTAAAATGTGAGGCAAAGA 6829


Search completed: June  9, 2006, 23:48:39
Job time : 212.38 secs
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2006, 23:31:05 ; Search time 1548.16 Seconds
(without alignments)
7309.894 Million cell updates/sec

Title: US-10-821-670A-26
Perfect score: 921
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

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3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
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8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
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11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	921	100.0	921	3	US-09-917-265-26	Sequence 26, Appl
c	2	921	100.0	921	3	US-09-917-265-28	Sequence 28, Appl
	3	921	100.0	921	9	US-10-821-670-26	Sequence 26, Appl
c	4	921	100.0	921	9	US-10-821-670-28	Sequence 28, Appl
	5	921	100.0	1533	3	US-09-917-265-43	Sequence 43, Appl
c	6	921	100.0	1533	3	US-09-917-265-45	Sequence 45, Appl
	7	921	100.0	1533	9	US-10-821-670-43	Sequence 43, Appl
c	8	921	100.0	1533	9	US-10-821-670-45	Sequence 45, Appl
	9	921	100.0	1599	3	US-09-917-265-38	Sequence 38, Appl
c	10	921	100.0	1599	3	US-09-917-265-40	Sequence 40, Appl
	11	921	100.0	1599	9	US-10-821-670-38	Sequence 38, Appl
c	12	921	100.0	1599	9	US-10-821-670-40	Sequence 40, Appl
	13	870	94.5	921	6	US-10-079-616-6	Sequence 6, Appli
	14	870	94.5	987	3	US-09-917-265-29	Sequence 29, Appl
c	15	870	94.5	987	3	US-09-917-265-31	Sequence 31, Appl
	16	870	94.5	987	9	US-10-821-670-29	Sequence 29, Appl
c	17	870	94.5	987	9	US-10-821-670-31	Sequence 31, Appl
	18	870	94.5	2193	6	US-10-079-616-5	Sequence 5, Appli
	19	868	94.2	985	3	US-09-917-265-55	Sequence 55, Appl
c	20	868	94.2	985	3	US-09-917-265-57	Sequence 57, Appl
	21	868	94.2	985	9	US-10-821-670-55	Sequence 55, Appl
c	22	868	94.2	985	9	US-10-821-670-57	Sequence 57, Appl
	23	819	88.9	921	6	US-10-079-616-7	Sequence 7, Appli
	24	768	83.4	990	7	US-10-041-672C-1	Sequence 1, Appli
	25	768	83.4	4522	7	US-10-041-672C-10	Sequence 10, Appl
	26	66	7.2	921	3	US-09-917-265-52	Sequence 52, Appl
c	27	66	7.2	921	3	US-09-917-265-54	Sequence 54, Appl
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ALIGNMENTS

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RESULT 1
US-09-917-265-26
; Sequence 26, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(921)
;   OTHER INFORMATION:
US-09-917-265-26

  Query Match             100.0%;  Score 921;  DB 3;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 2
US-09-917-265-28/c
; Sequence 28, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-28

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  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
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Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCAGT 1


RESULT 3
US-10-821-670-26
; Sequence 26, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(921)
US-10-821-670-26

  Query Match             100.0%;  Score 921;  DB 9;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 4
US-10-821-670-28/c
; Sequence 28, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-28

  Query Match             100.0%;  Score 921;  DB 9;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622
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Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCAGT 1
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RESULT 5
US-09-917-265-43
; Sequence 43, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)
; OTHER INFORMATION:
US-09-917-265-43

Query Match 100.0%; Score 921; DB 3; Length 1533;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921
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RESULT 6
US-09-917-265-45/c
; Sequence 45, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.

```
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-45

  Query Match             100.0%;  Score 921;  DB 3;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613


RESULT 7
US-10-821-670-43
; Sequence 43, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-10-821-670-43

  Query Match             100.0%;  Score 921;  DB 9;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921

Db        901 TGGGCATCCGTGTCCTGCAGT 921
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RESULT 8
US-10-821-670-45/c
; Sequence 45, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
US-10-821-670-45

Query Match 100.0%; Score 921; DB 9; Length 1533;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGT 921

Db        633 TGGGCATCCGTGTCCTGCAGT 613
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RESULT 9
US-09-917-265-38
; Sequence 38, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1599)
; OTHER INFORMATION:

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US-09-917-265-38

  Query Match             100.0%;  Score 921;  DB 3;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987


RESULT 10
US-09-917-265-40/c
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; Sequence 40, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-40

  Query Match             100.0%;  Score 921;  DB 3;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613


RESULT 11
US-10-821-670-38
; Sequence 38, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-10-821-670-38

  Query Match             100.0%;  Score 921;  DB 9;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987


RESULT 12
US-10-821-670-40/c
; Sequence 40, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-40

  Query Match             100.0%;  Score 921;  DB 9;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354
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Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613


RESULT 13
US-10-079-616-6
; Sequence 6, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-079-616-6

  Query Match           94.5%;  Score 870;  DB 6;  Length 921;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
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Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921
```

RESULT 14
US-09-917-265-29
; Sequence 29, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(987)
; OTHER INFORMATION:
US-09-917-265-29

Query Match 94.5%; Score 870; DB 3; Length 987;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 920; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987
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RESULT 15
US-09-917-265-31/c
; Sequence 31, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THER
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265-31

Query Match 94.5%; Score 870; DB 3; Length 987;
Best Local Similarity 99.9%; Pred. No. 0;

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  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        781 AACAGAGAAAAGAAAGAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCAGT 1


RESULT 16
US-10-821-670-29
; Sequence 29, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
US-10-821-670-29

  Query Match             94.5%;  Score 870;  DB 9;  Length 987;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987


RESULT 17
US-10-821-670-31/c
; Sequence 31, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-31

  Query Match             94.5%;  Score 870;  DB 9;  Length 987;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCAGT 1


RESULT 18
US-10-079-616-5
; Sequence 5, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
```

```
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2193 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-079-616-5

  Query Match             94.5%;  Score 870;  DB 6;  Length 2193;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 189

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 249

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 309

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 369

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 429

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 489

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 549

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        550 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 609

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 669

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 729

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 789

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 849

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 909

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 969

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 1029

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db       1030 TGGGCATCCGTGTCCTGCAGT 1050


RESULT 19
US-09-917-265-55
; Sequence 55, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(984)
;   OTHER INFORMATION:
US-09-917-265-55

  Query Match             94.2%;  Score 868;  DB 3;  Length 985;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
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Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCA 919
              ||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCA 985
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RESULT 20
US-09-917-265-57/c
; Sequence 57, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
; LENGTH: 985
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265-57

Query Match 94.2%; Score 868; DB 3; Length 985;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 918; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 860

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 800

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 740

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 680

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 620

Qy        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 560

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 500

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 440

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 380

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 320

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 260

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 200

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 140

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 80

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 20

Qy        901 TGGGCATCCGTGTCCTGCA 919
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Db         19 TGGGCATCCGTGTCCTGCA 1
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RESULT 21
US-10-821-670-55
; Sequence 55, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
; LENGTH: 985
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(984)
US-10-821-670-55

Query Match 94.2%; Score 868; DB 9; Length 985;
Best Local Similarity 99.9%; Pred. No. 0;

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  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCA 919
              ||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCA 985


RESULT 22
US-10-821-670-57/c
; Sequence 57, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-57

  Query Match             94.2%;  Score 868;  DB 9;  Length 985;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 860

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 800

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 740

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 680

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 620

Qy        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 560

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 500

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        499 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 440

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 380

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 320

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 260

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 200

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 140

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
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; SEQ ID NO 1
;   LENGTH: 990
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: feline IL-12 p40
US-10-041-672C-1

  Query Match             83.4%;  Score 768;  DB 7;  Length 990;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987


RESULT 25
US-10-041-672C-10
; Sequence 10, Application US/10041672C
; Publication No. US20030157059A1
; GENERAL INFORMATION:
;  APPLICANT: Mologen Forschungs-, Entwicklungs- und Vetriebs GmbH
;  APPLICANT:  Universitat Zurich
;  TITLE OF INVENTION: FELINE INTERLEUKIN-12 AS IMMUNOSTIMULANT
;  FILE REFERENCE: NHL-NP-36
;  CURRENT APPLICATION NUMBER: US/10/041,672C
;  CURRENT FILING DATE:  2002-01-08
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 4522
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pMol-fil12p40
US-10-041-672C-10

  Query Match             83.4%;  Score 768;  DB 7;  Length 4522;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches  918;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3113 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 3172

Qy         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       3173 GGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 3232

Qy        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3233 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 3292

Qy        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3293 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 3352

Qy        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3353 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 3412

Qy        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3413 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 3472

Qy        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3473 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 3532

Qy        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       3533 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 3592

Qy        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3593 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 3652

Qy        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3653 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 3712

Qy        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3713 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 3772
```

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Qy        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3773 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 3832

Qy        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3833 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 3892

Qy        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3893 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 3952

Qy        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       3953 AAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGGAGCAAC 4012

Qy        901 TGGGCATCCGTGTCCTGCAGT 921
              |||||||||||||||||||||
Db       4013 TGGGCATCCGTGTCCTGCAGT 4033


RESULT 26
US-09-917-265-52
; Sequence 52, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(921)
;   OTHER INFORMATION:
US-09-917-265-52

  Query Match             7.2%;  Score 66;  DB 3;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy        531 CTGCCC 536
              ||||||
Db        531 CTGCCC 536


RESULT 27
US-09-917-265-54/c
; Sequence 54, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-54

  Query Match             7.2%;  Score 66;  DB 3;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy        531 CTGCCC 536
              ||||||
Db        391 CTGCCC 386


RESULT 28
US-10-821-670-52
; Sequence 52, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(921)
US-10-821-670-52

  Query Match             7.2%;  Score 66;  DB 9;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy        531 CTGCCC 536
              ||||||
Db        531 CTGCCC 536


RESULT 29
US-10-821-670-54/c
; Sequence 54, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
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;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-54

  Query Match             7.2%;  Score 66;  DB 9;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy        531 CTGCCC 536
              ||||||
Db        391 CTGCCC 386


RESULT 30
US-09-917-265-58
; Sequence 58, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
;   OTHER INFORMATION:
US-09-917-265-58

  Query Match             7.2%;  Score 66;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        531 CTGCCC 536
              ||||||
Db        597 CTGCCC 602


RESULT 31
US-09-917-265-60/c
; Sequence 60, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-60

  Query Match             7.2%;  Score 66;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy        531 CTGCCC 536
              ||||||
Db        391 CTGCCC 386


RESULT 32
US-10-821-670-58
; Sequence 58, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
US-10-821-670-58

  Query Match             7.2%;  Score 66;  DB 9;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        531 CTGCCC 536
              ||||||
Db        597 CTGCCC 602


RESULT 33
US-10-821-670-60/c
; Sequence 60, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
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; SEQ ID NO 60
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-60

  Query Match             7.2%;  Score 66;  DB 9;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy        531 CTGCCC 536
              ||||||
Db        391 CTGCCC 386


RESULT 34
US-09-917-265-66
; Sequence 66, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
;   OTHER INFORMATION:
US-09-917-265-66

  Query Match             7.2%;  Score 66;  DB 3;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy        531 CTGCCC 536
              ||||||
Db        531 CTGCCC 536


RESULT 35
US-09-917-265-68/c
; Sequence 68, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-68

  Query Match             7.2%;  Score 66;  DB 3;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy        531 CTGCCC 536
              ||||||
Db       1003 CTGCCC 998


RESULT 36
US-10-821-670-66
; Sequence 66, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-10-821-670-66

  Query Match             7.2%;  Score 66;  DB 9;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy        531 CTGCCC 536
              ||||||
Db        531 CTGCCC 536


RESULT 37
US-10-821-670-68/c
; Sequence 68, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
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;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-68

  Query Match             7.2%;  Score 66;  DB 9;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy        531 CTGCCC 536
              ||||||
Db       1003 CTGCCC 998


RESULT 38
US-09-917-265-61
; Sequence 61, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
US-09-917-265-61

  Query Match             7.2%;  Score 66;  DB 3;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        531 CTGCCC 536
              ||||||
Db        597 CTGCCC 602


RESULT 39
US-09-917-265-63/c
; Sequence 63, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-63

  Query Match             7.2%;  Score 66;  DB 3;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy        531 CTGCCC 536
              ||||||
Db       1003 CTGCCC 998


RESULT 40
US-10-821-670-61
; Sequence 61, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-10-821-670-61

  Query Match             7.2%;  Score 66;  DB 9;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        531 CTGCCC 536
              ||||||
Db        597 CTGCCC 602


RESULT 41
US-10-821-670-63/c
; Sequence 63, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
;   LENGTH: 1599
```

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;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-63

  Query Match             7.2%;  Score 66;  DB 9;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy        531 CTGCCC 536
              ||||||
Db       1003 CTGCCC 998


RESULT 42
US-09-917-265-107
; Sequence 107, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 107
;   LENGTH: 2267
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (154)..(1140)
;   OTHER INFORMATION:
US-09-917-265-107

  Query Match             7.2%;  Score 66;  DB 3;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 749

Qy        531 CTGCCC 536
              ||||||
Db        750 CTGCCC 755


RESULT 43
US-09-917-265-109/c
; Sequence 109, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 109
;   LENGTH: 2267
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-109

  Query Match             7.2%;  Score 66;  DB 3;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1578 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1519

Qy        531 CTGCCC 536
              ||||||
Db       1518 CTGCCC 1513


RESULT 44
US-10-821-670-107
; Sequence 107, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 107
;   LENGTH: 2267
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (154)..(1140)
US-10-821-670-107

  Query Match             7.2%;  Score 66;  DB 9;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 749

Qy        531 CTGCCC 536
              ||||||
Db        750 CTGCCC 755


RESULT 45
US-10-821-670-109/c
; Sequence 109, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 109
;   LENGTH: 2267
;   TYPE: DNA
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```
;   ORGANISM: Canis familiaris
US-10-821-670-109

  Query Match             7.2%;  Score 66;  DB 9;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1578 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1519

Qy        531 CTGCCC 536
              ||||||
Db       1518 CTGCCC 1513


RESULT 46
US-11-136-527-4408
; Sequence 4408, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William M
;  TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
;  FILE REFERENCE: 031896-041000 (AM101086)
;  CURRENT APPLICATION NUMBER: US/11/136,527
;  CURRENT FILING DATE:  2005-05-25
;  PRIOR APPLICATION NUMBER: US 60/574,294
;  PRIOR FILING DATE: 2005-05-26
;  NUMBER OF SEQ ID NOS: 362830
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4408
;   LENGTH: 600
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-11-136-527-4408

  Query Match             5.5%;  Score 51;  DB 16;  Length 600;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-16;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        612 CAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCA 662
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCA 311


RESULT 47
US-11-136-527-312
; Sequence 312, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William M
;  TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
;  FILE REFERENCE: 031896-041000 (AM101086)
;  CURRENT APPLICATION NUMBER: US/11/136,527
;  CURRENT FILING DATE:  2005-05-25
;  PRIOR APPLICATION NUMBER: US 60/574,294
;  PRIOR FILING DATE: 2005-05-26
;  NUMBER OF SEQ ID NOS: 362830
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 312
;   LENGTH: 1024
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-11-136-527-312

  Query Match             5.5%;  Score 51;  DB 16;  Length 1024;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-16;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        612 CAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCA 662
              |||||||||||||||||||||||||||||||||||||||||||||||||||

Db        685 CAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCA 735


RESULT 48
US-09-754-014-2
; Sequence 2, Application US/09754014
; Patent No. US20020119940A1
;   GENERAL INFORMATION:
;        APPLICANT: Jeff No. US20020119940A1dstrom
;                   Bruce Freimark
;                   Deepa Deshpande
;        TITLE OF INVENTION: GENE EXPRESSION AND DELIVERY SYTEMS
;                            AND USES
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                      Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 90071-2066
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                          storage
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: IBM P.C. DOS 5.0
;             SOFTWARE: FastSEQ for Windows 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/754,014
;             FILING DATE: 03-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/948,958
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Berkman, Charles S.
;             REGISTRATION NUMBER: 38,077
;             REFERENCE/DOCKET NUMBER: 226/284
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 987 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-754-014-2

  Query Match             4.8%;  Score 44;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 49
US-09-836-866-2
; Sequence 2, Application US/09836866
; Patent No. US20020123473A1
;   GENERAL INFORMATION:
;        APPLICANT: No. US20020123473A1dstrom, Jeff
;                   Freimark, Bruce
;                   Deshpande, Deepa
;        TITLE OF INVENTION: IL-12 GENE EXPRESSION AND
;                            DELIVERY SYTEMS AND USES
;        NUMBER OF SEQUENCES: 8
;        CORRESPONDENCE ADDRESS:
```

```
;               ADDRESSEE: Lyon & Lyon
;               STREET: 633 West Fifth Street
;                       Suite 4700
;               CITY: Los Angeles
;               STATE: California
;               COUNTRY: U.S.A.
;               ZIP: 90071-2066
;          COMPUTER READABLE FORM:
;               MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                            storage
;               COMPUTER: IBM Compatible
;               OPERATING SYSTEM: IBM P.C. DOS 5.0
;               SOFTWARE: FastSEQ for Windows 2.0
;          CURRENT APPLICATION DATA:
;               APPLICATION NUMBER: US/09/836,866
;               FILING DATE: 16-Apr-2001
;               CLASSIFICATION: <Unknown>
;          PRIOR APPLICATION DATA:
;               APPLICATION NUMBER: 08/949,160
;               FILING DATE: <Unknown>
;          ATTORNEY/AGENT INFORMATION:
;               NAME: Warburg, Richard J.
;               REGISTRATION NUMBER: 32,327
;               REFERENCE/DOCKET NUMBER: 226/285
;          TELECOMMUNICATION INFORMATION:
;               TELEPHONE: (213) 489-1600
;               TELEFAX: (213) 955-0440
;               TELEX: 67-3510
;     INFORMATION FOR SEQ ID NO: 2:
;          SEQUENCE CHARACTERISTICS:
;               LENGTH: 987 base pairs
;               TYPE: nucleic acid
;               STRANDEDNESS: single
;               TOPOLOGY: linear
;          SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-836-866-2

  Query Match             4.8%;  Score 44;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 50
US-09-826-025-24
; Sequence 24, Application US/09826025
; Patent No. US20020162123A1
;   GENERAL INFORMATION:
;        APPLICANT: Chang, Lung-Ji
;        TITLE OF INVENTION: Combination Immunogene Therapy
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Medlen & Carroll, LLP
;             STREET: 220 Montgomery Street, Suite 2200
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: United States of America
;             ZIP: 94104
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/826,025
;             FILING DATE: 04-Apr-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/838,702
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ingolia, Diane E.
;             REGISTRATION NUMBER: 40,027
;             REFERENCE/DOCKET NUMBER: CHANG-02687
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 705-8410
;             TELEFAX: (415) 397-8338
;   INFORMATION FOR SEQ ID NO: 24:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 987 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: other nucleic acid
;             DESCRIPTION: /desc = "DNA"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-826-025-24

  Query Match             4.8%;  Score 44;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 51
US-10-785-577-24
; Sequence 24, Application US/10785577
; Publication No. US20040237129A1
;   GENERAL INFORMATION:
;        APPLICANT: Chang, Lung-Ji
;        TITLE OF INVENTION: Combination Immunogene Therapy
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Medlen & Carroll, LLP
;             STREET: 220 Montgomery Street, Suite 2200
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: United States of America
;             ZIP: 94104
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/785,577
;             FILING DATE: 23-Feb-2004
;             CLASSIFICATION: 424
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/838,702
;             FILING DATE: 9-Apr-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ingolia, Diane E.
;             REGISTRATION NUMBER: 40,027
;             REFERENCE/DOCKET NUMBER: CHANG-02687
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 705-8410
;             TELEFAX: (415) 397-8338
;   INFORMATION FOR SEQ ID NO: 24:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 987 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: other nucleic acid
;             DESCRIPTION: /desc = "DNA"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-785-577-24

  Query Match             4.8%;  Score 44;  DB 9;  Length 987;
```

```
  Best Local Similarity   100.0%;  Pred. No. 3.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 52
US-10-373-456-18
; Sequence 18, Application US/10373456
; Publication No. US20040009146A1
; GENERAL INFORMATION:
;  APPLICANT: Podhajcer, Osvaldo
;  TITLE OF INVENTION: Anti-Tumor Vaccine and Method
;  FILE REFERENCE: 1423P-US/101141-14
;  CURRENT APPLICATION NUMBER: US/10/373,456
;  CURRENT FILING DATE:  2003-02-25
;  PRIOR APPLICATION NUMBER: US 60/359,836
;  PRIOR FILING DATE: 2002-02-26
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 1005
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-373-456-18

  Query Match             4.8%;  Score 44;  DB 7;  Length 1005;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        669 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 712


RESULT 53
US-10-221-975A-1
; Sequence 1, Application US/10221975A
; Publication No. US20040023332A1
; GENERAL INFORMATION:
;  APPLICANT: Pohang University of Science and Technology
;  APPLICANT:  Progen Co., Ltd.
;  APPLICANT:  Sung, Young Chul
;  APPLICANT:  Lee, Sung Hee
;  APPLICANT:  Ha, Sang Jun
;  APPLICANT:  Song, Man Ki
;  APPLICANT:  Chang, Jun
;  TITLE OF INVENTION: Genes of IL-12p40 Subunit Mutated for Improving the Activity of
;  TITLE OF INVENTION:  IL-12 and Use Thereof for DNA Vaccine Adjuvant
;  FILE REFERENCE: 59520-00005
;  CURRENT APPLICATION NUMBER: US/10/221,975A
;  CURRENT FILING DATE:  2003-04-02
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 1007
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-221-975A-1

  Query Match             4.8%;  Score 44;  DB 8;  Length 1007;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        667 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 710


RESULT 54
US-10-373-456-20
; Sequence 20, Application US/10373456
; Publication No. US20040009146A1
; GENERAL INFORMATION:
;  APPLICANT: Podhajcer, Osvaldo
;  TITLE OF INVENTION: Anti-Tumor Vaccine and Method
;  FILE REFERENCE: 1423P-US/101141-14
;  CURRENT APPLICATION NUMBER: US/10/373,456
;  CURRENT FILING DATE:  2003-02-25
;  PRIOR APPLICATION NUMBER: US 60/359,836
;  PRIOR FILING DATE: 2002-02-26
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 1017
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-373-456-20

  Query Match             4.8%;  Score 44;  DB 7;  Length 1017;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        673 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 716


RESULT 55
US-10-267-384-194
; Sequence 194, Application US/10267384
; Publication No. US20030198623A1
;   GENERAL INFORMATION:
;        APPLICANT: Paoletti, Enzo
;                   Tartaglia, James
;                   Cox, William I.
;        TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
;        NUMBER OF SEQUENCES: 217
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Curtis, Morris & Safford
;             STREET: 530 Fifth Avenue
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10036
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/267,384
;             FILING DATE: 09-Oct-2002
;             CLASSIFICATION: 435
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Frommer, William S.
;             REGISTRATION NUMBER: 25,506
;             REFERENCE/DOCKET NUMBER: 454310-2530
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 840-3333
;             TELEFAX: (212) 840-0712
;             TELEX: 425066CURTMS
;   INFORMATION FOR SEQ ID NO: 194:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1018 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-10-267-384-194

  Query Match             4.8%;  Score 44;  DB 7;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-12;
```

```
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 56
US-10-603-064-4
; Sequence 4, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
;  APPLICANT: Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION: Multiple Cytokine Protein Complexes
;  FILE REFERENCE: LEX-010
;  CURRENT APPLICATION NUMBER: US/10/603,064
;  CURRENT FILING DATE:  2003-06-24
;  PRIOR APPLICATION NUMBER: US/09/634,368
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: 60/147,924
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 1389
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: human
;   OTHER INFORMATION: p40-IL-2 fusion protein coding sequence
US-10-603-064-4

  Query Match             4.8%;  Score 44;  DB 8;  Length 1389;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 57
US-10-349-507-2
; Sequence 2, Application US/10349507
; Publication No. US20030199002A1
; GENERAL INFORMATION:
;  APPLICANT: Hekimi , Siegfried
;  APPLICANT:  Jiang , Ning
;  APPLICANT:  Benard, Claire
;  APPLICANT:  Kebir , Hania
;  APPLICANT:  McCright, Brenton
;  APPLICANT:  Lakowski , Bernard
;  TITLE OF INVENTION: CLK-2 NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
;  FILE REFERENCE: 11202-006-999
;  CURRENT APPLICATION NUMBER: US/10/349,507
;  CURRENT FILING DATE:  2003-01-22
;  PRIOR APPLICATION NUMBER: 10/312,187
;  PRIOR FILING DATE: 2002-12-20
;  PRIOR APPLICATION NUMBER: PCT/CA01/00913
;  PRIOR FILING DATE: 2001-06-20
;  PRIOR APPLICATION NUMBER: 60/213,174
;  PRIOR FILING DATE: 2000-06-22
;  PRIOR APPLICATION NUMBER: 60/254,932
;  PRIOR FILING DATE: 2000-12-13
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 1397
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (41)...(1024)
US-10-349-507-2

  Query Match             4.8%;  Score 44;  DB 7;  Length 1397;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        701 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 744


RESULT 58
US-10-267-565-2
; Sequence 2, Application US/10267565
; Publication No. US20030204059A1
; GENERAL INFORMATION:
;  APPLICANT: Gately, Maurice
;  APPLICANT:  Gubler, Ulrich
;  APPLICANT:  Hulmes, Jeffery
;  APPLICANT:  Podlaski, Frank
;  APPLICANT:  Stern, Alvin
;  TITLE OF INVENTION: PURIFICATION AND CHARACTERIZATION OF CYTOTOXIC
;  TITLE OF INVENTION:  LYMPHOCYTE MATURATION FACTOR AND MONOCLONAL
;  TITLE OF INVENTION:  ANTIBODIES THERETO
;  FILE REFERENCE: 11126-005
;  CURRENT APPLICATION NUMBER: US/10/267,565
;  CURRENT FILING DATE:  2003-01-23
;  PRIOR APPLICATION NUMBER: 09/401,839
;  PRIOR FILING DATE: 1999-09-22
;  PRIOR APPLICATION NUMBER: 08/459,151
;  PRIOR FILING DATE: 1995-06-02
;  PRIOR APPLICATION NUMBER: 08/205,011
;  PRIOR FILING DATE: 1994-03-02
;  PRIOR APPLICATION NUMBER: 07/857,023
;  PRIOR FILING DATE: 1992-03-24
;  PRIOR APPLICATION NUMBER: 07/572,284
;  PRIOR FILING DATE: 1990-08-27
;  PRIOR APPLICATION NUMBER: 07/520,935
;  PRIOR FILING DATE: 1990-05-09
;  PRIOR APPLICATION NUMBER: 07/455,708
;  PRIOR FILING DATE: 1989-12-22
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 1397
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (41)...(1024)
US-10-267-565-2

  Query Match             4.8%;  Score 44;  DB 7;  Length 1397;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        701 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 744


RESULT 59
US-10-929-182-22
; Sequence 22, Application US/10929182
; Publication No. US20050064483A1
; GENERAL INFORMATION:
;  APPLICANT: Zang, Jingwu
;  APPLICANT:  Hong, Jian
;  TITLE OF INVENTION: Gene Expression Profiling Technology for Treatment Evaluation of
;  TITLE OF INVENTION:  Multiple Sclerosis
;  FILE REFERENCE: HO-P02859US1
;  CURRENT APPLICATION NUMBER: US/10/929,182
```

```
;  CURRENT FILING DATE:  2004-08-30
;  PRIOR APPLICATION NUMBER: US 60/498,731
;  PRIOR FILING DATE: 2003-08-28
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
;   LENGTH: 1399
;   TYPE: DNA
;   ORGANISM: HUMAN
US-10-929-182-22

  Query Match             4.8%;  Score 44;  DB 10;  Length 1399;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        703 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 746


RESULT 60
US-10-742-405-7
; Sequence 7, Application US/10742405
; Publication No. US20040213761A1
; GENERAL INFORMATION:
;  APPLICANT: Bowman, Edward P.
;  APPLICANT:  Chan, Jason R.
;  APPLICANT:  Moore, Kevin
;  APPLICANT:  Nguyen, Nhung
;  APPLICANT:  Churakova, Tatyana
;  APPLICANT:  Chen, Shi-Juan
;  APPLICANT:  Cua, Daniel J.
;  TITLE OF INVENTION: Uses of mammalian cytokine; related reagents
;  FILE REFERENCE: DX01578K
;  CURRENT APPLICATION NUMBER: US/10/742,405
;  CURRENT FILING DATE:  2003-12-18
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
;   LENGTH: 1580
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (7)..(1569)
US-10-742-405-7

  Query Match             4.8%;  Score 44;  DB 9;  Length 1580;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        673 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 716


RESULT 61
US-10-373-456-2
; Sequence 2, Application US/10373456
; Publication No. US20040009146A1
; GENERAL INFORMATION:
;  APPLICANT: Podhajcer, Osvaldo
;  TITLE OF INVENTION: Anti-Tumor Vaccine and Method
;  FILE REFERENCE: 1423P-US/101141-14
;  CURRENT APPLICATION NUMBER: US/10/373,456
;  CURRENT FILING DATE:  2003-02-25
;  PRIOR APPLICATION NUMBER: US 60/359,836
;  PRIOR FILING DATE: 2002-02-26
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 1828
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: p40-linker-p35 fragment cloned into MVL-hIL12lig vector (Fig. 11)
US-10-373-456-2

  Query Match             4.8%;  Score 44;  DB 7;  Length 1828;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        673 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 716


RESULT 62
US-10-228-811-4
; Sequence 4, Application US/10228811
; Publication No. US20030054392A1
; GENERAL INFORMATION:
;  APPLICANT: Wittig, Prof. Burghardt
;  APPLICANT:  Junghans, Claas
;  TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
;  TITLE OF INVENTION:  Therapy
;  FILE REFERENCE: XI 597/99
;  CURRENT APPLICATION NUMBER: US/10/228,811
;  CURRENT FILING DATE:  2002-08-27
;  PRIOR APPLICATION NUMBER: DE 196 48 625.4
;  PRIOR FILING DATE: 1996-11-13
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 1870
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (1)..(1870)
;   OTHER INFORMATION: Interleukin-12 (IL-12, p40-subunit); Oligo DNA Dumbbell
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1)..(2)
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to
;   OTHER INFORMATION: 2  can be modified with amino or caroxy features
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1869)..(1870)
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1869
;   OTHER INFORMATION: to 1870  can be modified with amino or caroxy features
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Strandness: both;  nucleic
;   OTHER INFORMATION: acid (linear),  hypothetical: No. US20030054392A1 anti-sense: No
US-10-228-811-4

  Query Match             4.8%;  Score 44;  DB 6;  Length 1870;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db       1293 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 1336


RESULT 63
US-10-172-399-7
; Sequence 7, Application US/10172399
; Publication No. US20030045495A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Chuan-Yuan
;  APPLICANT:  Dewhirst, Mark
;  APPLICANT:  Huang, Qian
;  TITLE OF INVENTION: A METHOD FOR SELECTIVE EXPRESSION OF THERAPEUTIC GENES BY HYPERTH
;  FILE REFERENCE: 180-129
;  CURRENT APPLICATION NUMBER: US/10/172,399
```

```
;  CURRENT FILING DATE:  2002-06-14
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
;   LENGTH: 2318
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (14)..(1000)
US-10-172-399-7

  Query Match             4.8%;  Score 44;  DB 6;  Length 2318;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        674 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 717


RESULT 64
US-10-476-961-3
; Sequence 3, Application US/10476961
; Publication No. US20040241843A1
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Isis Pharmaceuticals, Inc.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTSP-0393
;  CURRENT APPLICATION NUMBER: US/10/476,961
;  CURRENT FILING DATE:  2003-11-05
;  PRIOR APPLICATION NUMBER: 2001-05-07
;  PRIOR FILING DATE: 09/851,062
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 3
;   LENGTH: 2318
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (14)...(1000)
US-10-476-961-3

  Query Match             4.8%;  Score 44;  DB 9;  Length 2318;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        674 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 717


RESULT 65
US-10-429-802-44
; Sequence 44, Application US/10429802
; Publication No. US20030228285A1
; GENERAL INFORMATION:
;  APPLICANT: HUNG, MIEN-CHIE
;  APPLICANT:  WONG, KA YIN
;  APPLICANT:  ZOU, YIYU
;  TITLE OF INVENTION: BIPARTITE T-CELL FACTOR (TCF)-RESPONSIVE PROMOTER
;  FILE REFERENCE: UTSC:752US
;  CURRENT APPLICATION NUMBER: US/10/429,802
;  CURRENT FILING DATE:  2003-05-05
;  PRIOR APPLICATION NUMBER: 60/377,672
;  PRIOR FILING DATE: 2002-05-03
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
;   LENGTH: 2347
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-429-802-44

  Query Match             4.8%;  Score 44;  DB 7;  Length 2347;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        703 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 746


RESULT 66
US-10-430-503-35
; Sequence 35, Application US/10430503
; Publication No. US20040005684A1
; GENERAL INFORMATION:
;  APPLICANT: HUNG, MIEN-CHIE
;  APPLICANT:  LAN, KENG-LI
;  APPLICANT:  OU-YANG, FU
;  APPLICANT:  LIU, JAW-CHING
;  APPLICANT:  LAN, KENG-HSIN
;  TITLE OF INVENTION: TARGETING PROTEINS TO DELIVER THERAPEUTIC OR DIAGNOSTIC
;  TITLE OF INVENTION:  REAGENTS
;  FILE REFERENCE: UTSC:797US
;  CURRENT APPLICATION NUMBER: US/10/430,503
;  CURRENT FILING DATE:  2003-05-06
;  PRIOR APPLICATION NUMBER: 60/383,063
;  PRIOR FILING DATE: 2002-05-06
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
;   LENGTH: 2347
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-430-503-35

  Query Match             4.8%;  Score 44;  DB 7;  Length 2347;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||||||||||||||||
Db        703 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 746


RESULT 67
US-09-924-703-3
; Sequence 3, Application US/09924703
; Patent No. US20020137898A1
; GENERAL INFORMATION:
;  APPLICANT: TRINCHIERI, GIORGIO
;  APPLICANT:  PERUSSIA, BICE
;  APPLICANT:  CLARK, STEVEN C.
;  APPLICANT:  WONG, GORDON G.
;  APPLICANT:  HEWICK, RODNEY
;  APPLICANT:  KOBAYASHI, MICHIKO
;  TITLE OF INVENTION: ANTIBODIES TO NATURAL KILLER STIMULATORY FACTOR
;  FILE REFERENCE: 01142.0142.0100
;  CURRENT APPLICATION NUMBER: US/09/924,703
;  CURRENT FILING DATE:  2001-08-09
;  PRIOR APPLICATION NUMBER: 09/325,958
;  PRIOR FILING DATE: 1999-06-04
;  PRIOR APPLICATION NUMBER: 08/858,000
;  PRIOR FILING DATE: 1997-05-16
;  PRIOR APPLICATION NUMBER: 08/403,013
;  PRIOR FILING DATE: 1995-03-13
;  PRIOR APPLICATION NUMBER: 07/584,941
;  PRIOR FILING DATE: 1990-09-18
;  PRIOR APPLICATION NUMBER: 07/307,817
;  PRIOR FILING DATE: 1989-02-07
;  PRIOR APPLICATION NUMBER: 07/269,945
;  PRIOR FILING DATE: 1988-11-10
```

```
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 2362
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
;   OTHER INFORMATION: sequence of the 40 kD subunit of NKSF
;   NAME/KEY: CDS
;   LOCATION: (33)..(1016)
US-09-924-703-3

  Query Match             4.8%;  Score 44;  DB 3;  Length 2362;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        693 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 736


RESULT 68
US-10-358-395-3
; Sequence 3, Application US/10358395
; Publication No. US20040044186A1
; GENERAL INFORMATION:
;  APPLICANT: TRINCHIERI, GIORGIO
;  APPLICANT:  PERUSSIA, BICE
;  APPLICANT:  CLARK, STEVEN C.
;  APPLICANT:  WONG, GORDON G.
;  APPLICANT:  HEWICK, RODNEY
;  APPLICANT:  KOBAYASHI, MICHIKO
;  TITLE OF INVENTION: ANTIBODIES TO NATURAL KILLER STIMULATORY FACTOR
;  FILE REFERENCE: 01142.0142.0100
;  CURRENT APPLICATION NUMBER: US/10/358,395
;  CURRENT FILING DATE:  2003-02-05
;  PRIOR APPLICATION NUMBER: US/09/924,703
;  PRIOR FILING DATE: 2001-08-09
;  PRIOR APPLICATION NUMBER: 09/325,958
;  PRIOR FILING DATE: 1999-06-04
;  PRIOR APPLICATION NUMBER: 08/858,000
;  PRIOR FILING DATE: 1997-05-16
;  PRIOR APPLICATION NUMBER: 08/403,013
;  PRIOR FILING DATE: 1995-03-13
;  PRIOR APPLICATION NUMBER: 07/584,941
;  PRIOR FILING DATE: 1990-09-18
;  PRIOR APPLICATION NUMBER: 07/307,817
;  PRIOR FILING DATE: 1989-02-07
;  PRIOR APPLICATION NUMBER: 07/269,945
;  PRIOR FILING DATE: 1988-11-10
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 2362
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
;   OTHER INFORMATION: sequence of the 40 kD subunit of NKSF
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (33)..(1016)
US-10-358-395-3

  Query Match             4.8%;  Score 44;  DB 8;  Length 2362;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db        693 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 736


RESULT 69
US-10-373-456-1
; Sequence 1, Application US/10373456
; Publication No. US20040009146A1
; GENERAL INFORMATION:
;  APPLICANT: Podhajcer, Osvaldo
;  TITLE OF INVENTION: Anti-Tumor Vaccine and Method
;  FILE REFERENCE: 1423P-US/101141-14
;  CURRENT APPLICATION NUMBER: US/10/373,456
;  CURRENT FILING DATE:  2003-02-25
;  PRIOR APPLICATION NUMBER: US 60/359,836
;  PRIOR FILING DATE: 2002-02-26
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 2466
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: p35-IRES-p40 fragment cloned into MVL-hIL-12 and MVL-hIL-12-hIL-1
;   OTHER INFORMATION: 0 vectors (Fig 11)
US-10-373-456-1

  Query Match             4.8%;  Score 44;  DB 7;  Length 2466;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db       2130 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 2173


RESULT 70
US-10-136-837-1
; Sequence 1, Application US/10136837
; Publication No. US20030181405A1
; GENERAL INFORMATION:
;  APPLICANT: NORDSTROM, Jeffrey L
;  APPLICANT:  PERICLE, Federica
;  APPLICANT:  ROLLAND, Alain
;  APPLICANT:  RALSTON, Robert
;  TITLE OF INVENTION: Interferon Alpha Plasmids and Delivery Systems, and Methods of Ma
;  TITLE OF INVENTION:  Using the Same
;  FILE REFERENCE: 273/082 (GM15-1USC1)
;  CURRENT APPLICATION NUMBER: US/10/136,837
;  CURRENT FILING DATE:  2002-04-29
;  PRIOR APPLICATION NUMBER: US 09/268,135
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 5686
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Human IL-12 Plasmid pIN1143
US-10-136-837-1

  Query Match             4.8%;  Score 44;  DB 7;  Length 5686;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db       3879 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 3922


RESULT 71
US-09-828-825-1
; Sequence 1, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 8578
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: enhancer
;   LOCATION: (1)..(659)
;   OTHER INFORMATION: CMV IE
;   NAME/KEY: promoter
;   LOCATION: (669)..(750)
;   OTHER INFORMATION: CMV  IE
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA Promoter
;   NAME/KEY: mRNA
;   LOCATION: (1090)..(1984)
;   OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
;   NAME/KEY: RBS
;   LOCATION: (2013)..(2593)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: mRNA
;   LOCATION: (2627)..(4263)
;   OTHER INFORMATION: Human IL12.0 (2640-4223 coding sequence, flexible
;   OTHER INFORMATION: linker at 3624-3629)
;   NAME/KEY: promoter
;   LOCATION: (4352)..(4431)
;   OTHER INFORMATION: T3 RNA polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4362)..(4583)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4678)..(5133)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5197)..(6564)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (6975)..(7835)
;   OTHER INFORMATION: Ampicillin resistance
;   OTHER INFORMATION: Description of Artificial Sequence: Plasmid
;   NAME/KEY: CDS
;   LOCATION: (2640)..(4223)
;   OTHER INFORMATION: IL 12.0 coding sequence - 2 amino acid linker at
;   OTHER INFORMATION: 3624
US-09-828-825-1

  Query Match             4.8%;  Score 44;  DB 3;  Length 8578;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db       3300 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 3343


RESULT 72
US-09-828-825-3
; Sequence 3, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 8578
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
;   NAME/KEY: enhancer
;   LOCATION: (1)..(659)
;   OTHER INFORMATION: CMV IE Enhancer
;   NAME/KEY: promoter
;   LOCATION: (669)..(750)
;   OTHER INFORMATION: CMV IE Promoter
;   NAME/KEY: misc_feature
;   LOCATION: (890)..(1002)
;   OTHER INFORMATION: InTervening Sequence
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(1984)
;   OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
;   NAME/KEY: RBS
;   LOCATION: (2013)..(2593)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (2627)..(4263)
;   OTHER INFORMATION: Human IL12.0 sequence (2640-4217 is coding
;   OTHER INFORMATION: sequence)
;   NAME/KEY: promoter
;   LOCATION: (4346)..(4425)
;   OTHER INFORMATION: T3 RNA polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4356)..(4577)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4672)..(5127)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5191)..(6558)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (6969)..(7829)
;   OTHER INFORMATION: Ampicillin resistance
;   NAME/KEY: CDS
;   LOCATION: (2640)..(4217)
;   OTHER INFORMATION: IL12.0 coding sequence - no linker
US-09-828-825-3

  Query Match             4.8%;  Score 44;  DB 3;  Length 8578;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db       3300 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 3343


RESULT 73
US-09-828-825-7
; Sequence 7, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
```

```
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 8608
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: misc_feature
;   LOCATION: (890)..(1002)
;   OTHER INFORMATION: Intervening sequence
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(1984)
;   OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
;   NAME/KEY: RBS
;   LOCATION: (2013)..(2593)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (2627)..(4263)
;   OTHER INFORMATION: Human IL12.2 sequence (2460-4253 is coding
;   OTHER INFORMATION: sequence, 13 amino acid flexible linker at
;   OTHER INFORMATION: 3606-3676)
;   NAME/KEY: CDS
;   LOCATION: (2640)..(4253)
;   OTHER INFORMATION: IL12.2 coding sequence (13 amino acid linker)
;   NAME/KEY: promoter
;   LOCATION: (4362)..(4383)
;   OTHER INFORMATION: T3 RNA Polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4393)..(4614)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4709)..(5164)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5228)..(6595)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (7006)..(7866)
;   OTHER INFORMATION: Ampicillin resistance
US-09-828-825-7

  Query Match             4.8%;  Score 44;  DB 3;  Length 8608;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db       3300 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 3343


RESULT 74
US-09-828-825-5
; Sequence 5, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 8623
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: misc_feature
;   LOCATION: (890)..(1002)
;   OTHER INFORMATION: Intervening sequence
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(1984)
;   OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
;   NAME/KEY: RBS
;   LOCATION: (2013)..(2593)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (2627)..(4278)
;   OTHER INFORMATION: Human IL12.3 - 2640-4268 is coding sequence,
;   OTHER INFORMATION: flexible linker from 3606-3690
;   NAME/KEY: CDS
;   LOCATION: (2640)..(4268)
;   OTHER INFORMATION: IL 12.3 coding sequence - has 28 amino acid linker
;   OTHER INFORMATION: sequence
;   NAME/KEY: promoter
;   LOCATION: (4398)..(4407)
;   OTHER INFORMATION: T3 RNA polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4408)..(4629)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4724)..(5179)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5243)..(6610)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (7021)..(7881)
;   OTHER INFORMATION: Ampicillin resistance
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-828-825-5

  Query Match             4.8%;  Score 44;  DB 3;  Length 8623;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db       3300 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 3343


RESULT 75
US-09-828-825-15
; Sequence 15, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
```

; SEQ ID NO 15
; LENGTH: 8629
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
; NAME/KEY: misc_feature
; LOCATION: (1)..(750)
; OTHER INFORMATION: CMV enhancer and promoter
; NAME/KEY: promoter
; LOCATION: (1067)..(1085)
; OTHER INFORMATION: T7 RNA polymerase promoter
; NAME/KEY: misc_feature
; LOCATION: (1090)..(2726)
; OTHER INFORMATION: Human IL12.2 (coding sequence is 1103-2716, 10
; OTHER INFORMATION: amino acid linker at 2087-2116)
; NAME/KEY: CDS
; LOCATION: (1103)..(2716)
; OTHER INFORMATION: Human IL12.2 (10 amino acid linker)
; NAME/KEY: RBS
; LOCATION: (2752)..(3332)
; OTHER INFORMATION: IRES sequence
; NAME/KEY: misc_feature
; LOCATION: (3369)..(4263)
; OTHER INFORMATION: Human B7.1 sequence
; NAME/KEY: promoter
; LOCATION: (4383)..(4404)
; OTHER INFORMATION: T3 RNA Polymerase promoter
; NAME/KEY: polyA_signal
; LOCATION: (4414)..(4635)
; OTHER INFORMATION: SV40 fragment containing polyadenylation signal
; NAME/KEY: rep_origin
; LOCATION: (4730)..(5185)
; OTHER INFORMATION: f1 origin of replication
; NAME/KEY: misc_feature
; LOCATION: (5249)..(6616)
; OTHER INFORMATION: Neo r expression cassette
; NAME/KEY: misc_feature
; LOCATION: (7027)..(7887)
; OTHER INFORMATION: Ampicillin resistance gene
US-09-828-825-15

Query Match 4.8%; Score 44; DB 3; Length 8629;
Best Local Similarity 100.0%; Pred. No. 3.7e-12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
||||||||||||||||||||||||||||||||||||||||||||
Db 1763 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 1806

RESULT 76
US-09-828-825-9
; Sequence 9, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Seewoo
; APPLICANT: Kim, Han-soo
; TITLE OF INVENTION: Anti-cancer Cellular Vaccine
; FILE REFERENCE: 84906-102
; CURRENT APPLICATION NUMBER: US/09/828,825
; CURRENT FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: KR00-43498
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 8638
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
; NAME/KEY: misc_feature
; LOCATION: (1)..(750)
; OTHER INFORMATION: CMV enhancer and promoter
; NAME/KEY: misc_feature
; LOCATION: (890)..(1002)
; OTHER INFORMATION: Intervening sequence
; NAME/KEY: promoter
; LOCATION: (1067)..(1085)
; OTHER INFORMATION: T7 RNA polymerase promoter
; NAME/KEY: misc_feature
; LOCATION: (1090)..(1984)
; OTHER INFORMATION: Human B7.1 (1090-1954 is coding sequence)
; NAME/KEY: RBS
; LOCATION: (2013)..(2593)
; OTHER INFORMATION: IRES sequence
; NAME/KEY: misc_feature
; LOCATION: (2627)..(4293)
; OTHER INFORMATION: Human IL12.4 (coding sequence is 2640-4283, 33
; OTHER INFORMATION: amino acid linker at 3606-3706)
; NAME/KEY: CDS
; LOCATION: (2640)..(4283)
; OTHER INFORMATION: IL12.4 coding sequence (33 amino acid linker)
; NAME/KEY: promoter
; LOCATION: (4392)..(4413)
; OTHER INFORMATION: T3 RNA Polymerase promoter
; NAME/KEY: polyA_signal
; LOCATION: (4423)..(4644)
; OTHER INFORMATION: SV40 fragment containing polyadenylation signal
; NAME/KEY: rep_origin
; LOCATION: (4739)..(5194)
; OTHER INFORMATION: f1 origin of replication
; NAME/KEY: misc_feature
; LOCATION: (5258)..(6625)
; OTHER INFORMATION: Neo r expression cassette
; NAME/KEY: misc_feature
; LOCATION: (7036)..(7896)
; OTHER INFORMATION: Ampicillin resistance
US-09-828-825-9

Query Match 4.8%; Score 44; DB 3; Length 8638;
Best Local Similarity 100.0%; Pred. No. 3.7e-12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
||||||||||||||||||||||||||||||||||||||||||||
Db 3300 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 3343

RESULT 77
US-09-828-825-13
; Sequence 13, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Seewoo
; APPLICANT: Kim, Han-soo
; TITLE OF INVENTION: Anti-cancer Cellular Vaccine
; FILE REFERENCE: 84906-102
; CURRENT APPLICATION NUMBER: US/09/828,825
; CURRENT FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: KR00-43498
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 8644
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
; NAME/KEY: misc_feature
; LOCATION: (1)..(750)
; OTHER INFORMATION: CMV enhancer and promoter
; NAME/KEY: promoter
; LOCATION: (1067)..(1085)

```
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(2731)
;   OTHER INFORMATION: Human IL12.3 (1103-2731 is coding sequence, 15
;   OTHER INFORMATION: amino acid linker at 2087-2131)
;   NAME/KEY: CDS
;   LOCATION: (1103)..(2731)
;   OTHER INFORMATION: IL12.3 (15 amino acid linker)
;   NAME/KEY: RBS
;   LOCATION: (2767)..(3347)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (3384)..(4278)
;   OTHER INFORMATION: Human B7.1 sequence
;   NAME/KEY: promoter
;   LOCATION: (4398)..(4419)
;   OTHER INFORMATION: T3 RNA polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4429)..(4650)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4745)..(5200)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5264)..(5681)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (7042)..(7902)
;   OTHER INFORMATION: Ampicillin resistance gene
US-09-828-825-13

  Query Match             4.8%;  Score 44;  DB 3;  Length 8644;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db       1763 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 1806


RESULT 78
US-09-828-825-11
; Sequence 11, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 8659
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(2756)
;   OTHER INFORMATION: Human IL12.4 (coding sequence 1103-2746, 19 amino
;   OTHER INFORMATION: acid linker at 2087-2146)
;   NAME/KEY: CDS
;   LOCATION: (1103)..(2746)
;   OTHER INFORMATION: Human IL12.4 (19 amino acid linker)
;   NAME/KEY: RBS
;   LOCATION: (2782)..(3362)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (3399)..(4293)
;   OTHER INFORMATION: Human B7.1 sequence
;   NAME/KEY: promoter
;   LOCATION: (4413)..(4434)
;   OTHER INFORMATION: T3 RNA polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4444)..(4665)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4760)..(5215)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5279)..(6646)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (7057)..(7917)
;   OTHER INFORMATION: Ampicillin resistance gene
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-828-825-11

  Query Match             4.8%;  Score 44;  DB 3;  Length 8659;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
              |||||||||||||||||||||||||||||||||||||||||||
Db       1763 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 1806


RESULT 79
US-10-511-237-3
; Sequence 3, Application US/10511237
; Publication No. US20050233457A1
; GENERAL INFORMATION:
;  APPLICANT: Block, Andreas
;  TITLE OF INVENTION: Recombinant Viral Vectors for the Tetracycline-regulated Expressi
;  TITLE OF INVENTION:  Genes
;  FILE REFERENCE: 66741-043
;  CURRENT APPLICATION NUMBER: US/10/511,237
;  CURRENT FILING DATE:  2004-10-12
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 11453
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Adenoviral expression plasmid pShuttle.3r.hscIL-12 for regulated
;   OTHER INFORMATION: expression of human IL-12 following virus generation using AdEasy
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (327)..(713)
;   OTHER INFORMATION: VP16
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (714)..(1352)
;   OTHER INFORMATION: TetR
;   FEATURE:
;   NAME/KEY: Intron
;   LOCATION: (1353)..(1912)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: promoter
;   LOCATION: (1864)..(1902)
;   OTHER INFORMATION: TK-min
;   FEATURE:
;   NAME/KEY: protein_bind
;   LOCATION: (1913)..(2212)
;   OTHER INFORMATION: TetO7
```

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2213)..(2709)
; OTHER INFORMATION: CMV-min + Intron
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (2226)..(2264)
; OTHER INFORMATION: CMV-min
; FEATURE:
; NAME/KEY: gene
; LOCATION: (2710)..(4308)
; OTHER INFORMATION: Human singe-chain IL-12
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (4020)..(4023)
; OTHER INFORMATION: T/C, A/T, G/C, T/G
US-10-511-237-3

Query Match 4.8%; Score 44; DB 10; Length 11453;
Best Local Similarity 100.0%; Pred. No. 3.7e-12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
||||||||||||||||||||||||||||||||||||||||||||
Db 3370 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 3413

RESULT 80
US-10-511-237-1
; Sequence 1, Application US/10511237
; Publication No. US20050233457A1
; GENERAL INFORMATION:
; APPLICANT: Block, Andreas
; TITLE OF INVENTION: Recombinant Viral Vectors for the Tetracycline-regulated Expressi
; TITLE OF INVENTION: Genes
; FILE REFERENCE: 66741-043
; CURRENT APPLICATION NUMBER: US/10/511,237
; CURRENT FILING DATE: 2004-10-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 11569
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Adenoviral expression plasmid pAd.3r.hscIL-12 for regulated expre
; OTHER INFORMATION: human IL-12
; FEATURE:
; NAME/KEY: gene
; LOCATION: (327)..(713)
; OTHER INFORMATION: VP16
; FEATURE:
; NAME/KEY: gene
; LOCATION: (714)..(1352)
; OTHER INFORMATION: TetR
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (1353)..(1912)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1864)..(1902)
; OTHER INFORMATION: TK-min
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: (1913)..(2212)
; OTHER INFORMATION: TetO7
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2213)..(2709)
; OTHER INFORMATION: CMV-min + Intron
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (2226)..(2264)
; OTHER INFORMATION: CMV-min
; FEATURE:
; NAME/KEY: gene
; LOCATION: (2710)..(4308)
; OTHER INFORMATION: Human single-chain IL-12
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (4020)..(4023)
; OTHER INFORMATION: T/C, A/T, G/C, T/G
US-10-511-237-1

Query Match 4.8%; Score 44; DB 10; Length 11569;
Best Local Similarity 100.0%; Pred. No. 3.7e-12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641
||||||||||||||||||||||||||||||||||||||||||||
Db 3370 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 3413

RESULT 81
US-10-528-644A-53
; Sequence 53, Application US/10528644A
; Publication No. US20050287117A1
; GENERAL INFORMATION:
; APPLICANT: SUNG, Young Chul
; APPLICANT: YOUN, Jin-Won
; APPLICANT: YANG, Se-Hwan
; APPLICANT: PARK, Su-Hwan
; APPLICANT: LEE, Chang Geun
; TITLE OF INVENTION: A VACCINE ENHANCING THE PROTECTIVE IMMUNITY TO
; TITLE OF INVENTION: HEPATITIS C VIRUS USING PLASMID DNA AND RECOMBINANT ADENOVIRUS
; FILE REFERENCE: 428.1049
; CURRENT APPLICATION NUMBER: US/10/528,644A
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: PCT/KR03/01951
; PRIOR FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: KR 2002-0058712
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: KR 2002-68496
; PRIOR FILING DATE: 2002-11-06
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 53
; LENGTH: 2390
; TYPE: DNA
; ORGANISM: Homo sapiens (hIL-12m)
US-10-528-644A-53

Query Match 4.2%; Score 39; DB 10; Length 2390;
Best Local Similarity 100.0%; Pred. No. 1.7e-09;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 334 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 372
|||||||||||||||||||||||||||||||||||||||
Db 1803 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 1841

RESULT 82
US-10-240-376A-130
; Sequence 130, Application US/10240376A
; Publication No. US20040161747A1
; GENERAL INFORMATION:
; APPLICANT: Morahan, Grant
; TITLE OF INVENTION: A METHOD FOR SCREENING FOR AUTOIMMUNE
; TITLE OF INVENTION: DISEASE BY IDENTIFYING POLYMORPHISMS IN IL-12 p40
; FILE REFERENCE: DAVI186.001APC
; CURRENT APPLICATION NUMBER: US/10/240,376A
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: PCT/AU01/00340
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: PQ 6466

```
;  PRIOR FILING DATE: 2000-03-27
;  PRIOR APPLICATION NUMBER: US 60/204,366
;  PRIOR FILING DATE: 2000-05-15
;  NUMBER OF SEQ ID NOS: 140
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 130
;   LENGTH: 18340
;   TYPE: DNA
;   ORGANISM: mammalian
US-10-240-376A-130

  Query Match             4.2%;  Score 39;  DB 8;  Length 18340;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-09;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        334 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 372
              |||||||||||||||||||||||||||||||||||||||
Db      10439 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 10477


RESULT 83
US-10-029-386-16833/c
; Sequence 16833, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
;  TITLE OF INVENTION:  EXPRESSION ANALYSIS TWO
;  FILE REFERENCE: AEOMICA-X-2
;  CURRENT APPLICATION NUMBER: US/10/029,386
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 34288
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 16833
;   LENGTH: 270
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO CHR5.1
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.84
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.72
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.93
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.79
;   OTHER INFORMATION: NT HIT: AY008847.1, EVALUE 0.00e+00
;   OTHER INFORMATION: EST_HUMAN HIT: BF204907.1, EVALUE 9.20e-02
;   OTHER INFORMATION: SWISSPROT HIT: P29460, EVALUE 4.00e-41
US-10-029-386-16833

  Query Match             3.8%;  Score 35;  DB 7;  Length 270;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        247 CACAAAAAGGAAGATGGAATTTGGTCCACTGATAT 281
              |||||||||||||||||||||||||||||||||||
Db         41 CACAAAAAGGAAGATGGAATTTGGTCCACTGATAT 7


RESULT 84
US-10-029-386-3133/c
; Sequence 3133, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
;  TITLE OF INVENTION:  EXPRESSION ANALYSIS TWO
;  FILE REFERENCE: AEOMICA-X-2
;  CURRENT APPLICATION NUMBER: US/10/029,386
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 34288
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 3133
;   LENGTH: 556
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO CHR5.1
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.84
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.72
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.93
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.79
;   OTHER INFORMATION: NT HIT: AY008847.1, EVALUE 0.00e+00
;   OTHER INFORMATION: SWISSPROT HIT: P29460, EVALUE 5.00e-43
;   OTHER INFORMATION: EST_HUMAN HIT: BG389008.1, EVALUE 2.00e-01
US-10-029-386-3133

  Query Match             3.8%;  Score 35;  DB 7;  Length 556;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-07;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        247 CACAAAAAGGAAGATGGAATTTGGTCCACTGATAT 281
              |||||||||||||||||||||||||||||||||||
Db        236 CACAAAAAGGAAGATGGAATTTGGTCCACTGATAT 202


RESULT 85
US-09-823-549-77
; Sequence 77, Application US/09823549
; Publication No. US20020147998A1
; GENERAL INFORMATION:
;  APPLICANT: McConlogue, Lisa  C
;  APPLICANT:  Games, Kate D.
;  APPLICANT:  Yednock, Theodore A.
;  APPLICANT:  Hua, Tan
;  APPLICANT:  Messersmith, Elizabeth
;  APPLICANT:  Bard, Frederique
;  TITLE OF INVENTION: SCREENING MARKERS AND METHODS FOR NEURODEGENERATIVE DISORDERS
;  FILE REFERENCE: 015270-009110US
;  CURRENT APPLICATION NUMBER: US/09/823,549
;  CURRENT FILING DATE:  2001-03-30
;  PRIOR APPLICATION NUMBER: US 60/193,847
;  PRIOR FILING DATE: 2000-03-30
;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
;   LENGTH: 73
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: IL-12 p40, #1 marker
US-09-823-549-77

  Query Match             3.3%;  Score 30;  DB 3;  Length 73;
  Best Local Similarity   100.0%;  Pred. No. 0.0001;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        612 CAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||
Db          8 CAGCTTCTTCATCAGGGACATCATCAAACC 37


RESULT 86
US-10-685-992-77
; Sequence 77, Application US/10685992
; Publication No. US20040213739A1
; GENERAL INFORMATION:
;  APPLICANT: McConlogue, Lisa  C
;  APPLICANT:  Games, Kate D.
;  APPLICANT:  Yednock, Theodore A.
;  APPLICANT:  Hua, Tan
;  APPLICANT:  Messersmith, Elizabeth
;  APPLICANT:  Bard, Frederique
;  TITLE OF INVENTION: SCREENING MARKERS AND METHODS FOR NEURODEGENERATIVE DISORDERS
```

```
;  FILE REFERENCE: 015270-009110US
;  CURRENT APPLICATION NUMBER: US/10/685,992
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US/09/823,549
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: US 60/193,847
;  PRIOR FILING DATE: 2000-03-30
;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
;   LENGTH: 73
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: IL-12 p40, #1 marker
US-10-685-992-77

  Query Match             3.3%;  Score 30;  DB 9;  Length 73;
  Best Local Similarity   100.0%;  Pred. No. 0.0001;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        612 CAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||
Db          8 CAGCTTCTTCATCAGGGACATCATCAAACC 37


RESULT 87
US-10-603-064-3
; Sequence 3, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
;  APPLICANT: Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION: Multiple Cytokine Protein Complexes
;  FILE REFERENCE: LEX-010
;  CURRENT APPLICATION NUMBER: US/10/603,064
;  CURRENT FILING DATE:  2003-06-24
;  PRIOR APPLICATION NUMBER: US/09/634,368
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: 60/147,924
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1409
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p40-GM-CSF fusion protein coding sequence
US-10-603-064-3

  Query Match             3.3%;  Score 30;  DB 8;  Length 1409;
  Best Local Similarity   100.0%;  Pred. No. 0.00011;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        612 CAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||
Db        689 CAGCTTCTTCATCAGGGACATCATCAAACC 718


RESULT 88
US-10-603-064-2
; Sequence 2, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
;  APPLICANT: Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION: Multiple Cytokine Protein Complexes
;  FILE REFERENCE: LEX-010
;  CURRENT APPLICATION NUMBER: US/10/603,064
;  CURRENT FILING DATE:  2003-06-24
;  PRIOR APPLICATION NUMBER: US/09/634,368
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: 60/147,924
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 1472
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p40-IL-2 fusion protein coding sequence
US-10-603-064-2

  Query Match             3.3%;  Score 30;  DB 8;  Length 1472;
  Best Local Similarity   100.0%;  Pred. No. 0.00011;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        612 CAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||
Db        689 CAGCTTCTTCATCAGGGACATCATCAAACC 718


RESULT 89
US-10-603-064-12
; Sequence 12, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
;  APPLICANT: Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION: Multiple Cytokine Protein Complexes
;  FILE REFERENCE: LEX-010
;  CURRENT APPLICATION NUMBER: US/10/603,064
;  CURRENT FILING DATE:  2003-06-24
;  PRIOR APPLICATION NUMBER: US/09/634,368
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: 60/147,924
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 1569
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p35-linker-p40 fusion protein coding sequence
US-10-603-064-12

  Query Match             3.3%;  Score 30;  DB 8;  Length 1569;
  Best Local Similarity   100.0%;  Pred. No. 0.00011;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        612 CAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||
Db       1230 CAGCTTCTTCATCAGGGACATCATCAAACC 1259


RESULT 90
US-10-742-405-5
; Sequence 5, Application US/10742405
; Publication No. US20040213761A1
; GENERAL INFORMATION:
;  APPLICANT: Bowman, Edward P.
;  APPLICANT:  Chan, Jason R.
;  APPLICANT:  Moore, Kevin
;  APPLICANT:  Nguyen, Nhung
;  APPLICANT:  Churakova, Tatyana
;  APPLICANT:  Chen, Shi-Juan
;  APPLICANT:  Cua, Daniel J.
;  TITLE OF INVENTION: Uses of mammalian cytokine; related reagents
;  FILE REFERENCE: DX01578K
;  CURRENT APPLICATION NUMBER: US/10/742,405
```

```
;  CURRENT FILING DATE:  2003-12-18
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 1610
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (7)..(1599)
US-10-742-405-5

  Query Match             3.3%;  Score 30;  DB 9;  Length 1610;
  Best Local Similarity   100.0%;  Pred. No. 0.00011;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        612 CAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||
Db        681 CAGCTTCTTCATCAGGGACATCATCAAACC 710


RESULT 91
US-10-172-399-3
; Sequence 3, Application US/10172399
; Publication No. US20030045495A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Chuan-Yuan
;  APPLICANT:  Dewhirst, Mark
;  APPLICANT:  Huang, Qian
;  TITLE OF INVENTION: A METHOD FOR SELECTIVE EXPRESSION OF THERAPEUTIC GENES BY HYPERTH
;  FILE REFERENCE: 180-129
;  CURRENT APPLICATION NUMBER: US/10/172,399
;  CURRENT FILING DATE:  2002-06-14
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 1840
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (35)..(1042)
US-10-172-399-3

  Query Match             3.3%;  Score 30;  DB 6;  Length 1840;
  Best Local Similarity   100.0%;  Pred. No. 0.00011;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        612 CAGCTTCTTCATCAGGGACATCATCAAACC 641
              ||||||||||||||||||||||||||||||
Db        703 CAGCTTCTTCATCAGGGACATCATCAAACC 732


RESULT 92
US-10-603-064-11
; Sequence 11, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
;  APPLICANT: Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION: Multiple Cytokine Protein Complexes
;  FILE REFERENCE: LEX-010
;  CURRENT APPLICATION NUMBER: US/10/603,064
;  CURRENT FILING DATE:  2003-06-24
;  PRIOR APPLICATION NUMBER: US/09/634,368
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: 60/147,924
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 2013
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p35-linker-p40-IL-2 fusion protein coding sequence
US-10-603-064-11

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  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db       1230 CAGCTTCTTCATCAGGGACATCATCAAACC 1259


RESULT 93
US-10-603-064-13
; Sequence 13, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
;  APPLICANT: Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION: Multiple Cytokine Protein Complexes
;  FILE REFERENCE: LEX-010
;  CURRENT APPLICATION NUMBER: US/10/603,064
;  CURRENT FILING DATE:  2003-06-24
;  PRIOR APPLICATION NUMBER: US/09/634,368
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: 60/147,924
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
;   LENGTH: 2709
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: Fc-p35-linker-p40-IL-2 fusion protein coding
;   OTHER INFORMATION: sequence
US-10-603-064-13

  Query Match             3.3%;  Score 30;  DB 8;  Length 2709;
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  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        612 CAGCTTCTTCATCAGGGACATCATCAAACC 641
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Db       1926 CAGCTTCTTCATCAGGGACATCATCAAACC 1955


RESULT 94
US-10-136-837-3
; Sequence 3, Application US/10136837
; Publication No. US20030181405A1
; GENERAL INFORMATION:
;  APPLICANT: NORDSTROM, Jeffrey L
;  APPLICANT:  PERICLE, Federica
;  APPLICANT:  ROLLAND, Alain
;  APPLICANT:  RALSTON, Robert
;  TITLE OF INVENTION: Interferon Alpha Plasmids and Delivery Systems, and Methods of Ma
;  TITLE OF INVENTION:  Using the Same
;  FILE REFERENCE: 273/082 (GM15-1USC1)
;  CURRENT APPLICATION NUMBER: US/10/136,837
;  CURRENT FILING DATE:  2002-04-29
;  PRIOR APPLICATION NUMBER: US 09/268,135
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 5966
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
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;   FEATURE:
;   OTHER INFORMATION: Mouse IL-12 pIN0961
US-10-136-837-3

  Query Match             3.3%;  Score 30;  DB 7;  Length 5966;
  Best Local Similarity   100.0%;  Pred. No. 0.00011;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db       5342 CAGCTTCTTCATCAGGGACATCATCAAACC 5371


RESULT 95
US-10-511-237-2
; Sequence 2, Application US/10511237
; Publication No. US20050233457A1
; GENERAL INFORMATION:
;  APPLICANT: Block, Andreas
;  TITLE OF INVENTION: Recombinant Viral Vectors for the Tetracycline-regulated Expressi
;  TITLE OF INVENTION:  Genes
;  FILE REFERENCE: 66741-043
;  CURRENT APPLICATION NUMBER: US/10/511,237
;  CURRENT FILING DATE:  2004-10-12
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 11458
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Adenoviral expression plasmid pAd.3r.mscIL-12 for regulated
;   OTHER INFORMATION: expression of murine IL-12
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (327)..(713)
;   OTHER INFORMATION: VP16
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (714)..(1352)
;   OTHER INFORMATION: TetR
;   FEATURE:
;   NAME/KEY: Intron
;   LOCATION: (1353)..(1912)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: promoter
;   LOCATION: (1864)..(1902)
;   OTHER INFORMATION: TK-min
;   FEATURE:
;   NAME/KEY: protein_bind
;   LOCATION: (1913)..(2212)
;   OTHER INFORMATION: TetO7
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2213)..(2687)
;   OTHER INFORMATION: CMV-min + Intron
;   FEATURE:
;   NAME/KEY: promoter
;   LOCATION: (2226)..(2264)
;   OTHER INFORMATION: CMV-min
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (2688)..(4325)
;   OTHER INFORMATION: Murine single-chain IL-12
US-10-511-237-2

  Query Match             3.3%;  Score 30;  DB 10;  Length 11458;
  Best Local Similarity   100.0%;  Pred. No. 0.00011;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db       3362 CAGCTTCTTCATCAGGGACATCATCAAACC 3391


RESULT 96
US-09-917-265-86/c
; Sequence 86, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THER
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 86
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-917-265-86

  Query Match             2.7%;  Score 25;  DB 3;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 0.047;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         25 AGCAACTGGGCATCCGTGTCCTGCA 1


RESULT 97
US-10-719-956-231796
; Sequence 231796, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Rat
;  FILE REFERENCE: 3527.1
;  CURRENT APPLICATION NUMBER: US/10/719,956
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,836
;  PRIOR FILING DATE: 2002 11 20
;  NUMBER OF SEQ ID NOS: 699466
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 231796
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-10-719-956-231796

  Query Match             2.7%;  Score 25;  DB 8;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 0.047;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        612 CAGCTTCTTCATCAGGGACATCATC 636
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Db          1 CAGCTTCTTCATCAGGGACATCATC 25


RESULT 98
US-10-821-670-86/c
; Sequence 86, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
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;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 86
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-10-821-670-86

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  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 99
US-11-136-527-18285
; Sequence 18285, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William M
;  TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
;  FILE REFERENCE: 031896-041000 (AM101086)
;  CURRENT APPLICATION NUMBER: US/11/136,527
;  CURRENT FILING DATE:  2005-05-25
;  PRIOR APPLICATION NUMBER: US 60/574,294
;  PRIOR FILING DATE: 2005-05-26
;  NUMBER OF SEQ ID NOS: 362830
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18285
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Probe
US-11-136-527-18285

  Query Match             2.7%;  Score 25;  DB 16;  Length 25;
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  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 CTTCTTCATCAGGGACATCATCAAA 25


RESULT 100
US-11-136-527-18288
; Sequence 18288, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William M
;  TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
;  FILE REFERENCE: 031896-041000 (AM101086)
;  CURRENT APPLICATION NUMBER: US/11/136,527
;  CURRENT FILING DATE:  2005-05-25
;  PRIOR APPLICATION NUMBER: US 60/574,294
;  PRIOR FILING DATE: 2005-05-26
;  NUMBER OF SEQ ID NOS: 362830
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18288
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Probe
US-11-136-527-18288

  Query Match             2.7%;  Score 25;  DB 16;  Length 25;
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  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        616 TTCTTCATCAGGGACATCATCAAAC 640
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Db          1 TTCTTCATCAGGGACATCATCAAAC 25


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OM nucleic - nucleic search, using sw model

Run on: June 9, 2006, 23:41:15 ; Search time 21.3095 Seconds
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5485.659 Million cell updates/sec

Title: US-10-821-670A-26
Perfect score: 921
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 253354 seqs, 63461778 residues

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6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	18	2.0	5934	7	US-11-313-450-13	Sequence 13, Appl
	3	18	2.0	6371	7	US-11-251-465-8	Sequence 8, Appli
c	4	17	1.8	862	6	US-10-953-349-15338	Sequence 15338, A
c	5	17	1.8	1000	7	US-11-233-726-17	Sequence 17, Appl
	6	17	1.8	1061	6	US-10-953-349-3012	Sequence 3012, Ap
	7	17	1.8	1498	6	US-10-953-349-9710	Sequence 9710, Ap
c	8	17	1.8	3228	7	US-11-217-529-190982	Sequence 190982,
c	9	16	1.7	231	6	US-10-471-571A-4869	Sequence 4869, Ap
	10	16	1.7	305	6	US-10-548-484-9	Sequence 9, Appli
	11	16	1.7	305	6	US-10-548-484-10	Sequence 10, Appl
	12	16	1.7	561	6	US-10-488-619-3012	Sequence 3012, Ap
c	13	16	1.7	577	6	US-10-953-349-38575	Sequence 38575, A
	14	16	1.7	634	6	US-10-953-349-39182	Sequence 39182, A
	15	16	1.7	726	6	US-10-548-484-16	Sequence 16, Appl
	16	16	1.7	742	6	US-10-196-749-359	Sequence 359, App
c	17	16	1.7	921	6	US-10-471-571A-689	Sequence 689, App
c	18	16	1.7	945	7	US-11-217-529-79675	Sequence 79675, A
	19	16	1.7	1039	6	US-10-953-349-27059	Sequence 27059, A
	20	16	1.7	1083	7	US-11-217-529-4517	Sequence 4517, Ap
	21	16	1.7	1098	7	US-11-217-529-75941	Sequence 75941, A
	22	16	1.7	1226	6	US-10-953-349-9694	Sequence 9694, Ap
	23	16	1.7	1232	6	US-10-953-349-3568	Sequence 3568, Ap
c	24	16	1.7	1621	6	US-10-953-349-22615	Sequence 22615, A
	25	16	1.7	1747	6	US-10-953-349-33373	Sequence 33373, A
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c	27	16	1.7	1975	7	US-11-313-836-53	Sequence 53, Appl
c	28	16	1.7	2117	6	US-10-953-349-37153	Sequence 37153, A
	29	16	1.7	2270	7	US-11-293-697-1627	Sequence 1627, Ap
c	30	16	1.7	2278	7	US-11-293-697-928	Sequence 928, App
c	31	16	1.7	2324	7	US-11-293-697-1624	Sequence 1624, Ap
c	32	16	1.7	2538	7	US-11-293-697-1068	Sequence 1068, Ap
c	33	16	1.7	2682	7	US-11-266-446-7	Sequence 7, Appli
c	34	16	1.7	2703	6	US-10-953-349-36221	Sequence 36221, A
c	35	16	1.7	2829	7	US-11-293-697-539	Sequence 539, App
	36	16	1.7	2846	6	US-10-505-928-444	Sequence 444, App
	37	16	1.7	2872	7	US-11-145-307A-3	Sequence 3, Appli
c	38	16	1.7	3271	6	US-10-953-349-5832	Sequence 5832, Ap
	39	16	1.7	5310	7	US-11-217-529-77298	Sequence 77298, A
c	40	16	1.7	6266	7	US-11-253-190-4	Sequence 4, Appli
c	41	16	1.7	12659	6	US-10-953-349-5546	Sequence 5546, Ap
c	42	16	1.7	151830	6	US-10-519-335-37	Sequence 37, Appl
c	43	15	1.6	20	7	US-11-266-409-12	Sequence 12, Appl
c	44	15	1.6	25	7	US-11-217-529-28477	Sequence 28477, A
c	45	15	1.6	25	7	US-11-217-529-94239	Sequence 94239, A
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c	47	15	1.6	25	7	US-11-217-529-121503	Sequence 121503,
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	49	15	1.6	261	7	US-11-217-529-4828	Sequence 4828, Ap
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	51	15	1.6	354	7	US-11-217-529-82243	Sequence 82243, A
	52	15	1.6	423	7	US-11-217-529-80395	Sequence 80395, A
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	54	15	1.6	498	6	US-10-471-571A-5447	Sequence 5447, Ap
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	57	15	1.6	508	6	US-10-560-723-10	Sequence 10, Appl
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c	59	15	1.6	531	7	US-11-217-529-174237	Sequence 174237,
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	63	15	1.6	702	6	US-10-488-619-1757	Sequence 1757, Ap
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c	66	15	1.6	795	6	US-10-488-619-1758	Sequence 1758, Ap
c	67	15	1.6	798	6	US-10-953-349-3534	Sequence 3534, Ap
	68	15	1.6	843	7	US-11-217-529-970	Sequence 970, App
	69	15	1.6	852	6	US-10-953-349-25	Sequence 25, Appl
	70	15	1.6	865	6	US-10-953-349-39	Sequence 39, Appl
	71	15	1.6	880	6	US-10-953-349-5007	Sequence 5007, Ap
	72	15	1.6	922	6	US-10-953-349-15440	Sequence 15440, A
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	76	15	1.6	1077	7	US-11-217-529-173436	Sequence 173436,
	77	15	1.6	1089	7	US-11-217-529-6206	Sequence 6206, Ap
c	78	15	1.6	1101	6	US-10-953-349-32952	Sequence 32952, A
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c	80	15	1.6	1122	6	US-10-953-349-31251	Sequence 31251, A
	81	15	1.6	1129	6	US-10-953-349-17431	Sequence 17431, A
c	82	15	1.6	1157	6	US-10-953-349-19240	Sequence 19240, A
c	83	15	1.6	1178	6	US-10-953-349-19188	Sequence 19188, A
c	84	15	1.6	1194	7	US-11-217-529-81713	Sequence 81713, A
c	85	15	1.6	1228	6	US-10-953-349-25037	Sequence 25037, A
	86	15	1.6	1243	6	US-10-953-349-37059	Sequence 37059, A
c	87	15	1.6	1244	6	US-10-953-349-21963	Sequence 21963, A
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c	97	15	1.6	1428	7	US-11-217-529-2039	Sequence 2039, Ap
c	98	15	1.6	1436	6	US-10-953-349-30996	Sequence 30996, A

99	15	1.6	1444	6	US-10-953-349-289	Sequence 289, App
c 100	15	1.6	1452	6	US-10-505-928-318	Sequence 318, App
c 101	15	1.6	1479	7	US-11-217-529-76855	Sequence 76855, A
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103	15	1.6	1489	6	US-10-953-349-31882	Sequence 31882, A
c 104	15	1.6	1503	7	US-11-217-529-76539	Sequence 76539, A
105	15	1.6	1519	6	US-10-953-349-19905	Sequence 19905, A
c 106	15	1.6	1582	6	US-10-953-349-11557	Sequence 11557, A
107	15	1.6	1600	6	US-10-953-349-3805	Sequence 3805, Ap
108	15	1.6	1645	6	US-10-953-349-22110	Sequence 22110, A
c 109	15	1.6	1648	6	US-10-953-349-10297	Sequence 10297, A
110	15	1.6	1671	7	US-11-217-529-78801	Sequence 78801, A
111	15	1.6	1683	7	US-11-217-529-82600	Sequence 82600, A
112	15	1.6	1690	6	US-10-196-749-449	Sequence 449, App
113	15	1.6	1704	7	US-11-217-529-81313	Sequence 81313, A
114	15	1.6	1725	7	US-11-217-529-77188	Sequence 77188, A
c 115	15	1.6	1733	7	US-11-293-697-1577	Sequence 1577, Ap
c 116	15	1.6	1736	7	US-11-293-697-981	Sequence 981, App
117	15	1.6	1737	7	US-11-217-529-1440	Sequence 1440, Ap
118	15	1.6	1743	6	US-10-471-571A-4661	Sequence 4661, Ap
c 119	15	1.6	1758	6	US-10-953-349-3183	Sequence 3183, Ap
120	15	1.6	1767	7	US-11-217-529-6013	Sequence 6013, Ap
c 121	15	1.6	1785	7	US-11-217-529-81561	Sequence 81561, A
122	15	1.6	1838	6	US-10-953-349-37949	Sequence 37949, A
c 123	15	1.6	1843	6	US-10-511-937-620	Sequence 620, App
c 124	15	1.6	1889	6	US-10-953-349-7228	Sequence 7228, Ap
c 125	15	1.6	1915	6	US-10-953-349-11008	Sequence 11008, A
126	15	1.6	1949	7	US-11-293-697-89	Sequence 89, Appl
c 127	15	1.6	1962	7	US-11-217-529-82242	Sequence 82242, A
c 128	15	1.6	1974	7	US-11-217-529-80089	Sequence 80089, A
129	15	1.6	2035	6	US-10-511-937-2831	Sequence 2831, Ap
130	15	1.6	2045	6	US-10-953-349-40229	Sequence 40229, A
131	15	1.6	2046	6	US-10-471-571A-991	Sequence 991, App
c 132	15	1.6	2071	7	US-11-293-697-10	Sequence 10, Appl
c 133	15	1.6	2136	7	US-11-217-529-78809	Sequence 78809, A
c 134	15	1.6	2209	6	US-10-953-349-23348	Sequence 23348, A
c 135	15	1.6	2236	6	US-10-511-937-516	Sequence 516, App
c 136	15	1.6	2276	6	US-10-953-349-20232	Sequence 20232, A
c 137	15	1.6	2295	7	US-11-293-697-946	Sequence 946, App
c 138	15	1.6	2324	6	US-10-511-937-585	Sequence 585, App
139	15	1.6	2366	7	US-11-293-697-1960	Sequence 1960, Ap
c 140	15	1.6	2520	6	US-10-953-349-7725	Sequence 7725, Ap
c 141	15	1.6	2532	7	US-11-217-529-77060	Sequence 77060, A
c 142	15	1.6	2615	6	US-10-196-749-523	Sequence 523, App
143	15	1.6	2640	7	US-11-238-282-18	Sequence 18, Appl
144	15	1.6	2650	7	US-11-293-697-241	Sequence 241, App
145	15	1.6	2766	7	US-11-293-697-1119	Sequence 1119, Ap
146	15	1.6	2787	7	US-11-293-697-653	Sequence 653, App
c 147	15	1.6	2810	7	US-11-305-477-2	Sequence 2, Appli
148	15	1.6	2883	7	US-11-333-838-3	Sequence 3, Appli
c 149	15	1.6	2925	7	US-11-217-529-78225	Sequence 78225, A
c 150	15	1.6	2926	7	US-11-293-697-327	Sequence 327, App
c 151	15	1.6	2961	6	US-10-511-455-53	Sequence 53, Appl
c 152	15	1.6	2961	7	US-11-293-697-49	Sequence 49, Appl
153	15	1.6	3041	7	US-11-293-697-1534	Sequence 1534, Ap
c 154	15	1.6	3054	7	US-11-217-529-2509	Sequence 2509, Ap
c 155	15	1.6	3112	7	US-11-293-697-1458	Sequence 1458, Ap
156	15	1.6	3366	7	US-11-333-838-2	Sequence 2, Appli
c 157	15	1.6	3428	6	US-10-511-455-51	Sequence 51, Appl
158	15	1.6	3442	7	US-11-293-697-1578	Sequence 1578, Ap
159	15	1.6	3560	7	US-11-293-697-654	Sequence 654, App
c 160	15	1.6	3624	7	US-11-217-529-3816	Sequence 3816, Ap
161	15	1.6	3674	6	US-10-473-173-2	Sequence 2, Appli
c 162	15	1.6	4059	7	US-11-106-014-47	Sequence 47, Appl
163	15	1.6	4534	6	US-10-473-691B-1	Sequence 1, Appli
164	15	1.6	4573	6	US-10-505-928-409	Sequence 409, App
165	15	1.6	4585	6	US-10-505-928-47	Sequence 47, Appl
166	15	1.6	4686	7	US-11-217-529-3096	Sequence 3096, Ap
167	15	1.6	4842	6	US-10-196-749-289	Sequence 289, App
168	15	1.6	4863	7	US-11-217-529-2436	Sequence 2436, Ap
169	15	1.6	4995	7	US-11-217-529-2505	Sequence 2505, Ap
c 170	15	1.6	5262	7	US-11-217-529-76367	Sequence 76367, A
171	15	1.6	5515	6	US-10-524-021-1	Sequence 1, Appli
172	15	1.6	5711	6	US-10-480-434A-15	Sequence 15, Appl
c 173	15	1.6	5934	7	US-11-313-450-13	Sequence 13, Appl
c 174	15	1.6	5997	7	US-11-313-450-1	Sequence 1, Appli
c 175	15	1.6	6003	7	US-11-313-450-5	Sequence 5, Appli
c 176	15	1.6	6018	7	US-11-313-450-3	Sequence 3, Appli
177	15	1.6	6218	6	US-10-505-928-460	Sequence 460, App
c 178	15	1.6	6328	7	US-11-263-326-101	Sequence 101, App
c 179	15	1.6	6328	7	US-11-263-326-102	Sequence 102, App
c 180	15	1.6	6328	7	US-11-263-326-103	Sequence 103, App
c 181	15	1.6	6328	7	US-11-263-326-146	Sequence 146, App
c 182	15	1.6	6328	7	US-11-263-326-147	Sequence 147, App
c 183	15	1.6	6328	7	US-11-263-326-148	Sequence 148, App
c 184	15	1.6	6328	7	US-11-263-326-149	Sequence 149, App
c 185	15	1.6	6328	7	US-11-263-326-150	Sequence 150, App
c 186	15	1.6	6328	7	US-11-263-326-151	Sequence 151, App
c 187	15	1.6	6328	7	US-11-263-326-152	Sequence 152, App
c 188	15	1.6	6371	7	US-11-251-465-8	Sequence 8, Appli
c 189	15	1.6	6596	7	US-11-263-326-105	Sequence 105, App
c 190	15	1.6	6599	7	US-11-263-326-106	Sequence 106, App
c 191	15	1.6	6599	7	US-11-263-326-107	Sequence 107, App
c 192	15	1.6	6599	7	US-11-263-326-109	Sequence 109, App
c 193	15	1.6	6732	7	US-11-217-529-1872	Sequence 1872, Ap
c 194	15	1.6	7280	6	US-10-505-928-842	Sequence 842, App
195	15	1.6	8019	7	US-11-217-529-76544	Sequence 76544, A
c 196	15	1.6	8292	6	US-10-501-814-2	Sequence 2, Appli
c 197	15	1.6	8370	7	US-11-263-326-90	Sequence 90, Appl
c 198	15	1.6	8377	7	US-11-263-326-95	Sequence 95, Appl
c 199	15	1.6	8380	7	US-11-263-326-89	Sequence 89, Appl
c 200	15	1.6	8381	7	US-11-263-326-1	Sequence 1, Appli

ALIGNMENTS

```
RESULT 1
US-10-471-571A-1285/c
; Sequence 1285, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 1285
;   LENGTH: 960
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-1285

  Query Match             2.0%;  Score 18;  DB 6;  Length 960;
  Best Local Similarity   100.0%;  Pred. No. 4.1;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        609 CAGCAGCTTCTTCATCAG 626
              ||||||||||||||||||
Db        142 CAGCAGCTTCTTCATCAG 125


RESULT 2
US-11-313-450-13
; Sequence 13, Application US/11313450
; Publication No. US20060110778A1
; GENERAL INFORMATION:
;  APPLICANT: Adorante, Joeseph S.
;  APPLICANT:  Ehring, George R.
;  TITLE OF INVENTION: High-Throughput Screens For Identifying
;  TITLE OF INVENTION:  Selective Persistent Sodium Channels Channel Blockers
;  FILE REFERENCE: 17407 CIP (AP)
```

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;  CURRENT APPLICATION NUMBER: US/11/313,450
;  CURRENT FILING DATE:  2005-12-19
;  PRIOR APPLICATION NUMBER: 09/989797
;  PRIOR FILING DATE: 2001-11-20
;  PRIOR APPLICATION NUMBER: 60/252771
;  PRIOR FILING DATE: 2000-11-22
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 5934
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-313-450-13

  Query Match             2.0%;  Score 18;  DB 7;  Length 5934;
  Best Local Similarity   100.0%;  Pred. No. 4.3;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        250 AAAAAGGAAGATGGAATT 267
              ||||||||||||||||||
Db       4975 AAAAAGGAAGATGGAATT 4992


RESULT 3
US-11-251-465-8
; Sequence 8, Application US/11251465
; Publication No. US20060094061A1
; GENERAL INFORMATION:
;  APPLICANT: Brys, Reginald
;  APPLICANT:  Vandeghinste, Nick
;  APPLICANT:  Tomme, Peter
;  APPLICANT:  Klaassen, Hubertus
;  TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
;  TITLE OF INVENTION:  Same, Useful In The Treatment Of Joint Degenerative And
;  TITLE OF INVENTION:  Inflammatory Diseases
;  FILE REFERENCE: P30,172-A USA
;  CURRENT APPLICATION NUMBER: US/11/251,465
;  CURRENT FILING DATE:  2005-10-14
;  PRIOR APPLICATION NUMBER: 60/619,384
;  PRIOR FILING DATE: 2004-10-15
;  NUMBER OF SEQ ID NOS: 880
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
;   LENGTH: 6371
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-251-465-8

  Query Match             2.0%;  Score 18;  DB 7;  Length 6371;
  Best Local Similarity   100.0%;  Pred. No. 4.4;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        250 AAAAAGGAAGATGGAATT 267
              ||||||||||||||||||
Db       5023 AAAAAGGAAGATGGAATT 5040


RESULT 4
US-10-953-349-15338/c
; Sequence 15338, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15338
;   LENGTH: 862
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-15338

  Query Match             1.8%;  Score 17;  DB 6;  Length 862;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        876 CTACTATAGCTCATCCT 892
              |||||||||||||||||
Db        620 CTACTATAGCTCATCCT 604


RESULT 5
US-11-233-726-17/c
; Sequence 17, Application US/11233726
; Publication No. US20060090216A1
; GENERAL INFORMATION:
;  APPLICANT: APUYA, Nestor
;  APPLICANT:  KWOK, Shing
;  APPLICANT:  ALEXANDROV, Nickolai
;  APPLICANT:  TATARINOVA, Tatiana
;  APPLICANT:  FANG, Yiwen
;  APPLICANT:  PENNELL, Roger
;  APPLICANT:  LU, Yu-Ping
;  APPLICANT:  MEDRANO, Leonard
;  APPLICANT:  FELDMANN, Kenneth A.
;  APPLICANT:  COOK, Zhihong C.
;  TITLE OF INVENTION: Promoter, Promoter Control Elements, And Combinations, And Uses Th
;  FILE REFERENCE: 2750-1619PUS2
;  CURRENT APPLICATION NUMBER: US/11/233,726
;  CURRENT FILING DATE:  2005-02-23
;  PRIOR APPLICATION NUMBER: 60/612,891
;  PRIOR FILING DATE: 2004-09-23
;  PRIOR APPLICATION NUMBER: 60/613,134
;  PRIOR FILING DATE: 2004-09-23
;  PRIOR APPLICATION NUMBER: 60/637,174
;  PRIOR FILING DATE: 2004-12-16
;  NUMBER OF SEQ ID NOS: 46
; SEQ ID NO 17
;   LENGTH: 1000
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1000)
;   OTHER INFORMATION: Ceres Promoter construct YP0382 as found in Promoter Report #130
US-11-233-726-17

  Query Match             1.8%;  Score 17;  DB 7;  Length 1000;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        167 AAGTCAAAGAATTTGCA 183
              |||||||||||||||||
Db        623 AAGTCAAAGAATTTGCA 607


RESULT 6
US-10-953-349-3012
; Sequence 3012, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3012
;   LENGTH: 1061
;   TYPE: DNA
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;   ORGANISM: Arabidopsis thaliana
US-10-953-349-3012

  Query Match             1.8%;  Score 17;  DB 6;  Length 1061;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        304 AAAAATAAGATCTTTCT 320
              |||||||||||||||||
Db         63 AAAAATAAGATCTTTCT 79


RESULT 7
US-10-953-349-9710
; Sequence 9710, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9710
;   LENGTH: 1498
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-9710

  Query Match             1.8%;  Score 17;  DB 6;  Length 1498;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        117 CTCTGACCAGAGCAGTG 133
              |||||||||||||||||
Db        553 CTCTGACCAGAGCAGTG 569


RESULT 8
US-11-217-529-190982/c
; Sequence 190982, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 190982
;   LENGTH: 3228
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-190982

  Query Match             1.8%;  Score 17;  DB 7;  Length 3228;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         90 TCCTGAAGAAGATGACA 106
              |||||||||||||||||
Db       1929 TCCTGAAGAAGATGACA 1913


RESULT 9
US-10-471-571A-4869/c
; Sequence 4869, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 4869
;   LENGTH: 231
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-4869

  Query Match             1.7%;  Score 16;  DB 6;  Length 231;
  Best Local Similarity   100.0%;  Pred. No. 45;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        612 CAGCTTCTTCATCAGG 627
              ||||||||||||||||
Db        178 CAGCTTCTTCATCAGG 163


RESULT 10
US-10-548-484-9
; Sequence 9, Application US/10548484
; Publication No. US20060107343A1
; GENERAL INFORMATION:
;  APPLICANT: Ishihara Sangyo Kaisha, Ltd.
;  TITLE OF INVENTION: Plant Cells And Plant Bodies With Modified Cell Growth, Developmer
;  TITLE OF INVENTION:  Differentiation
;  FILE REFERENCE: IS-09PCT
;  CURRENT APPLICATION NUMBER: US/10/548,484
;  CURRENT FILING DATE:  2005-09-09
;  PRIOR APPLICATION NUMBER: JP 2003-66064
;  PRIOR FILING DATE: 2003-03-12
;  NUMBER OF SEQ ID NOS: 100
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 305
;   TYPE: DNA
;   ORGANISM: Oryza sativa
US-10-548-484-9

  Query Match             1.7%;  Score 16;  DB 6;  Length 305;
  Best Local Similarity   100.0%;  Pred. No. 45;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         94 GAAGAAGATGACATCA 109
              ||||||||||||||||
Db         55 GAAGAAGATGACATCA 70


RESULT 11
US-10-548-484-10
; Sequence 10, Application US/10548484
; Publication No. US20060107343A1
; GENERAL INFORMATION:
;  APPLICANT: Ishihara Sangyo Kaisha, Ltd.
;  TITLE OF INVENTION: Plant Cells And Plant Bodies With Modified Cell Growth, Developmer
;  TITLE OF INVENTION:  Differentiation
;  FILE REFERENCE: IS-09PCT
;  CURRENT APPLICATION NUMBER: US/10/548,484
;  CURRENT FILING DATE:  2005-09-09
;  PRIOR APPLICATION NUMBER: JP 2003-66064
;  PRIOR FILING DATE: 2003-03-12
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;  NUMBER OF SEQ ID NOS: 100
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 305
;   TYPE: DNA
;   ORGANISM: Oryza sativa
US-10-548-484-10

  Query Match             1.7%;  Score 16;  DB 6;  Length 305;
  Best Local Similarity   100.0%;  Pred. No. 45;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         94 GAAGAAGATGACATCA 109
              ||||||||||||||||
Db         55 GAAGAAGATGACATCA 70


RESULT 12
US-10-488-619-3012
; Sequence 3012, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3012
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-488-619-3012

  Query Match             1.7%;  Score 16;  DB 6;  Length 561;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        839 ACAAGGATGCCAAGAT 854
              ||||||||||||||||
Db        336 ACAAGGATGCCAAGAT 351


RESULT 13
US-10-953-349-38575/c
; Sequence 38575, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38575
;   LENGTH: 577
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-38575

  Query Match             1.7%;  Score 16;  DB 6;  Length 577;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        269 GGTCCACTGATATCTT 284
              ||||||||||||||||
Db        436 GGTCCACTGATATCTT 421


RESULT 14
US-10-953-349-39182
; Sequence 39182, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39182
;   LENGTH: 634
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-39182

  Query Match             1.7%;  Score 16;  DB 6;  Length 634;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        838 CACAAGGATGCCAAGA 853
              ||||||||||||||||
Db        281 CACAAGGATGCCAAGA 296


RESULT 15
US-10-548-484-16
; Sequence 16, Application US/10548484
; Publication No. US20060107343A1
; GENERAL INFORMATION:
;  APPLICANT: Ishihara Sangyo Kaisha, Ltd.
;  TITLE OF INVENTION: Plant Cells And Plant Bodies With Modified Cell Growth, Developmer
;  TITLE OF INVENTION:  Differentiation
;  FILE REFERENCE: IS-09PCT
;  CURRENT APPLICATION NUMBER: US/10/548,484
;  CURRENT FILING DATE:  2005-09-09
;  PRIOR APPLICATION NUMBER: JP 2003-66064
;  PRIOR FILING DATE: 2003-03-12
;  NUMBER OF SEQ ID NOS: 100
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 726
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (542)..(542)
;   OTHER INFORMATION: n stands for any base
US-10-548-484-16

  Query Match             1.7%;  Score 16;  DB 6;  Length 726;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         94 GAAGAAGATGACATCA 109
              ||||||||||||||||
Db        567 GAAGAAGATGACATCA 582


RESULT 16
US-10-196-749-359
; Sequence 359, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
```

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;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C340
;  CURRENT APPLICATION NUMBER: US/10/196,749
;  CURRENT FILING DATE:  2002-07-16
;  PRIOR APPLICATION NUMBER: 10/052586
;  PRIOR FILING DATE: 2002-01-15
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059266
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063120
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063121
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063486
;  PRIOR FILING DATE: 1997-10-21
;  PRIOR APPLICATION NUMBER: 60/063540
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063541
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063544
;  PRIOR FILING DATE: 1997-10-28
;  Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 359
;   LENGTH: 742
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-196-749-359

  Query Match             1.7%;  Score 16;  DB 6;  Length 742;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          97 GAAGATGACATCACCT 112
               ||||||||||||||||
Db         361 GAAGATGACATCACCT 376


RESULT 17
US-10-471-571A-689/c
; Sequence 689, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 689
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-689

  Query Match             1.7%;  Score 16;  DB 6;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 47;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         611 GCAGCTTCTTCATCAG 626
               ||||||||||||||||
Db         398 GCAGCTTCTTCATCAG 383


RESULT 18
US-11-217-529-79675/c
; Sequence 79675, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79675
;   LENGTH: 945
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-79675

  Query Match             1.7%;  Score 16;  DB 7;  Length 945;
  Best Local Similarity   100.0%;  Pred. No. 47;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         609 CAGCAGCTTCTTCATC 624
               ||||||||||||||||
Db         214 CAGCAGCTTCTTCATC 199


RESULT 19
US-10-953-349-27059
; Sequence 27059, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27059
;   LENGTH: 1039
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-10-953-349-27059

  Query Match             1.7%;  Score 16;  DB 6;  Length 1039;
  Best Local Similarity   100.0%;  Pred. No. 47;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         379 AGTACCGATTTGAAAT 394
               ||||||||||||||||
Db         407 AGTACCGATTTGAAAT 422


RESULT 20
US-11-217-529-4517
; Sequence 4517, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
```

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;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4517
;   LENGTH: 1083
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-4517

  Query Match             1.7%;  Score 16;  DB 7;  Length 1083;
  Best Local Similarity   100.0%;  Pred. No. 47;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 AACTGGAGAAAAACGT 23
              ||||||||||||||||
Db        467 AACTGGAGAAAAACGT 482


RESULT 21
US-11-217-529-75941
; Sequence 75941, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75941
;   LENGTH: 1098
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-75941

  Query Match             1.7%;  Score 16;  DB 7;  Length 1098;
  Best Local Similarity   100.0%;  Pred. No. 47;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        665 TGAAGCCATTAAAAAA 680
              ||||||||||||||||
Db        254 TGAAGCCATTAAAAAA 269


RESULT 22
US-10-953-349-9694
; Sequence 9694, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9694
;   LENGTH: 1226
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-9694

  Query Match             1.7%;  Score 16;  DB 6;  Length 1226;
  Best Local Similarity   100.0%;  Pred. No. 47;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        310 AAGATCTTTCTAAAAT 325
              ||||||||||||||||
Db        973 AAGATCTTTCTAAAAT 988


RESULT 23
US-10-953-349-3568
; Sequence 3568, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3568
;   LENGTH: 1232
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-3568

  Query Match             1.7%;  Score 16;  DB 6;  Length 1232;
  Best Local Similarity   100.0%;  Pred. No. 47;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        603 CTACACCAGCAGCTTC 618
              ||||||||||||||||
Db        592 CTACACCAGCAGCTTC 607


RESULT 24
US-10-953-349-22615/c
; Sequence 22615, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22615
;   LENGTH: 1621
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-22615

  Query Match             1.7%;  Score 16;  DB 6;  Length 1621;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        736 TCCTACTTCTCCTTAA 751
              ||||||||||||||||
Db       1184 TCCTACTTCTCCTTAA 1169


RESULT 25
US-10-953-349-33373
```

; Sequence 33373, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33373
; LENGTH: 1747
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
US-10-953-349-33373

Query Match 1.7%; Score 16; DB 6; Length 1747;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 401 TCAAAAGCAGCAGAGG 416
||||||||||||||||
Db 1268 TCAAAAGCAGCAGAGG 1283

RESULT 26
US-11-217-529-4576
; Sequence 4576, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4576
; LENGTH: 1797
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4576

Query Match 1.7%; Score 16; DB 7; Length 1797;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 750 AACATTTGGCGTACAG 765
||||||||||||||||
Db 729 AACATTTGGCGTACAG 744

RESULT 27
US-11-313-836-53/c
; Sequence 53, Application US/11313836
; Publication No. US20060116508A1
; GENERAL INFORMATION:
; APPLICANT: Glucksman, Maria Alexandra
; APPLICANT: Williamson, Mark J.
; APPLICANT: Tsia, Fong-Ying
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Chiang, Lillian Wei-Ming
; APPLICANT: Hunter, John Joseph
; APPLICANT: Wood, Andrew
; APPLICANT: Jenkins, Lorayne P.
; TITLE OF INVENTION: NOVEL 27411, 23413, 22438, 23553,
; TITLE OF INVENTION: 25278, 26212, NARC SC1, NARC 10A, NARC 1, NARC 12, NARC 13,
; TITLE OF INVENTION: NARC17, NARC 25, NARC 3, NARC 4, NARC 7, NARC 8, NARC 11,
; TITLE OF INVENTION: NARC 14A, NARC 15, NARC 16, NARC 19, NARC 20, NARC 26, NARC
; TITLE OF INVENTION: 27, NARC 28, NARC 30, NARC 5, NARC 6, NARC 9, NARC 10C, NARC
; TITLE OF INVENTION: 8B, NARC 9, NARC2A, NARC 16B, NARC 1C, NARC 1A, NARC 25,
; TITLE OF INVENTION: 86604 AND 32222 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-062OMNIM
; CURRENT APPLICATION NUMBER: US/11/313,836
; CURRENT FILING DATE: 2005-12-21
; PRIOR APPLICATION NUMBER: US/10/426,776
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 10/229,662
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 09/795,691
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/185,517
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 10/105,992
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/406,045
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: 10/314,881
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 09/773,426
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 09/495,823
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 09/692,785
; PRIOR FILING DATE: 2000-10-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 1975
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-313-836-53

Query Match 1.7%; Score 16; DB 7; Length 1975;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 409 AGCAGAGGCTCCTCTG 424
||||||||||||||||
Db 225 AGCAGAGGCTCCTCTG 210

RESULT 28
US-10-953-349-37153/c
; Sequence 37153, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37153
; LENGTH: 2117
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
US-10-953-349-37153

Query Match 1.7%; Score 16; DB 6; Length 2117;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        802 CTCTCCGTGGACAAGA 817
              ||||||||||||||||
Db       1588 CTCTCCGTGGACAAGA 1573


RESULT 29
US-11-293-697-1627
; Sequence 1627, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1627
;   LENGTH: 2270
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1627

  Query Match             1.7%;  Score 16;  DB 7;  Length 2270;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        835 TGCCACAAGGATGCCA 850
              ||||||||||||||||
Db       1151 TGCCACAAGGATGCCA 1166


RESULT 30
US-11-293-697-928/c
; Sequence 928, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 928
;   LENGTH: 2278
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-928

  Query Match             1.7%;  Score 16;  DB 7;  Length 2278;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        409 AGCAGAGGCTCCTCTG 424
              ||||||||||||||||
Db        442 AGCAGAGGCTCCTCTG 427


RESULT 31
US-11-293-697-1624/c
; Sequence 1624, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1624
;   LENGTH: 2324
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1624

  Query Match             1.7%;  Score 16;  DB 7;  Length 2324;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        881 ATAGCTCATCCTGGAG 896
              ||||||||||||||||
Db       1957 ATAGCTCATCCTGGAG 1942


RESULT 32
US-11-293-697-1068/c
; Sequence 1068, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1068
;   LENGTH: 2538
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1068

  Query Match             1.7%;  Score 16;  DB 7;  Length 2538;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        299 AATCCAAAAATAAGAT 314
              ||||||||||||||||
Db       2405 AATCCAAAAATAAGAT 2390


RESULT 33
US-11-266-446-7/c
; Sequence 7, Application US/11266446
; Publication No. US20060112452A1
; GENERAL INFORMATION:
;  APPLICANT: Keetman, Ulrich
;  APPLICANT:  Duwenig, Elke
;  APPLICANT:  Loyall, Linda P
;  APPLICANT:  Herbers, Karin
;  APPLICANT:  Hillebrand, Helke
;  TITLE OF INVENTION: EXPRESSION CASSETTES FOR SEED-PREFERENTIAL EXPRESSION IN PLANTS
;  FILE REFERENCE: 12810-00165-US
;  CURRENT APPLICATION NUMBER: US/11/266,446
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04026295.8
;  PRIOR FILING DATE: 2004-11-05
;  PRIOR APPLICATION NUMBER: EP 04029024.9
;  PRIOR FILING DATE: 2004-12-08
;  PRIOR APPLICATION NUMBER: EP 05002262.3
;  PRIOR FILING DATE: 2005-02-03
;  PRIOR APPLICATION NUMBER: EP 05002850.5
;  PRIOR FILING DATE: 2005-02-11
;  NUMBER OF SEQ ID NOS: 156
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
```

```
;   LENGTH: 2682
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (93)..(2387)
;   OTHER INFORMATION: coding for 5-methyltetrahydro-pteroyltriglutamate homocysteine
;   OTHER INFORMATION: methyltransferase (At5g17920)
US-11-266-446-7

  Query Match             1.7%;  Score 16;  DB 7;  Length 2682;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        802 CTCTCCGTGGACAAGA 817
              ||||||||||||||||
Db       1562 CTCTCCGTGGACAAGA 1547


RESULT 34
US-10-953-349-36221/c
; Sequence 36221, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36221
;   LENGTH: 2703
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-36221

  Query Match             1.7%;  Score 16;  DB 6;  Length 2703;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        108 CACCTGGACCTCTGAC 123
              ||||||||||||||||
Db       1550 CACCTGGACCTCTGAC 1535


RESULT 35
US-11-293-697-539/c
; Sequence 539, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 539
;   LENGTH: 2829
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-539

  Query Match             1.7%;  Score 16;  DB 7;  Length 2829;
  Best Local Similarity   100.0%;  Pred. No. 49;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        294 GAAAGAATCCAAAAAT 309
              ||||||||||||||||
Db        330 GAAAGAATCCAAAAAT 315


RESULT 36
US-10-505-928-444
; Sequence 444, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
;  APPLICANT: Ludwig Institute for Cancer Research et al.
;  TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
;  FILE REFERENCE: 28967/39178
;  CURRENT APPLICATION NUMBER: US/10/505,928
;  CURRENT FILING DATE:  2004-08-27
;  PRIOR APPLICATION NUMBER: US 60/363,019
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: PatentIn 3.2
; SEQ ID NO 444
;   LENGTH: 2846
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-505-928-444

  Query Match             1.7%;  Score 16;  DB 6;  Length 2846;
  Best Local Similarity   100.0%;  Pred. No. 49;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        779 ACAACAGAGAAAAGAA 794
              ||||||||||||||||
Db        599 ACAACAGAGAAAAGAA 614


RESULT 37
US-11-145-307A-3
; Sequence 3, Application US/11145307A
; Publication No. US20060094035A1
; GENERAL INFORMATION:
;  APPLICANT: Arcturus Bioscience, Inc.
;  APPLICANT:  Erlander, Mark G.
;  APPLICANT:  Ma, Xiao-Jun
;  TITLE OF INVENTION: Identification of Tumors
;  FILE REFERENCE: 022041-002020US
;  CURRENT APPLICATION NUMBER: US/11/145,307A
;  CURRENT FILING DATE:  2005-06-03
;  PRIOR APPLICATION NUMBER: US 60/577,084
;  PRIOR FILING DATE: 2004-06-04
;  NUMBER OF SEQ ID NOS: 268
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 2872
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-145-307A-3

  Query Match             1.7%;  Score 16;  DB 7;  Length 2872;
  Best Local Similarity   100.0%;  Pred. No. 49;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        248 ACAAAAAGGAAGATGG 263
              ||||||||||||||||
Db       1864 ACAAAAAGGAAGATGG 1879


RESULT 38
US-10-953-349-5832/c
; Sequence 5832, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
```

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;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5832
;   LENGTH: 3271
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-5832

  Query Match             1.7%;  Score 16;  DB 6;  Length 3271;
  Best Local Similarity   100.0%;  Pred. No. 49;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         88 ACTCCTGAAGAAGATG 103
              ||||||||||||||||
Db        824 ACTCCTGAAGAAGATG 809


RESULT 39
US-11-217-529-77298
; Sequence 77298, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77298
;   LENGTH: 5310
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-77298

  Query Match             1.7%;  Score 16;  DB 7;  Length 5310;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        263 GAATTTGGTCCACTGA 278
              ||||||||||||||||
Db       4376 GAATTTGGTCCACTGA 4391


RESULT 40
US-11-253-190-4/c
; Sequence 4, Application US/11253190
; Publication No. US20060115839A1
; GENERAL INFORMATION:
;  APPLICANT: Halazonetis, Thanos D
;  TITLE OF INVENTION: METHODS OF IDENTIFYING AN AGENT THAT MODULATES AN INTERACTION
;  TITLE OF INVENTION:  BETWEEN 53BP1 AND HISTONE H3, AND USES THEREOF
;  FILE REFERENCE: HALA0001-100
;  CURRENT APPLICATION NUMBER: US/11/253,190
;  CURRENT FILING DATE:  2005-10-17
;  PRIOR APPLICATION NUMBER: US 60/620,461
;  PRIOR FILING DATE: 2004-10-19
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
;   LENGTH: 6266
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-253-190-4

  Query Match             1.7%;  Score 16;  DB 7;  Length 6266;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        113 GGACCTCTGACCAGAG 128
              ||||||||||||||||
Db       1220 GGACCTCTGACCAGAG 1205


RESULT 41
US-10-953-349-5546/c
; Sequence 5546, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5546
;   LENGTH: 12659
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-5546

  Query Match             1.7%;  Score 16;  DB 6;  Length 12659;
  Best Local Similarity   100.0%;  Pred. No. 51;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        148 GGTAAAACTCTGACCA 163
              ||||||||||||||||
Db       5793 GGTAAAACTCTGACCA 5778


RESULT 42
US-10-519-335-37/c
; Sequence 37, Application US/10519335
; Publication No. US20060099210A1
; GENERAL INFORMATION:
;  APPLICANT: Cavarec, Laurent
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Destenaves, Benoit
;  APPLICANT:  Gonthier, Catherine
;  APPLICANT:  Elias, Isabelle
;  TITLE OF INVENTION: NOVEL KCNQ POLYPEPTIDES, MODULATORS THEREOF, AND THEIR USES IN THE
;  TITLE OF INVENTION:  TREATMENT OF MENTAL DISORDERS
;  FILE REFERENCE: G-194US03PCT
;  CURRENT APPLICATION NUMBER: US/10/519,335
;  CURRENT FILING DATE:  2004-12-22
;  PRIOR APPLICATION NUMBER: US 60/391,359
;  PRIOR FILING DATE: 2002-06-25
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
;   LENGTH: 151830
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (10)..(10)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (60402)..(60402)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (61110)..(61110)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
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;   NAME/KEY: misc_feature
;   LOCATION: (98207)..(98207)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (98208)..(98208)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (98209)..(98209)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (98210)..(98210)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (98211)..(98211)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (99743)..(99743)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (108055)..(108055)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (109094)..(109094)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (109125)..(109125)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (118900)..(118900)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (119024)..(119052)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (119053)..(119112)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (119115)..(119121)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (119123)..(119123)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (141674)..(141674)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (142063)..(142063)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (142137)..(142137)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (142967)..(142967)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (143077)..(143077)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (143506)..(143506)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (143587)..(143587)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (143629)..(143629)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (149079)..(149079)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (5363)..(5363)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (8080)..(8080)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (10296)..(10296)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (14528)..(14528)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (15336)..(15336)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (15457)..(15457)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (16288)..(16288)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (16306)..(16307)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (16316)..(16316)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (16397)..(16397)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (56012)..(56012)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (57662)..(57662)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: 5'UTR
;   LOCATION: (1)..(54)
;   OTHER INFORMATION: exon 1
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (55)..(124)
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;   OTHER INFORMATION: exon 1
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (91147)..(91244)
;   OTHER INFORMATION: exon 2
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (93669)..(93834)
;   OTHER INFORMATION: exon 3
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (96310)..(96422)
;   OTHER INFORMATION: exon 4
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (99546)..(99723)
;   OTHER INFORMATION: exon 5
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (125441)..(125605)

  Query Match             1.7%;  Score 16;  DB 6;  Length 151830;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        518 AGGAGGGCAGTGCCTG 533
              ||||||||||||||||
Db       8739 AGGAGGGCAGTGCCTG 8724


RESULT 43
US-11-266-409-12/c
; Sequence 12, Application US/11266409
; Publication No. US20060093578A1
; GENERAL INFORMATION:
;  APPLICANT: SUZUMURA, AKIO
;  TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATING MULTIPLE SCLEROSIS
;  FILE REFERENCE: 279847US40
;  CURRENT APPLICATION NUMBER: US/11/266,409
;  CURRENT FILING DATE:  2005-11-04
;  PRIOR APPLICATION NUMBER: US 60/624,851
;  PRIOR FILING DATE: 2004-11-04
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA
US-11-266-409-12

  Query Match             1.6%;  Score 15;  DB 7;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        733 CATTCCTACTTCTCC 747
              |||||||||||||||
Db         17 CATTCCTACTTCTCC 3


RESULT 44
US-11-217-529-28477/c
; Sequence 28477, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28477
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-28477

  Query Match             1.6%;  Score 15;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        287 GGGAACAGAAAGAAT 301
              |||||||||||||||
Db         23 GGGAACAGAAAGAAT 9


RESULT 45
US-11-217-529-94239/c
; Sequence 94239, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 94239
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-94239

  Query Match             1.6%;  Score 15;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        850 AAGATCCGCGTGCAA 864
              |||||||||||||||
Db         24 AAGATCCGCGTGCAA 10


RESULT 46
US-11-217-529-115861/c
; Sequence 115861, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
```

```
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 115861
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-115861

  Query Match             1.6%;  Score 15;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        292 CAGAAAGAATCCAAA 306
              |||||||||||||||
Db         18 CAGAAAGAATCCAAA 4


RESULT 47
US-11-217-529-121503/c
; Sequence 121503, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 121503
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-121503

  Query Match             1.6%;  Score 15;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        745 TCCTTAACATTTGGC 759
              |||||||||||||||
Db         19 TCCTTAACATTTGGC 5


RESULT 48
US-10-857-260-37
; Sequence 37, Application US/10857260
; Publication No. US20060110742A1
; GENERAL INFORMATION:
;  APPLICANT: Lyons, Leslie A.
;  APPLICANT:  Grahn, Robert
;  APPLICANT:  Erdman, Carolyn
;  APPLICANT:  The Regents of the University of California
;  TITLE OF INVENTION: Carrier Tests for Polycystic Kidney Disease in the Cat
;  FILE REFERENCE: 02307O-146800US
;  CURRENT APPLICATION NUMBER: US/10/857,260
;  CURRENT FILING DATE:  2004-05-28
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
;   LENGTH: 209
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: human (Hsap) PKD1 exon 29
US-10-857-260-37

  Query Match             1.6%;  Score 15;  DB 6;  Length 209;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        356 CCTGCTGGTGGCTGA 370
              |||||||||||||||
Db         27 CCTGCTGGTGGCTGA 41


RESULT 49
US-11-217-529-4828
; Sequence 4828, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4828
;   LENGTH: 261
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-4828

  Query Match             1.6%;  Score 15;  DB 7;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        774 CAAGAACAACAGAGA 788
              |||||||||||||||
Db         15 CAAGAACAACAGAGA 29


RESULT 50
US-11-301-554-899
; Sequence 899, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
;  APPLICANT: Henderson, Robert A.
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Watanabe, Yoshihiro
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Sleath, Paul R.
;  APPLICANT:  Johnson, Jeffrey C.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Durham, Margarita
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  McNabb, Andria
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.478C21
;  CURRENT APPLICATION NUMBER: US/11/301,554
;  CURRENT FILING DATE:  2005-12-13
;  PRIOR APPLICATION NUMBER: US 10/283,017
;  PRIOR FILING DATE: 2002-10-28
;  PRIOR APPLICATION NUMBER: US 10/113,872
;  PRIOR FILING DATE: 2002-03-28
;  PRIOR APPLICATION NUMBER: US 10/017,754
;  PRIOR FILING DATE: 2001-10-29
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;  PRIOR APPLICATION NUMBER: US 09/902,941
;  PRIOR FILING DATE: 2001-07-10
;  PRIOR APPLICATION NUMBER: US 09/849,626
;  PRIOR FILING DATE: 2001-05-03
;  PRIOR APPLICATION NUMBER: US 09/736,457
;  PRIOR FILING DATE: 2000-12-13
;  PRIOR APPLICATION NUMBER: US 09/702,705
;  PRIOR FILING DATE: 2000-10-30
;  PRIOR APPLICATION NUMBER: US 09/677,419
;  PRIOR FILING DATE: 2000-10-06
;  PRIOR APPLICATION NUMBER: US 09/671,325
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US 09/658,824
;  PRIOR FILING DATE: 2000-09-08
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2157
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 899
;   LENGTH: 277
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-301-554-899

  Query Match             1.6%;  Score 15;  DB 7;  Length 277;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        671 CATTAAAAAATTCTC 685
              |||||||||||||||
Db         10 CATTAAAAAATTCTC 24


RESULT 51
US-11-217-529-82243
; Sequence 82243, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82243
;   LENGTH: 354
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-82243

  Query Match             1.6%;  Score 15;  DB 7;  Length 354;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        788 AAAAGAAAGACAGAC 802
              |||||||||||||||
Db         19 AAAAGAAAGACAGAC 33


RESULT 52
US-11-217-529-80395
; Sequence 80395, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80395
;   LENGTH: 423
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-80395

  Query Match             1.6%;  Score 15;  DB 7;  Length 423;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         90 TCCTGAAGAAGATGA 104
              |||||||||||||||
Db        324 TCCTGAAGAAGATGA 338


RESULT 53
US-10-488-619-382
; Sequence 382, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations W
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 382
;   LENGTH: 456
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(456)
;   OTHER INFORMATION: n is g, c, a or t
US-10-488-619-382

  Query Match             1.6%;  Score 15;  DB 6;  Length 456;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        785 GAGAAAAGAAAGACA 799
              |||||||||||||||
Db        251 GAGAAAAGAAAGACA 265


RESULT 54
US-10-471-571A-5447
; Sequence 5447, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
```

; SEQ ID NO 5447
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-471-571A-5447

Query Match 1.6%; Score 15; DB 6; Length 498;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 273 CACTGATATCTTAAG 287
||||||||||||||||
Db 360 CACTGATATCTTAAG 374

RESULT 55
US-10-473-173-325/c
; Sequence 325, Application US/10473173
; Publication No. US20060088823A1
; GENERAL INFORMATION:
; APPLICANT: VAN ANDEL INSTITUTE
; TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell
; TITLE OF INVENTION: Carcinoma: Prognosis and Drug Target Identification
; FILE REFERENCE: 38345-170094
; CURRENT APPLICATION NUMBER: US/10/473,173
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/279,411
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 498
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 325
; LENGTH: 506
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-473-173-325

Query Match 1.6%; Score 15; DB 6; Length 506;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 477 AGTGGACAACAGGGA 491
||||||||||||||||
Db 258 AGTGGACAACAGGGA 244

RESULT 56
US-10-488-619-94/c
; Sequence 94, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 94
; LENGTH: 506
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-488-619-94

Query Match 1.6%; Score 15; DB 6; Length 506;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 477 AGTGGACAACAGGGA 491
||||||||||||||||
Db 258 AGTGGACAACAGGGA 244

RESULT 57
US-10-560-723-10
; Sequence 10, Application US/10560723
; Publication No. US20060115821A1
; GENERAL INFORMATION:
; APPLICANT: EXONHIT THERAPEUTICALS
; TITLE OF INVENTION: PROSTATE SPECIFIC GENES AND THE USE THEREOF AS TARGETS FOR PROSTAT
; TITLE OF INVENTION: CANCER THERAPY AND DIAGNOSIS
; FILE REFERENCE: B0213WO
; CURRENT APPLICATION NUMBER: US/10/560,723
; CURRENT FILING DATE: 2005-12-15
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-560-723-10

Query Match 1.6%; Score 15; DB 6; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 811 GACAAGACCTCAGCC 825
|||||||||||||||
Db 261 GACAAGACCTCAGCC 275

RESULT 58
US-10-953-349-31038
; Sequence 31038, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31038
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (511)..(511)
; OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-31038

Query Match 1.6%; Score 15; DB 6; Length 525;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 817 ACCTCAGCCAAGGTC 831
|||||||||||||||
Db 410 ACCTCAGCCAAGGTC 424

RESULT 59
US-11-217-529-174237/c
; Sequence 174237, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285

```
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174237
;   LENGTH: 531
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-174237

  Query Match             1.6%;  Score 15;  DB 7;  Length 531;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        793 AAAGACAGACTCTCC 807
              |||||||||||||||
Db        261 AAAGACAGACTCTCC 247


RESULT 60
US-10-953-349-13816/c
; Sequence 13816, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13816
;   LENGTH: 566
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-13816

  Query Match             1.6%;  Score 15;  DB 6;  Length 566;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        610 AGCAGCTTCTTCATC 624
              |||||||||||||||
Db        255 AGCAGCTTCTTCATC 241


RESULT 61
US-10-953-349-15128/c
; Sequence 15128, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15128
;   LENGTH: 605
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-15128

  Query Match             1.6%;  Score 15;  DB 6;  Length 605;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        210 AGGAGGCGAGGTTCT 224
              |||||||||||||||
Db        134 AGGAGGCGAGGTTCT 120


RESULT 62
US-10-953-349-1547/c
; Sequence 1547, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1547
;   LENGTH: 621
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-1547

  Query Match             1.6%;  Score 15;  DB 6;  Length 621;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         93 TGAAGAAGATGACAT 107
              |||||||||||||||
Db        148 TGAAGAAGATGACAT 134


RESULT 63
US-10-488-619-1757
; Sequence 1757, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1757
;   LENGTH: 702
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-488-619-1757

  Query Match             1.6%;  Score 15;  DB 6;  Length 702;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        763 CAGGTCCAGGGCAAG 777
              |||||||||||||||
Db         41 CAGGTCCAGGGCAAG 55


RESULT 64
US-11-217-529-78302/c
; Sequence 78302, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
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```
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78302
;   LENGTH: 723
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-78302

  Query Match             1.6%;  Score 15;  DB 7;  Length 723;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        292 CAGAAAGAATCCAAA 306
              |||||||||||||||
Db        515 CAGAAAGAATCCAAA 501


RESULT 65
US-10-953-349-30607
; Sequence 30607, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30607
;   LENGTH: 734
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-10-953-349-30607

  Query Match             1.6%;  Score 15;  DB 6;  Length 734;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        184 GATGCTGGCCAGTAT 198
              |||||||||||||||
Db        328 GATGCTGGCCAGTAT 342


RESULT 66
US-10-488-619-1758/c
; Sequence 1758, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1758
;   LENGTH: 795
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(795)
;   OTHER INFORMATION: n is g, c, a or t
US-10-488-619-1758

  Query Match             1.6%;  Score 15;  DB 6;  Length 795;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        763 CAGGTCCAGGGCAAG 777
              |||||||||||||||
Db        726 CAGGTCCAGGGCAAG 712


RESULT 67
US-10-953-349-3534/c
; Sequence 3534, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3534
;   LENGTH: 798
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-3534

  Query Match             1.6%;  Score 15;  DB 6;  Length 798;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        611 GCAGCTTCTTCATCA 625
              |||||||||||||||
Db        577 GCAGCTTCTTCATCA 563


RESULT 68
US-11-217-529-970
; Sequence 970, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 970
;   LENGTH: 843
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-970

  Query Match             1.6%;  Score 15;  DB 7;  Length 843;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        786 AGAAAAGAAAGACAG 800
              |||||||||||||||
Db        480 AGAAAAGAAAGACAG 494


RESULT 69
US-10-953-349-25
; Sequence 25, Application US/10953349
```

```
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
;   LENGTH: 852
;   TYPE: DNA
;   ORGANISM: Brassica napus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (697)..(697)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (753)..(753)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-25

  Query Match             1.6%;  Score 15;  DB 6;  Length 852;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        248 ACAAAAAGGAAGATG 262
              |||||||||||||||
Db        547 ACAAAAAGGAAGATG 561


RESULT 70
US-10-953-349-39
; Sequence 39, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39
;   LENGTH: 865
;   TYPE: DNA
;   ORGANISM: Brassica napus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (529)..(529)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-39

  Query Match             1.6%;  Score 15;  DB 6;  Length 865;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        404 AAAGCAGCAGAGGCT 418
              |||||||||||||||
Db        678 AAAGCAGCAGAGGCT 692


RESULT 71
US-10-953-349-5007
; Sequence 5007, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5007
;   LENGTH: 880
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-5007

  Query Match             1.6%;  Score 15;  DB 6;  Length 880;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         90 TCCTGAAGAAGATGA 104
              |||||||||||||||
Db        478 TCCTGAAGAAGATGA 492


RESULT 72
US-10-953-349-15440
; Sequence 15440, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15440
;   LENGTH: 922
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-15440

  Query Match             1.6%;  Score 15;  DB 6;  Length 922;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        846 TGCCAAGATCCGCGT 860
              |||||||||||||||
Db        791 TGCCAAGATCCGCGT 805


RESULT 73
US-10-953-349-12006/c
; Sequence 12006, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12006
;   LENGTH: 1021
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (682)..(682)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (691)..(691)
;   OTHER INFORMATION: n is a, c, g, or t
```

```
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (729)..(729)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (761)..(761)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (804)..(804)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-12006

  Query Match             1.6%;  Score 15;  DB 6;  Length 1021;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        411 CAGAGGCTCCTCTGA 425
              |||||||||||||||
Db         74 CAGAGGCTCCTCTGA 60


RESULT 74
US-11-217-529-78549
; Sequence 78549, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78549
;   LENGTH: 1041
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-78549

  Query Match             1.6%;  Score 15;  DB 7;  Length 1041;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        663 ACTGAAGCCATTAAA 677
              |||||||||||||||
Db        376 ACTGAAGCCATTAAA 390


RESULT 75
US-10-953-349-4246/c
; Sequence 4246, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4246
;   LENGTH: 1049
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-4246

  Query Match             1.6%;  Score 15;  DB 6;  Length 1049;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        431 AAGAGGTGACTTGTG 445
              |||||||||||||||
Db        462 AAGAGGTGACTTGTG 448


RESULT 76
US-11-217-529-173436
; Sequence 173436, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 173436
;   LENGTH: 1077
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-173436

  Query Match             1.6%;  Score 15;  DB 7;  Length 1077;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        166 CAAGTCAAAGAATTT 180
              |||||||||||||||
Db        283 CAAGTCAAAGAATTT 297


RESULT 77
US-11-217-529-6206
; Sequence 6206, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6206
;   LENGTH: 1089
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-6206

  Query Match             1.6%;  Score 15;  DB 7;  Length 1089;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
```

```
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        556 CCCATTGAAGTCGTG 570
              |||||||||||||||
Db        478 CCCATTGAAGTCGTG 492


RESULT 78
US-10-953-349-32952/c
; Sequence 32952, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32952
;   LENGTH: 1101
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-32952

  Query Match             1.6%;  Score 15;  DB 6;  Length 1101;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        811 GACAAGACCTCAGCC 825
              |||||||||||||||
Db       1092 GACAAGACCTCAGCC 1078


RESULT 79
US-11-266-446-63/c
; Sequence 63, Application US/11266446
; Publication No. US20060112452A1
; GENERAL INFORMATION:
;  APPLICANT: Keetman, Ulrich
;  APPLICANT:  Duwenig, Elke
;  APPLICANT:  Loyall, Linda P
;  APPLICANT:  Herbers, Karin
;  APPLICANT:  Hillebrand, Helke
;  TITLE OF INVENTION: EXPRESSION CASSETTES FOR SEED-PREFERENTIAL EXPRESSION IN PLANTS
;  FILE REFERENCE: 12810-00165-US
;  CURRENT APPLICATION NUMBER: US/11/266,446
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04026295.8
;  PRIOR FILING DATE: 2004-11-05
;  PRIOR APPLICATION NUMBER: EP 04029024.9
;  PRIOR FILING DATE: 2004-12-08
;  PRIOR APPLICATION NUMBER: EP 05002262.3
;  PRIOR FILING DATE: 2005-02-03
;  PRIOR APPLICATION NUMBER: EP 05002850.5
;  PRIOR FILING DATE: 2005-02-11
;  NUMBER OF SEQ ID NOS: 156
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 63
;   LENGTH: 1102
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (82)..(846)
;   OTHER INFORMATION: coding for reticulon family protein (RTNLB3) (At1g64090)
US-11-266-446-63

  Query Match             1.6%;  Score 15;  DB 7;  Length 1102;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        431 AAGAGGTGACTTGTG 445
              |||||||||||||||
Db        462 AAGAGGTGACTTGTG 448


RESULT 80
US-10-953-349-31251/c
; Sequence 31251, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31251
;   LENGTH: 1122
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-10-953-349-31251

  Query Match             1.6%;  Score 15;  DB 6;  Length 1122;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        239 TCCTGATACACAAAA 253
              |||||||||||||||
Db       1044 TCCTGATACACAAAA 1030


RESULT 81
US-10-953-349-17431
; Sequence 17431, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17431
;   LENGTH: 1129
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-17431

  Query Match             1.6%;  Score 15;  DB 6;  Length 1129;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         89 CTCCTGAAGAAGATG 103
              |||||||||||||||
Db        893 CTCCTGAAGAAGATG 907


RESULT 82
US-10-953-349-19240/c
; Sequence 19240, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
```

```
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19240
;   LENGTH: 1157
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-19240

  Query Match             1.6%;  Score 15;  DB 6;  Length 1157;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        411 CAGAGGCTCCTCTGA 425
              |||||||||||||||
Db         74 CAGAGGCTCCTCTGA 60


RESULT 83
US-10-953-349-19188/c
; Sequence 19188, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19188
;   LENGTH: 1178
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-19188

  Query Match             1.6%;  Score 15;  DB 6;  Length 1178;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        173 AAGAATTTGCAGATG 187
              |||||||||||||||
Db        280 AAGAATTTGCAGATG 266


RESULT 84
US-11-217-529-81713/c
; Sequence 81713, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81713
;   LENGTH: 1194
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-81713

  Query Match             1.6%;  Score 15;  DB 7;  Length 1194;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        306 AAATAAGATCTTTCT 320
              |||||||||||||||
Db        719 AAATAAGATCTTTCT 705


RESULT 85
US-10-953-349-25037/c
; Sequence 25037, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25037
;   LENGTH: 1228
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-25037

  Query Match             1.6%;  Score 15;  DB 6;  Length 1228;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        173 AAGAATTTGCAGATG 187
              |||||||||||||||
Db        399 AAGAATTTGCAGATG 385


RESULT 86
US-10-953-349-37059
; Sequence 37059, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37059
;   LENGTH: 1243
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-37059

  Query Match             1.6%;  Score 15;  DB 6;  Length 1243;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         88 ACTCCTGAAGAAGAT 102
              |||||||||||||||
Db        823 ACTCCTGAAGAAGAT 837


RESULT 87
US-10-953-349-21963/c
; Sequence 21963, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
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;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21963
;   LENGTH: 1244
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-21963

  Query Match             1.6%;  Score 15;  DB 6;  Length 1244;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        724 AGCACCCCACATTCC 738
              |||||||||||||||
Db        362 AGCACCCCACATTCC 348


RESULT 88
US-11-217-529-77875
; Sequence 77875, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77875
;   LENGTH: 1257
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-77875

  Query Match             1.6%;  Score 15;  DB 7;  Length 1257;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        381 TACCGATTTGAAATT 395
              |||||||||||||||
Db       1017 TACCGATTTGAAATT 1031


RESULT 89
US-10-953-349-21887/c
; Sequence 21887, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21887
;   LENGTH: 1259
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-21887

  Query Match             1.6%;  Score 15;  DB 6;  Length 1259;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        145 TCTGGTAAAACTCTG 159
              |||||||||||||||
Db        137 TCTGGTAAAACTCTG 123


RESULT 90
US-10-953-349-28383
; Sequence 28383, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28383
;   LENGTH: 1262
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-10-953-349-28383

  Query Match             1.6%;  Score 15;  DB 6;  Length 1262;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         88 ACTCCTGAAGAAGAT 102
              |||||||||||||||
Db        831 ACTCCTGAAGAAGAT 845


RESULT 91
US-11-217-529-191180/c
; Sequence 191180, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 191180
;   LENGTH: 1290
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-191180

  Query Match             1.6%;  Score 15;  DB 7;  Length 1290;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        740 ACTTCTCCTTAACAT 754
              |||||||||||||||
Db        571 ACTTCTCCTTAACAT 557


RESULT 92
US-10-953-349-5441
; Sequence 5441, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
```

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5441
; LENGTH: 1301
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5441

Query Match 1.6%; Score 15; DB 6; Length 1301;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 683 CTCGGCATGTGGAAG 697
||||||||||||||||
Db 878 CTCGGCATGTGGAAG 892

RESULT 93
US-10-953-349-14176
; Sequence 14176, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14176
; LENGTH: 1343
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (84)..(84)
; OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-14176

Query Match 1.6%; Score 15; DB 6; Length 1343;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 404 AAAGCAGCAGAGGCT 418
|||||||||||||||
Db 652 AAAGCAGCAGAGGCT 666

RESULT 94
US-10-953-349-29639
; Sequence 29639, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29639
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-953-349-29639

Query Match 1.6%; Score 15; DB 6; Length 1344;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 160 ACCATCCAAGTCAAA 174
|||||||||||||||
Db 800 ACCATCCAAGTCAAA 814

RESULT 95
US-10-953-349-34749
; Sequence 34749, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34749
; LENGTH: 1364
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
US-10-953-349-34749

Query Match 1.6%; Score 15; DB 6; Length 1364;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 92 CTGAAGAAGATGACA 106
|||||||||||||||
Db 583 CTGAAGAAGATGACA 597

RESULT 96
US-10-953-349-23846/c
; Sequence 23846, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23846
; LENGTH: 1415
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-23846

Query Match 1.6%; Score 15; DB 6; Length 1415;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 403 AAAAGCAGCAGAGGC 417
|||||||||||||||
Db 1010 AAAAGCAGCAGAGGC 996

RESULT 97
US-11-217-529-2039/c
; Sequence 2039, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA

; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2039
; LENGTH: 1428
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-2039

Query Match 1.6%; Score 15; DB 7; Length 1428;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 287 GGGAACAGAAAGAAT 301
||||||||||||||||
Db 1051 GGGAACAGAAAGAAT 1037

RESULT 98
US-10-953-349-30996/c
; Sequence 30996, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30996
; LENGTH: 1436
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-953-349-30996

Query Match 1.6%; Score 15; DB 6; Length 1436;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 803 TCTCCGTGGACAAGA 817
||||||||||||||||
Db 161 TCTCCGTGGACAAGA 147

RESULT 99
US-10-953-349-289
; Sequence 289, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 289
; LENGTH: 1444
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-289

Query Match 1.6%; Score 15; DB 6; Length 1444;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 94 GAAGAAGATGACATC 108
||||||||||||||||
Db 950 GAAGAAGATGACATC 964

RESULT 100
US-10-505-928-318/c
; Sequence 318, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 318
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-318

Query Match 1.6%; Score 15; DB 6; Length 1452;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 ATGTTGTAGAGTTGG 40
||||||||||||||||
Db 1190 ATGTTGTAGAGTTGG 1176

Search completed: June 9, 2006, 23:43:26
Job time : 23.3095 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 12, 2006, 15:14:42 ; Search time 4162.82 Seconds
(without alignments)
7073.997 Million cell updates/sec

Title: US-10-821-670A-27
Perfect score: 1646
Sequence: 1 IWELEKNVYVVELDWHPDAP.....QARDRYYSSSWSNWASVSCS 307

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/abss/ABSSWEB_spool/US10821670/runat_07062006_110102_26152/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss06h
-USER=US10821670_@CGN_1_1_5308_@runat_07062006_110102_26152 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: gb_pat:*
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4: gb_pl:*
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10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1646	100.0	921	2	AR595948	AR595948 Sequence
c 2	1646	100.0	921	2	AR595949	AR595949 Sequence
3	1646	100.0	1006	14	FCIL12P40	Y07762 Felis catus
4	1646	100.0	1533	2	AR595959	AR595959 Sequence
c 5	1646	100.0	1533	2	AR595960	AR595960 Sequence
6	1646	100.0	1599	2	AR595956	AR595956 Sequence
c 7	1646	100.0	1599	2	AR595957	AR595957 Sequence
8	1639	99.6	921	2	AR242436	AR242436 Sequence
9	1639	99.6	921	2	AR242437	AR242437 Sequence
10	1639	99.6	921	2	AR280204	AR280204 Sequence
11	1639	99.6	921	2	AR280205	AR280205 Sequence
12	1639	99.6	921	2	AR322419	AR322419 Sequence
13	1639	99.6	921	2	AR322420	AR322420 Sequence
14	1639	99.6	987	2	AR595950	AR595950 Sequence
c 15	1639	99.6	987	2	AR595951	AR595951 Sequence
16	1639	99.6	990	2	AX076200	AX076200 Sequence
17	1639	99.6	990	2	AX076482	AX076482 Sequence
18	1639	99.6	2193	2	AR242435	AR242435 Sequence
19	1639	99.6	2193	2	AR280203	AR280203 Sequence
20	1639	99.6	2193	2	AR322418	AR322418 Sequence
21	1639	99.6	4522	2	AX076209	AX076209 Sequence
22	1639	99.6	4522	2	AX076476	AX076476 Sequence
23	1635	99.3	985	2	AR595967	AR595967 Sequence
c 24	1635	99.3	985	2	AR595968	AR595968 Sequence
25	1634	99.3	990	14	FCU83184	U83184 Felis catus
26	1547	94.0	1015	14	CFU49100	U49100 Canis famil
27	1546	93.9	921	2	AR595965	AR595965 Sequence
c 28	1546	93.9	921	2	AR595966	AR595966 Sequence
29	1546	93.9	987	2	AR595969	AR595969 Sequence
c 30	1546	93.9	987	2	AR595970	AR595970 Sequence
31	1546	93.9	990	2	AR151071	AR151071 Sequence
32	1546	93.9	990	2	BD014663	BD014663 Process f
33	1546	93.9	990	2	E15017	E15017 Canine mRNA
34	1546	93.9	990	2	AR316470	AR316470 Sequence
35	1546	93.9	1533	2	AR595973	AR595973 Sequence
c 36	1546	93.9	1533	2	AR595974	AR595974 Sequence
37	1546	93.9	1599	2	AR595971	AR595971 Sequence
c 38	1546	93.9	1599	2	AR595972	AR595972 Sequence
39	1546	93.9	2267	2	AR596011	AR596011 Sequence
c 40	1546	93.9	2267	2	AR596012	AR596012 Sequence
41	1537	93.4	990	2	BD014653	BD014653 Process f
42	1533	93.1	990	2	AR151061	AR151061 Sequence
43	1533	93.1	990	2	AR316460	AR316460 Sequence
44	1511.5	91.8	924	2	BD171282	BD171282 Novel can
45	1511.5	91.8	2154	2	BD171281	BD171281 Novel can

ALIGNMENTS

RESULT 1
AR595948
LOCUS AR595948 921 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 26 from patent US 6818444.
ACCESSION AR595948
VERSION AR595948.1 GI:56646929
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 921)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 26 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .921
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.: 1.14e-174 Length: 921
Score: 1646.00 Matches: 307
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0

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DB:                    2             Gaps:          0

US-10-821-670A-27 (1-307) x AR595948 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
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Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
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Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
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Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
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Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
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Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
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Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
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Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
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Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
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Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
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Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
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Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
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Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
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Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
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Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
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Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
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RESULT 2
AR595949/c
LOCUS       AR595949                921 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 28 from patent US 6818444.
ACCESSION   AR595949
VERSION     AR595949.1  GI:56646930
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 28 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .921
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ORIGIN

Alignment Scores:
Pred. No.:                1.14e-174      Length:          921
Score:                    1646.00        Matches:         307
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-27 (1-307) x AR595949 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
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Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
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Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
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Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
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Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
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Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
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Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
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Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
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Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
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Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
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Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
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Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
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Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
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Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
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Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        301 TrpAlaSerValSerCysSer 307
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Db         21 TGGGCATCCGTGTCCTGCAGT 1
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RESULT 3
FCIL12P40
LOCUS FCIL12P40 1006 bp mRNA linear MAM 18-APR-2005
DEFINITION Felis catus mRNA for interleukin-12 p40 chain.
ACCESSION Y07762
VERSION Y07762.1 GI:2102664
KEYWORDS interleukin-12 p40.
SOURCE Felis catus (cat)
ORGANISM Felis catus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae; Felinae; Felis.
REFERENCE 1
AUTHORS Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
TITLE Molecular cloning of cat interleukin-12
JOURNAL Immunogenetics 45 (6), 462-463 (1997)
PUBMED 9089110
REFERENCE 2 (bases 1 to 1006)
AUTHORS Schijns,V.E.C.J.
TITLE Direct Submission
JOURNAL Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division, Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL Utrecht, NETHERLANDS
FEATURES Location/Qualifiers
source 1. .1006
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/mol_type="mRNA"
/db_xref="taxon:9685"
/cell_type="lymphocyte"
/tissue_type="peripheral blood"
gene 1. .1006
/gene="IL-12.p40"
CDS 1. .990
/gene="IL-12.p40"
/note="heterodimer with IL-12 p35 chain"
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ORIGIN

Alignment Scores:
Pred. No.: 1.29e-174 Length: 1006

Score: 1646.00 Matches: 307
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 14 Gaps: 0

US-10-821-670A-27 (1-307) x FCIL12P40 (1-1006)

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Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
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Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
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Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
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Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
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Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
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Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
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Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
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Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
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Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
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Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
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Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
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Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
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Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
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Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
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Qy        301 TrpAlaSerValSerCysSer 307
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RESULT 4

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AR595959
LOCUS       AR595959               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 43 from patent US 6818444.
ACCESSION   AR595959
VERSION     AR595959.1  GI:56646940
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 43 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:                2.35e-174      Length:          1533
Score:                    1646.00        Matches:         307
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-27 (1-307) x AR595959 (1-1533)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
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Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
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Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
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Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
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Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
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Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
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Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
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Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
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Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 5
AR595960/c
LOCUS       AR595960               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 45 from patent US 6818444.
ACCESSION   AR595960
VERSION     AR595960.1  GI:56646941
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 45 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                2.35e-174      Length:          1533
Score:                    1646.00        Matches:         307
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-27 (1-307) x AR595960 (1-1533)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        301 TrpAlaSerValSerCysSer 307
                |||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613

RESULT 6
AR595956
LOCUS       AR595956                1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 38 from patent US 6818444.
ACCESSION   AR595956
VERSION     AR595956.1  GI:56646937
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 38 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.49e-174       Length:         1599
Score:                  1646.00         Matches:        307
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-27 (1-307) x AR595956 (1-1599)
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Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        301 TrpAlaSerValSerCysSer 307
                |||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987

RESULT 7
AR595957/c
LOCUS       AR595957                1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 40 from patent US 6818444.
ACCESSION   AR595957
VERSION     AR595957.1  GI:56646938
KEYWORDS    .
SOURCE      Unknown.
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  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 40 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.49e-174      Length:         1599
Score:                  1646.00        Matches:        307
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-27 (1-307) x AR595957 (1-1599)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613

RESULT 8
AR242436
LOCUS       AR242436                 921 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 6 from patent US 6472509.
ACCESSION   AR242436
VERSION     AR242436.1  GI:27288853
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 6 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              6.99e-174      Length:         921
Score:                  1639.00        Matches:        306
Percent Similarity:     99.7%          Conservative:   0
Best Local Similarity:  99.7%          Mismatches:     1
Query Match:            99.6%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-27 (1-307) x AR242436 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 9
AR242437
LOCUS       AR242437                 921 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 7 from patent US 6472509.
ACCESSION   AR242437
VERSION     AR242437.1  GI:27288854
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 7 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              6.99e-174      Length:         921
Score:                  1639.00        Matches:        306
Percent Similarity:     99.7%          Conservative:   0
Best Local Similarity:  99.7%          Mismatches:     1
Query Match:            99.6%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-27 (1-307) x AR242437 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 10
AR280204
LOCUS       AR280204                 921 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 6 from patent US 6518045.
ACCESSION   AR280204
VERSION     AR280204.1  GI:29715594
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
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  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 6 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              6.99e-174       Length:         921
Score:                  1639.00         Matches:        306
Percent Similarity:     99.7%           Conservative:   0
Best Local Similarity:  99.7%           Mismatches:     1
Query Match:            99.6%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-27 (1-307) x AR280204 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 11
AR280205
LOCUS       AR280205                921 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 7 from patent US 6518045.
ACCESSION   AR280205
VERSION     AR280205.1  GI:29715595
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 7 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              6.99e-174       Length:         921
Score:                  1639.00         Matches:        306
Percent Similarity:     99.7%           Conservative:   0
Best Local Similarity:  99.7%           Mismatches:     1
Query Match:            99.6%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-27 (1-307) x AR280205 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420
```

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Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 12
AR322419
LOCUS       AR322419                 921 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 6 from patent US 6566097.
ACCESSION   AR322419
VERSION     AR322419.1  GI:33708172
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 6 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:                6.99e-174      Length:          921
Score:                    1639.00        Matches:         306
Percent Similarity:       99.7%          Conservative:    0
Best Local Similarity:    99.7%          Mismatches:      1
Query Match:              99.6%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-27 (1-307) x AR322419 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 13
AR322420
LOCUS       AR322420                 921 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 7 from patent US 6566097.
ACCESSION   AR322420
VERSION     AR322420.1  GI:33708173
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
```

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  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 7 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:                6.99e-174      Length:          921
Score:                    1639.00        Matches:         306
Percent Similarity:       99.7%          Conservative:    0
Best Local Similarity:    99.7%          Mismatches:      1
Query Match:              99.6%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-27 (1-307) x AR322420 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 14
AR595950
LOCUS       AR595950                 987 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 29 from patent US 6818444.
ACCESSION   AR595950
VERSION     AR595950.1  GI:56646931
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 29 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                7.7e-174       Length:          987
Score:                    1639.00        Matches:         306
Percent Similarity:       99.7%          Conservative:    0
Best Local Similarity:    99.7%          Mismatches:      1
Query Match:              99.6%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-27 (1-307) x AR595950 (1-987)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
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Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987

RESULT 15
AR595951/c
LOCUS       AR595951                 987 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 31 from patent US 6818444.
ACCESSION   AR595951
VERSION     AR595951.1  GI:56646932
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 31 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              7.7e-174        Length:         987
Score:                  1639.00         Matches:        306
Percent Similarity:     99.7%           Conservative:   0
Best Local Similarity:  99.7%           Mismatches:     1
Query Match:            99.6%           Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-27 (1-307) x AR595951 (1-987)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCAGT 1


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Job time : 4168.82 secs
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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 9, 2006, 23:43:41 ; Search time 655.34 Seconds
(without alignments)
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Title: US-10-821-670A-27
Perfect score: 1646
Sequence: 1 IWELEKNVYVVELDWHPDAP.....QARDRYYSSSWSNWASVSCS 307

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1646	100.0	921	6	ABK98942	Abk98942 Feline in
c 2	1646	100.0	921	6	ABK98943	Abk98943 Feline in
c 3	1646	100.0	921	14	ADV34681	Adv34681 Feline si
4	1646	100.0	921	14	ADV34679	Adv34679 Feline si
c 5	1646	100.0	1533	6	ABK98954	Abk98954 Feline in
6	1646	100.0	1533	6	ABK98953	Abk98953 Feline in
c 7	1646	100.0	1533	14	ADV34697	Adv34697 Feline si
8	1646	100.0	1533	14	ADV34695	Adv34695 Feline si
9	1646	100.0	1599	6	ABK98950	Abk98950 Feline in
c 10	1646	100.0	1599	6	ABK98951	Abk98951 Feline in
11	1646	100.0	1599	14	ADV34691	Adv34691 Feline si
c 12	1646	100.0	1599	14	ADV34693	Adv34693 Feline si
13	1639	99.6	921	2	AAV56627	Aav56627 Feline FL
14	1639	99.6	921	2	AAV56626	Aav56626 Feline FL
15	1639	99.6	987	6	ABK98944	Abk98944 Feline in
c 16	1639	99.6	987	6	ABK98945	Abk98945 Feline in
17	1639	99.6	987	14	ADV34682	Adv34682 Feline si
c 18	1639	99.6	987	14	ADV34684	Adv34684 Feline si
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20	1639	99.6	990	4	AAF26085	Aaf26085 Feline IL
21	1639	99.6	2193	2	AAV56625	Aav56625 Feline FL
22	1639	99.6	4522	4	AAF26076	Aaf26076 Feline IL
23	1639	99.6	4522	4	AAF26094	Aaf26094 Plasmid p
c 24	1635	99.3	985	6	ABK98962	Abk98962 Feline in
25	1635	99.3	985	6	ABK98961	Abk98961 Feline in
26	1635	99.3	985	14	ADV34707	Adv34707 Feline N-
c 27	1635	99.3	985	14	ADV34709	Adv34709 Feline N-
28	1547	94.0	1015	13	ADT04849	Adt04849 Canine in
29	1546	93.9	921	6	ABK98959	Abk98959 Canine in
c 30	1546	93.9	921	6	ABK98960	Abk98960 Canine in
c 31	1546	93.9	921	14	ADV34706	Adv34706 Canine si
32	1546	93.9	921	14	ADV34704	Adv34704 Canine si
33	1546	93.9	987	6	ABK98963	Abk98963 Canine in
c 34	1546	93.9	987	6	ABK98964	Abk98964 Canine in
c 35	1546	93.9	987	14	ADV34712	Adv34712 Canine si
36	1546	93.9	987	14	ADV34710	Adv34710 Canine si
37	1546	93.9	990	2	AAV13817	Aav13817 Canine IL
38	1546	93.9	990	2	AAX03162	Aax03162 Nucleic a
39	1546	93.9	990	2	AAX35625	Aax35625 Nucleic a
40	1546	93.9	990	4	AAI64388	Aai64388 Canine co
41	1546	93.9	1533	6	ABK98967	Abk98967 Canine in
c 42	1546	93.9	1533	6	ABK98968	Abk98968 Canine in
c 43	1546	93.9	1533	14	ADV34718	Adv34718 Canine si
44	1546	93.9	1533	14	ADV34716	Adv34716 Canine si
45	1546	93.9	1599	6	ABK98965	Abk98965 Canine in

ALIGNMENTS

RESULT 1
ABK98942
ID ABK98942 standard; cDNA; 921 BP.
XX
AC ABK98942;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p40-921 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX

PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69302.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 1; Page 49-50; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 921 BP; 277 A; 227 C; 230 G; 187 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	3.89e-156	Length:	921
Score:	1646.00	Matches:	307
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-27 (1-307) x ABK98942 (1-921)

```
Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921
```

RESULT 2
ABK98943/c
ID ABK98943 standard; cDNA; 921 BP.
XX
AC ABK98943;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p40-921 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Disclosure; Page 51; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of

```
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 921 BP; 187 A; 230 C; 227 G; 277 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              3.89e-156       Length:         921
Score:                  1646.00         Matches:        307
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-27 (1-307) x ABK98943 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCAGT 1

RESULT 3
ADV34681/c
ID   ADV34681 standard; DNA; 921 BP.
XX
AC   ADV34681;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain mature IL-12p40 complementary DNA, nFeIL-12p40 921.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 28; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain mature IL-12p40 subunit
CC   complementary DNA.
XX
SQ   Sequence 921 BP; 187 A; 230 C; 227 G; 277 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              3.89e-156       Length:         921
Score:                  1646.00         Matches:        307
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-27 (1-307) x ADV34681 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCAGT 1
```

```
RESULT 4
ADV34679
ID   ADV34679 standard; cDNA; 921 BP.
XX
AC   ADV34679;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain mature IL-12p40 protein cDNA, nFeIL-12p40 921.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
```

```
FH   Key             Location/Qualifiers
FT   CDS             1. .921
FT                   /*tag=  a
FT                   /product= "PFeIL-12p40 307 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34680.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 23; SEQ ID NO 26; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain mature IL-12p40 subunit
CC   protein encoding cDNA.
XX
SQ   Sequence 921 BP; 277 A; 227 C; 230 G; 187 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.:              3.89e-156       Length:         921
Score:                  1646.00         Matches:        307
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-27 (1-307) x ADV34679 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921
```

```
RESULT 5
ABK98954/c
ID   ABK98954 standard; cDNA; 1533 BP.
XX
AC   ABK98954;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1533 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 66-67; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;
```

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Alignment Scores:
Pred. No.:              7.69e-156      Length:          1533
Score:                  1646.00        Matches:         307
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            100.0%         Indels:          0
DB:                     6              Gaps:            0

US-10-821-670A-27 (1-307) x ABK98954 (1-1533)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        301 TrpAlaSerValSerCysSer 307
                |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613
```

RESULT 6
ABK98953
ID ABK98953 standard; cDNA; 1533 BP.
XX
AC ABK98953;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12-1533 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69307.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 63-64; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	7.69e-156	Length:	1533
Score:	1646.00	Matches:	307
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-27 (1-307) x ABK98953 (1-1533)

```
Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900
```

```
Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 7
ADV34697/c
ID   ADV34697 standard; DNA; 1533 BP.
XX
AC   ADV34697;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 complementary DNA, nFeIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 45; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 complementary DNA.
XX
SQ   Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              7.69e-156      Length:          1533
Score:                  1646.00        Matches:         307
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            100.0%         Indels:          0
DB:                     14             Gaps:            0

US-10-821-670A-27 (1-307) x ADV34697 (1-1533)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613

RESULT 8
ADV34695
ID   ADV34695 standard; cDNA; 1533 BP.
XX
AC   ADV34695;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1533
FT                   /*tag=  a
FT                   /product= "PFeIL-12 511 protein"
FT                   /partial
```

```
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34696.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 43; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              7.69e-156      Length:          1533
Score:                  1646.00        Matches:         307
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            100.0%         Indels:          0
DB:                     14             Gaps:            0

US-10-821-670A-27 (1-307) x ADV34695 (1-1533)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 9
ABK98950
ID   ABK98950 standard; cDNA; 1599 BP.
XX
AC   ABK98950;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1599 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69306.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
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PS   Claim 6; Page 58-60; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              8.13e-156      Length:          1599
Score:                  1646.00        Matches:         307
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            100.0%         Indels:          0
DB:                     6              Gaps:            0

US-10-821-670A-27 (1-307) x ABK98950 (1-1599)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987

RESULT 10
ABK98951/c
ID   ABK98951 standard; cDNA; 1599 BP.
XX
AC   ABK98951;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1599 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 61-62; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              8.13e-156      Length:          1599
```

```
Score:                 1646.00       Matches:       307
Percent Similarity:    100.0%        Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:           100.0%        Indels:        0
DB:                    6             Gaps:          0

US-10-821-670A-27 (1-307) x ABK98951 (1-1599)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613
```

RESULT 11

```
ADV34691
ID   ADV34691 standard; cDNA; 1599 BP.
XX
AC   ADV34691;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1599
FT                   /*tag=  a
FT                   /product= "PFeIL-12p533 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34692.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 38; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:             8.13e-156     Length:        1599
Score:                 1646.00       Matches:       307
Percent Similarity:    100.0%        Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:           100.0%        Indels:        0
DB:                    14            Gaps:          0

US-10-821-670A-27 (1-307) x ADV34691 (1-1599)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
```

```
                                                                                                                    
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
                                                                                                                    
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
                                                                                                                    
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
                                                                                                                    
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
                                                                                                                    
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
                                                                                                                    
Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
                                                                                                                    
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
                                                                                                                    
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
                                                                                                                    
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
                                                                                                                    
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
                                                                                                                    
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
                                                                                                                    
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
                                                                                                                    
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        301 TrpAlaSerValSerCysSer 307
                                                                                                                    
Db        967 TGGGCATCCGTGTCCTGCAGT 987

RESULT 12
ADV34693/c
ID   ADV34693 standard; DNA; 1599 BP.
XX
AC   ADV34693;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 complementary DNA, nFeIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 40; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 complementary DNA.
XX
SQ   Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                8.13e-156       Length:          1599
Score:                    1646.00         Matches:         307
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              100.0%          Indels:          0
DB:                       14              Gaps:            0

US-10-821-670A-27 (1-307) x ADV34693 (1-1599)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
                                                                                                                    
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
                                                                                                                    
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
                                                                                                                    
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
                                                                                                                    
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
                                                                                                                    
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
                                                                                                                    
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
                                                                                                                    
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
                                                                                                                    
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
                                                                                                                    
```

```
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613

RESULT 13
AAV56627
ID   AAV56627 standard; cDNA; 921 BP.
XX
AC   AAV56627;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp40 cDNA mature transcript #2.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP001824.
XX
PR   04-JUN-1996;   96JP-00165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76174.
XX
PT   Novel feline cytokine protein - useful for treating feline auto:immune
PT   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS   Claim 21; Page 56-57; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine mature protein, FLAFp40.
CC   This protein can be used in the production of a FLAFp35/FLAFp40
CC   heterodimer which can potentiate the cytotoxic activity of feline
CC   cytotoxic T lymphocyte cells. Such proteins are used for treatment of
CC   feline autoimmune diseases e.g. as caused by feline herpes virus or
CC   feline calcivirus
XX
SQ   Sequence 921 BP; 276 A; 228 C; 230 G; 187 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.98e-155      Length:          921
Score:                    1639.00        Matches:         306
Percent Similarity:       99.7%          Conservative:    0
Best Local Similarity:    99.7%          Mismatches:      1
Query Match:              99.6%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-27 (1-307) x AAV56627 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
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Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 14
AAV56626
ID   AAV56626 standard; cDNA; 921 BP.
XX
AC   AAV56626;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp40 cDNA mature transcript #1.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP001824.
XX
PR   04-JUN-1996;   96JP-00165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76174.
XX
PT   Novel feline cytokine protein - useful for treating feline auto:immune
PT   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS   Claim 20; Page 55; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine mature protein, FLAFp40.
CC   This protein can be used in the production of a FLAFp35/FLAFp40
CC   heterodimer which can potentiate the cytotoxic activity of feline
CC   cytotoxic T lymphocyte cells. Such proteins are used for treatment of
CC   feline autoimmune diseases e.g. as caused by feline herpes virus or
CC   feline calcivirus
XX
SQ   Sequence 921 BP; 276 A; 227 C; 231 G; 187 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.98e-155      Length:         921
Score:                  1639.00        Matches:        306
Percent Similarity:     99.7%          Conservative:   0
Best Local Similarity:  99.7%          Mismatches:     1
Query Match:            99.6%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-27 (1-307) x AAV56626 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 15
ABK98944
ID   ABK98944 standard; cDNA; 987 BP.
XX
AC   ABK98944;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p40-987 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
```

XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69303.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 1; Page 51-53; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 987 BP; 283 A; 250 C; 246 G; 208 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.17e-155	Length:	987
Score:	1639.00	Matches:	306
Percent Similarity:	99.7%	Conservative:	0
Best Local Similarity:	99.7%	Mismatches:	1
Query Match:	99.6%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-27 (1-307) x ABK98944 (1-987)

```
Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987
```

Search completed: June 10, 2006, 01:17:56
Job time : 661.34 secs

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 10, 2006, 00:20:47 ; Search time 3762.81 Seconds
(without alignments)
6843.525 Million cell updates/sec

Title: US-10-821-670A-27
Perfect score: 1646
Sequence: 1 IWELEKNVYVVELDWHPDAP.....QARDRYYSSSWSNWASVSCS 307

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10821670/runat_07062006_110104_26172/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
-USER=US10821670_@CGN_1_1_27300_@runat_07062006_110104_26172 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1100.5	66.9	1839	6	AK162981	AK162981 Mus muscu
	2	1087.5	66.1	2908	6	AK155593	AK155593 Mus muscu
	3	1028.5	62.5	735	5	CD559605	CD559605 AGENCOURT
	4	1028.5	62.5	756	5	CK130264	CK130264 AGENCOURT
	5	1015.5	61.7	747	5	CD559607	CD559607 AGENCOURT
	6	1001	60.8	772	5	CD559604	CD559604 AGENCOURT
c	7	957	58.1	785	5	CD559448	CD559448 AGENCOURT
c	8	955.5	58.0	736	5	CD559453	CD559453 AGENCOURT
c	9	952.5	57.9	772	5	CD559450	CD559450 AGENCOURT
c	10	947.5	57.6	762	5	CD559451	CD559451 AGENCOURT
	11	898.5	54.6	745	5	CD559602	CD559602 AGENCOURT
c	12	898.5	54.6	766	5	CD559449	CD559449 AGENCOURT
c	13	890.5	54.1	754	5	CD559452	CD559452 AGENCOURT
c	14	816	49.6	725	5	CD559454	CD559454 AGENCOURT
	15	700	42.5	724	5	CD559603	CD559603 AGENCOURT
	16	693.5	42.1	1042	5	CD559606	CD559606 AGENCOURT
	17	683.5	41.5	649	5	CJ134671	CJ134671 CJ134671
	18	519.5	31.6	475	7	BF704417	BF704417 MI-P-E6-a
	19	431.5	26.2	417	8	CO949904	CO949904 UMC-pd12c
	20	386	23.5	387	4	BY167742	BY167742 BY167742
	21	378	23.0	535	11	AZ441303	AZ441303 1M0232M24
	22	377	22.9	432	4	BY154173	BY154173 BY154173
	23	357	21.7	700	12	CE093997	CE093997 tigr-gss-
	24	353	21.4	423	4	BY218447	BY218447 BY218447
c	25	351	21.3	569	11	AZ853726	AZ853726 2M0157M01
	26	338.5	20.6	252	10	DV799576	DV799576 est_t_tru
	27	337	20.5	375	4	BY222535	BY222535 BY222535
	28	331	20.1	346	4	BY164658	BY164658 BY164658
	29	319	19.4	355	4	BY221814	BY221814 BY221814
c	30	223.5	13.6	812	10	DT349218	DT349218 JGI_CAAX1
	31	202	12.3	666	4	BY749553	BY749553 BY749553
	32	191.5	11.6	755	10	DV591060	DV591060 AGENCOURT
	33	190.5	11.6	748	10	DV593962	DV593962 AGENCOURT
	34	185	11.2	1277	14	DQ037702	DQ037702 Homo sapi
	35	184	11.2	1277	14	DQ037703	DQ037703 Pan trogl
	36	183	11.1	2548	6	AK046337	AK046337 Mus muscu
	37	181	11.0	705	8	CX261472	CX261472 1314997 N
	38	181	11.0	2373	6	AK141197	AK141197 Mus muscu
	39	180	10.9	850	3	BU291084	BU291084 603603708
	40	178	10.8	1118	14	AY403646	AY403646 Mus muscu
	41	178	10.8	1881	6	AK137026	AK137026 Mus muscu
c	42	177	10.8	665	4	CA062264	CA062264 ssalrgb52
c	43	177	10.8	689	10	DW558518	DW558518 EST_ssal_
	44	176	10.7	1008	4	BX364435	BX364435 BX364435
	45	176	10.7	1118	14	AY403644	AY403644 Homo sapi

ALIGNMENTS

RESULT 1
AK162981
LOCUS AK162981 1839 bp mRNA linear HTC 21-SEP-2005
DEFINITION Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430014H12 product:interleukin 12b, full insert sequence.
ACCESSION AK162981
VERSION AK162981.1 GI:74188061
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,

Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

PUBMED 11076861

REFERENCE 4

AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

CONSRTM RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409 (6821), 685-690 (2001)

PUBMED 11217851

REFERENCE 5

AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420 (6915), 563-573 (2002)

PUBMED 12466851

REFERENCE 6

AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE The transcriptional landscape of the mammalian genome

JOURNAL Science 309 (5740), 1559-1563 (2005)

PUBMED 16141072

REFERENCE 7

AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.

CONSRTM RIKEN Genome Exploration Research Group

TITLE Antisense transcription in the mammalian transcriptome

JOURNAL Science 309 (5740), 1564-1566 (2005)

PUBMED 16141073

REFERENCE 8 (bases 1 to 1839)

AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

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                     /mol_type="mRNA"
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     CDS             58. .1065
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ORIGIN

Alignment Scores:
Pred. No.:              3.52e-112       Length:         1839
Score:                  1100.50         Matches:        211
Percent Similarity:     77.7%           Conservative:   33
Best Local Similarity:  67.2%           Mismatches:     57
Query Match:            66.9%           Indels:         13
DB:                     6               Gaps:           4

US-10-821-670A-27 (1-307) x AK162981 (1-1839)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
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Db        124 ATGTGGGAGCTGGAGAAAGACGTTTATGTTGTAGAGGTGGACTGGACTCCCGATGCCCCT 183

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
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Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||         |||:::|||||||||||||||||||||||||   ||||||||||||
Db        244 GACCAGAGACATGGAGTCATAGGCTCTGGAAAGACCCTGACCATCACTGTCAAAGAGTTT 303

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||   ||||||||||||   |||
Db        304 CTAGATGCTGGCCAGTACACCTGCCACAAAGGAGGCGAGACTCTGAGCCACTCACATCTG 363

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              |||:::|||||||||||:::|||||||||||||||:::||||||         |||
Db        364 CTGCTCCACAAGAAGGAAAATGGAATTTGGTCCACTGAAATTTTA---------AAAAAT 414

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
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Db        415 TTCAAAAACAAGACTTTCCTGAAGTGTGAAGCACCAAATTACTCCGGACGGTTCACGTGC 474

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
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Db        475 TCATGGCTGGTGCAAAGAAACATGGACTTGAAGTTCAACATCAAGAGCAGTAGCAGTTCC 534

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
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Db        535 CCTGACTCTCGGGCAGTGACATGTGGAATGGCGTCTCTGTCTGCAGAGAAGGTCACACTG 594

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              |||   |||||||||:::||||||:::|||   |||||||||         ||||||
Db        595 GACCAAAGGGACTATGAGAAGTATTCAGTGTCCTGCCAGGAGGATGTCACCTGCCCAACT 654

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              |||||||||:::||||||||||||:::   ::::::|||       :::   |||||||||
Db        655 GCCGAGGAGACCCTGCCCATTGAACTGGCGTTGGAAGCACGGCAGCAGAATAAATATGAG 714

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
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Db        715 AACTACAGCACCAGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTTG 774

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
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Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              |||||||||||||||||||||||||||||   |||   |||::::::|||   |||
Db        832 TGGAGCACTCCCCATTCCTACTTCTCCCTCAAGTTCTTTGTTCGAATCCAGCGCAAGAAA 891

Qy        261 AsnArgGluLys----------------------LysAspArgLeuSerValAspLys 272
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Db        892 GAAAAGATGAAGGAGACAGAGGAGGGGTGTAACCAGAAAGGTGCGTTCCTCGTAGAGAAG 951

Qy        273 ThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaArgAspArg 292
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Qy        293 TyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 306
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RESULT 2
AK155593
LOCUS       AK155593               2908 bp    mRNA    linear   HTC 21-SEP-2005
DEFINITION  Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN
            full-length enriched library, clone:F730005O03 product:interleukin
            12b, full insert sequence.
ACCESSION   AK155593
VERSION     AK155593.1  GI:74212721
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
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Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

CONSRTM RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409 (6821), 685-690 (2001)

PUBMED 11217851

REFERENCE 5

AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420 (6915), 563-573 (2002)

PUBMED 12466851

REFERENCE 6

AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE The transcriptional landscape of the mammalian genome

JOURNAL Science 309 (5740), 1559-1563 (2005)

PUBMED 16141072

REFERENCE 7

AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.

CONSRTM RIKEN Genome Exploration Research Group

TITLE Antisense transcription in the mammalian transcriptome

JOURNAL Science 309 (5740), 1564-1566 (2005)

PUBMED 16141073

REFERENCE 8 (bases 1 to 2908)

AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

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/db_xref="taxon:10090"
/clone="F730005O03"
/cell_type="B6-derived CD11 +ve dendritic cells"
/clone_lib="RIKEN full-length enriched mouse cDNA library"

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ORIGIN

Alignment Scores:
Pred. No.:              2e-110          Length:         2908
Score:                  1087.50         Matches:        211
Percent Similarity:     77.5%           Conservative:   33
Best Local Similarity:  67.0%           Mismatches:     57
Query Match:            66.1%           Indels:         14
DB:                     6               Gaps:           4

US-10-821-670A-27 (1-307) x AK155593 (1-2908)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
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Db        527 ATGTGGGAGCTGGAGAAAGACGTTTATGTTGTAGAGGTGGACTGGACTCCCGATGCCCCT 586

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
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Db        587 GGAGAAACAGTGAACCTCACCTGTGACACGCCTGAAGAAGATGACATCACCTGGACCTCA 646

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
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Db        647 GACCAGAGACATGGAGTCATAGGCTCTGGAAAGACCCTGACCATCACTGTCAAAGAGTTT 706

Qy         61 AlaAspAlaGlyGln-TyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLe 80
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Qy         80 uLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGl 100
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Qy        100 uSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCy 120
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Db        818 TTTCAAAAACAAGACTTTCCTGAAGTGTGAAGCACCAAATTACTCCGGACGGTTCACGTG 877

Qy        120 sTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySe 140
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Qy        160 lAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAl 180
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Qy        180 aAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGl 200
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Db       1058 TGCCGAGGAGACCCTGCCCATTGAACTGGCGTTGGAAGCACGGCAGCAGAATAAATATGA 1117

Qy        200 uAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLe 220
              ||||||:::::||||||||||||||||||||||||||||||||||||||||||||||||
Db       1118 GAACTACAGCACCAGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAGAACTT 1177

Qy        220 uGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspTh 240
              ||||:::|||||||||||||||:::   |||||||||||||||||||||||||||::
Db       1178 GCAGATGAAGCCTTTGAAGAACTCACAG---GTGGAGGTCAGCTGGGAGTACCCTGACTC 1234

Qy        240 rTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAs 260
              :|||||||||||||||||||||||||||   |||   |||::::::|||   |||
Db       1235 CTGGAGCACTCCCCATTCCTACTTCTCCCTCAAGTTCTTTGTTCGAATCCAGCGCAAGAA 1294

Qy        260 nAsnArgGluLys----------------------LysAspArgLeuSerValAspLy 272
                 :::   |||                        |||          |||:::||
Db       1295 AGAAAAGATGAAGGAGACAGAGGAGGGGGTGTAACCAGAAAGGTGCGTTCCTCGTAGAGAA 1354

Qy        272 sThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaArgAspAr 292
              |||||||   :::|||   |||   |||         :::   |||||||||:::||||||
Db       1355 GACATCTACCGAAGTCCAATGC---AAAGGCGGGAATGTCTGCGTGCAAGCTCAGGATCG 1411

Qy        292 gTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 306
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              |||||||:::||||||   |||   ||||||   |||   |||
Db       1412 CTATTACAATTCCTCATGCAGCAAGTGGGCATGTGTTCCCTGC 1454

RESULT 3
CD559605
LOCUS       CD559605                735 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496534 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971870 5', mRNA sequence.
ACCESSION   CD559605
VERSION     CD559605.2  GI:38558937
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 735)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585673.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 01
            High quality sequence stop: 709.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971870"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              1.16e-104       Length:         735
Score:                  1028.50         Matches:        190
Percent Similarity:     94.5%           Conservative:   16
Best Local Similarity:  87.2%           Mismatches:     11
Query Match:            62.5%           Indels:         1
DB:                     5               Gaps:           1

US-10-821-670A-27 (1-307) x CD559605 (1-735)
```

```
Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||:::|||:::|||||||||||||||||||||||:::||||||||||||
Db         83 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 142

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||:::|||||||||||||||   ||||||||||||
Db        143 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 202

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 262

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
                 ||||||||||||||||||||||||||||||||||||||||||||||||||    |||
Db        263 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 322

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              |||:::|||||||||||||||||||||||||||||||||||||||||||:::::|||||||||
Db        323 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 382

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
                 |||||||||   ||||||:::|||||||||||||||||||||||||||||||||||
Db        383 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 442

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||   ||||||||||||||   |||:::||||||||||||||||||||
Db        443 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAGAGCAGCAGAGGCTCT 502

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||   ||||||||||||||||||||||||||||||:::||||||
Db        503 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 562

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||::::::|||   :::|||:::||||||||||||||   ||||||||||||||||
Db        563 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 619

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||:::||||||||||:::||||||||||||||||||||
Db        620 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAA 679

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 218
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        680 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 733

RESULT 4
CK130264
LOCUS       CK130264                 756 bp    mRNA    linear   EST 02-DEC-2003
DEFINITION  AGENCOURT_14496566 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971871 5', mRNA sequence.
ACCESSION   CK130264
VERSION     CK130264.1  GI:38622200
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 756)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 02
            High quality sequence start: 5
            High quality sequence stop: 731.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971871"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:                1.21e-104      Length:          756
Score:                    1028.50        Matches:         190
Percent Similarity:       94.1%          Conservative:    16
Best Local Similarity:    86.8%          Mismatches:      12
Query Match:              62.5%          Indels:          1
DB:                       5              Gaps:            1

US-10-821-670A-27 (1-307) x CK130264 (1-756)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||:::|||:::|||||||||||||||||||||||:::||||||||||||
Db        100 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 159

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||:::|||||||||||||||   ||||||||||||
Db        160 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 219

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 279

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
                 ||||||||||||||||||||||||||||||||||||||||||||||||||    |||
Db        280 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 339

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              |||:::|||||||||||||||||||||||||||||||||||||||||||:::::|||||||||
Db        340 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 399

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
                 |||||||||   ||||||:::|||||||||||||||||||||||||||||||||||
Db        400 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 459

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||   ||||||||||||||   |||:::||||||||||||||||||||
Db        460 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 519

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||   ||||||||||||||||||||||||||||||:::||||||
Db        520 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 579
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Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||::::::|||   :::|||:::|||||||||||||||   ||||||||||||||||
Db        580 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 636

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              |||||||||||||||||||||||||:::|||||||||:::|||||||||||||||||||
Db        637 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAA 696

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsn 219
              |||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        697 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCNAACCTGACCCACCCAAGAAC 753

RESULT 5
CD559607
LOCUS       CD559607                747 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14497061 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971868 5', mRNA sequence.
ACCESSION   CD559607
VERSION     CD559607.2  GI:38558941
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 747)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585675.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: g  column: 11
            High quality sequence start: 14
            High quality sequence stop: 671.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971868"
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                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN
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Alignment Scores:
Pred. No.:              3.44e-103       Length:          747
Score:                  1015.50         Matches:         187
Percent Similarity:     93.6%           Conservative:    17
Best Local Similarity:  85.8%           Mismatches:      13
Query Match:            61.7%           Indels:          1
DB:                     5               Gaps:            1

US-10-821-670A-27 (1-307) x CD559607 (1-747)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||:::|||:::|||||||||||||||||||||||:::||||||||||||
Db         95 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 154

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||:::|||||||||||||||   ||||||||||||
Db        155 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 214

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        215 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 274

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        275 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 334

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              |||:::|||||||||||||||||||||||||||||||||||||||:::::|||||||||
Db        335 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 394

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              |||||||||   ||||||:::||||||||||||||||||||||||||||||||||||||
Db        395 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 454

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||   ||||||||||||||||   |||:::|||||||||||||||||||
Db        455 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 514

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||   ||||||||||||||||||||||||||||||||:::||||||
Db        515 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 574

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||::::::|||   :::|||:::|||||||||||||||   ||||||||||||||||
Db        575 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 631

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              |||||||||||||||||||||||||:::||||||   :::|||||||||:::||||||
Db        632 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATTGCGTTCACAAGCTCCAGTATGAA 691

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 218
              |||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        692 AACTACACCCGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAA 745

RESULT 6
CD559604
LOCUS       CD559604                772 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496598 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971872 5', mRNA sequence.
ACCESSION   CD559604
VERSION     CD559604.2  GI:38558934
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 772)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585672.
            Contact: Daniela S. Gerhard, Ph.D.
```

```
          Office of Cancer Genomics
          National Cancer Institute / NIH
          Bldg. 31 Rm10A07 Bethesda, MD 20892
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Narayan Bhat
           cDNA Library Preparation: Bhat Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: IRBK2  row: h  column: 03
          High quality sequence start: 13
          High quality sequence stop: 750.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:6971872"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              1.55e-101       Length:         772
Score:                  1001.00         Matches:        188
Percent Similarity:     93.6%           Conservative:   16
Best Local Similarity:  86.2%           Mismatches:     13
Query Match:            60.8%           Indels:         2
DB:                     5               Gaps:           1

US-10-821-670A-27 (1-307) x CD559604 (1-772)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||:::|||:::|||||||||||||||||||||||:::||||||||||||
Db        104 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 163

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||:::|||||||||||||||   ||||||||||||
Db        164 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 223

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 GACCAGAGCAGTGAGGTCCTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 283

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
                 ||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        284 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 343

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              |||:::|||||||||||||||||||||||||||||||||||||:::::::|||||||||
Db        344 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 403

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              |||||||||   ||||||:::|||||||||||||||||||||||||||||||||||||||
Db        404 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 463

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||   ||||||||||||||||   |||:::||||||||||||||||||||
Db        464 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 523

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||   ||||||||||||||||||||||||||||:::||||||
Db        524 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 583

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||::::::|||   :::|||:::||||||||||||||   ||||||||||||||||
Db        584 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 640

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||:::||||||||:::||||||||||||||||||
Db        641 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAA 700

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 218
              ||||||||||||||||||||||||||||||||   ||||||   ||||||
Db        701 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAA-CCTGACCAACCCAAA 753

RESULT 7
CD559448/c
LOCUS       CD559448                785 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496712 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971874 5', mRNA sequence.
ACCESSION   CD559448
VERSION     CD559448.2  GI:38453466
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 785)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585516.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 05
            High quality sequence stop: 696.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971874"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
```

of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	1.41e-96	Length:	785
Score:	957.00	Matches:	186
Percent Similarity:	89.5%	Conservative:	18
Best Local Similarity:	81.6%	Mismatches:	23
Query Match:	58.1%	Indels:	3
DB:	5	Gaps:	1

US-10-821-670A-27 (1-307) x CD559448 (1-785)

```
Qy         80 LeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLys 99
              |||         :::|||||||||||||   ||||||||||   |||::::::||||||
Db        771 CTCTGCTGCTCACAAAAGGAAGATGGAAT-TGGTCCACTGATAT-TTAAAGGACCAGAAA 714

Qy        100 GluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThr 119
              |||   |||||||||   ||||||:::||||||||||||||||||||||||||||||||||
Db        713 GAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACC 654

Qy        120 CysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGly 139
              ||||||||||||||   ||||||||||||||   |||:::||||||||||||||||||
Db        653 TGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGC 594

Qy        140 SerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArg 159
              ||||||||||||||   ||||||||||||||||||||||||||||:::||||||
Db        593 TCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGA 534

Qy        160 ValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysPro 179
              ||||||::::::|||   :::|||:::||||||||||||||   ||||||||||||
Db        533 GGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCA 477

Qy        180 AlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyr 199
              |||||||||||||||||||||||||||:::||||||||||:::||||||||||||||||
Db        476 GCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTAT 417

Qy        200 GluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsn 219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        416 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAAC 357

Qy        220 LeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAsp 239
              ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        356 TTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGAC 297

Qy        240 ThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLys 259
              |||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        296 ACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAG 237

Qy        260 AsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCys 279
              :::   ||||||||||||||||:::      ||||||||||||||   |||:::|||
Db        236 AGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGC 177

Qy        280 HisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSer 299
              |||:::|||   |||   |||:::|||:::||||||||||||||||||||||||||||
Db        176 CGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGC 117

Qy        300 AsnTrpAlaSerValSerCysSer 307
              ||||||||||||   ||||||
Db        116 GAATGGGCATCTGTGCCCTGCAGT 93
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RESULT 8
CD559453/c

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LOCUS       CD559453                736 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14497154 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971869 5', mRNA sequence.
ACCESSION   CD559453
VERSION     CD559453.2  GI:38453475
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 736)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585521.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: g  column: 12
            High quality sequence stop: 683.
FEATURES             Location/Qualifiers
     source          1. .736
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971869"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN
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Alignment Scores:

Pred. No.:	1.9e-96	Length:	736
Score:	955.50	Matches:	181
Percent Similarity:	90.8%	Conservative:	17
Best Local Similarity:	83.0%	Mismatches:	19
Query Match:	58.0%	Indels:	2
DB:	5	Gaps:	1

US-10-821-670A-27 (1-307) x CD559453 (1-736)

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Qy         90 TrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCys 109
              ||||||||||   |||::::::||||||||   |||||||   ||||||:::|||
Db        727 TGGTCCACTGATAT-TTAAAGGACCAGAAAGAACCCAAAAATAAGACCTTTCTAAGATGC 669

Qy        110 GluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAsp 129
              ||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db        668 GAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGACAATCAGTACTGAT 609
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```
Qy        130 LeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGluValThrCysGly 149
Db        608 TTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGA 549

Qy        150 AlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThr 169
Db        548 GCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAACAAGGAGTAT---GAGTACTCA 492

Qy        170 ValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluVal 189
Db        491 GTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTC 432

Qy        190 ValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArg 209
Db        431 ATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGG 372

Qy        210 AspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 229
Db        371 GACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 312

Qy        230 HisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSer 249
Db        311 CAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACATTCCTACTTCTCC 252

Qy        250 LeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSer 269
Db        251 CTGACATTCTGCGTTCAGGTCCAGGGCAAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTC 192

Qy        270 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 289
Db        191 ACGGACAAGACCTCAGCCACGGTCATCTGCCGCAAAAATGCCAGCATTAGCGTGCGGGCC 132

Qy        290 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSer 307
Db        131 CAGGACCGCTACTATAGCTCATCTTGGAGCGAATGGGCATCTGTGCCCTGCAGT 78

RESULT 9
CD559450/c
LOCUS       CD559450                772 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496612 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971872 5', mRNA sequence.
ACCESSION   CD559450
VERSION     CD559450.2  GI:38453469
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 772)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585518.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 03
            High quality sequence start: 2
            High quality sequence stop: 753.
FEATURES             Location/Qualifiers
     source          1. .772
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                     /mol_type="mRNA"
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                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:                4.43e-96        Length:          772
Score:                    952.50          Matches:         184
Percent Similarity:       90.2%           Conservative:    18
Best Local Similarity:    82.1%           Mismatches:      21
Query Match:              57.9%           Indels:          3
DB:                       5               Gaps:            1

US-10-821-670A-27 (1-307) x CD559450 (1-772)

Qy         84 LysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsn 103
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Qy        104 LysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeu 123
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Qy        124 ThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSerAspPro 143
Db        650 ACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCTGACCCC 591

Qy        144 GlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArg 163
Db        590 CAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAACAAG 531

Qy        164 AspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGlu 183
Db        530 GAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCTGAGGAG 474

Qy        184 SerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThr 203
Db        473 AGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACC 414

Qy        204 SerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGlnLeuLys 223
Db        413 AGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAG 354

Qy        224 ProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThrTrpSerThr 243
Db        353 CCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACT 294

Qy        244 ProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGlu 263
Db        293 CCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGCAAGAGAGAA 234

Qy        264 LysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHisLysAspAla 283
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Qy        284 LysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSer 303
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Db        173 AGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAATGGGCATCT 114

Qy        304 ValSerCysSer 307
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Db        113 GTGCCCTGCAGT 102
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RESULT 10
CD559451/c
LOCUS CD559451 762 bp mRNA linear EST 19-NOV-2003
DEFINITION AGENCOURT_14496580 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971871 5', mRNA sequence.
ACCESSION CD559451
VERSION CD559451.2 GI:38453471
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 762)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585519.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: IRBK2 row: h column: 02
High quality sequence start: 38
High quality sequence stop: 761.
FEATURES Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971871"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.data Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.: 1.59e-95 Length: 762
Score: 947.50 Matches: 183

Percent Similarity: 90.1% Conservative: 17
Best Local Similarity: 82.4% Mismatches: 21
Query Match: 57.6% Indels: 3
DB: 5 Gaps: 1

US-10-821-670A-27 (1-307) x CD559451 (1-762)

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Qy         86 GluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIle 105
              |||||||||   ||||||||||||   |||:::::|||||||||   |||||||||
Db        759 GAAGATGGAAT-TGGTCCACTGATAT-TTAAAGGACCAGAAAGAACCCAAAAATAAGACC 702

Qy        106 PheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAla 125
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        701 TCTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGACA 642

Qy        126 IleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlu 145
              ||||||||||||||   |||:::||||||||||||||||||||||||||||||||||||
Db        641 ATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGG 582

Qy        146 ValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyr 165
              |||||||||||||||||||||||||||||:::||||||   ||||||::::::|||
Db        581 GTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAACAAGGAGTAT 522

Qy        166 LysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeu 185
                 :::|||:::||||||||||||||   ||||||||||||||||||||||||||||||
Db        521 ---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCTGAGGAGAGTCTG 465

Qy        186 ProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSer 205
              ||||||||||||:::||||||||||:::||||||||||||||||||||||||||||||||
Db        464 CCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACCAGCAGC 405

Qy        206 PhePheIleArgAspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeu 225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        404 TTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTA 345

Qy        226 LysAsnSerArgHisValGluValSerTrpGluTyrProAspThrTrpSerThrProHis 245
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db        344 AAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACAT 285

Qy        246 SerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLys 265
              ||||||||||||||||||||   ||||||||||||||||:::   ||||||||||||
Db        284 TCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGCAAGAGAGAAAAGAAA 225

Qy        266 AspArgLeuSerValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIle 285
              ||||||:::      ||||||||||||||   |||:::|||   |||:::|||   |||
Db        224 GATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGCAAAAATGCCAGCATT 165

Qy        286 ArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSer 305
              |||:::|||:::||||||||||||||||||||||||||   ||||||||||||
Db        164 AGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAATGGGCATCTGTGCCC 105

Qy        306 CysSer 307
              ||||||
Db        104 TGCAGT 99
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RESULT 11
CD559602
LOCUS CD559602 745 bp mRNA linear EST 26-NOV-2003
DEFINITION AGENCOURT_14496684 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971874 5', mRNA sequence.
ACCESSION CD559602
VERSION CD559602.2 GI:38558930
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 745)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585670.

```
           Contact: Daniela S. Gerhard, Ph.D.
           Office of Cancer Genomics
           National Cancer Institute / NIH
           Bldg. 31 Rm10A07 Bethesda, MD 20892
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: IRBK2  row: h  column: 05
           High quality sequence start: 2
           High quality sequence stop: 644.
FEATURES             Location/Qualifiers
     source          1. .745
                     /organism="Homo sapiens"
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                     /clone="IMAGE:6971874"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              5e-90          Length:        745
Score:                  898.50         Matches:       173
Percent Similarity:     89.8%          Conservative:  21
Best Local Similarity:  80.1%          Mismatches:    19
Query Match:            54.6%          Indels:        4
DB:                     5              Gaps:          3

US-10-821-670A-27 (1-307) x CD559602 (1-745)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||:::|||:::|||||||||||||||||||||||:::||||||||||||
Db         72 ATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCT 131

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||:::|||||||||||||||   ||||||||||||
Db        132 GGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTG 191

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 GACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTT 251

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        252 GGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTG 311

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              |||:::||||||||||||||||||||||||||||||||||||||:::::|||||||||
Db        312 CTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAA 371

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||   ||||||:::|||||||||||||||||||||||||||||||||||||||
Db        372 CCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGC 431

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||   ||||||||||||||||   |||:::|||||||||||||||||||
Db        432 TGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCT 491

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||   ||||||||||||||||||||||||||||||:::||||||
Db        492 TCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGG 551

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||::::::|||   :::|||:::||||||||||||||   ||||||||||||||||
Db        552 GACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCT 608

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||:::|||||||||   |||||||||      :::
Db        609 GCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGT-CACAAGCTCATGTTGAAA 667

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspPro 216
                 :::         ||||||:::   :::   ::::::   ||||||
Db        668 ATACAC---CACGGCTTCTTTCTCTGAAAT---CTTCAATCTGACCCA 709

RESULT 12
CD559449/c
LOCUS       CD559449                 766 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496649 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971873 5', mRNA sequence.
ACCESSION   CD559449
VERSION     CD559449.2  GI:38453467
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 766)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585517.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 04
            High quality sequence stop: 641.
FEATURES             Location/Qualifiers
     source          1. .766
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971873"
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                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
```

PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	5.21e-90	Length:	766
Score:	898.50	Matches:	168
Percent Similarity:	90.6%	Conservative:	15
Best Local Similarity:	83.2%	Mismatches:	18
Query Match:	54.6%	Indels:	1
DB:	5	Gaps:	1

US-10-821-670A-27 (1-307) x CD559449 (1-766)

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Qy        106 PheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAla 125
              ||||||:::|||||||||||   |||||||||||||||||   ||||||||||||
Db        693 TTTCTAAGATGCGAGGCCAAGAAGTATTCTGGACGTTTCACCTGGTGGTGGCTGACGACA 634

Qy        126 IleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlu 145
              ||||||||||||||||   |||:::|||||||||||||||||||||||||||||||||
Db        633 ATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGG 574

Qy        146 ValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyr 165
              ||||||||||||||||||||||||||||||:::||||||   ||||||:::::::|||
Db        573 GTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAACAAGGAGTAT 514

Qy        166 LysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeu 185
                  :::|||:::|||||||||||||||   ||||||||||||||||||||||||||||
Db        513 ---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCTGAGGAGAGTCTG 457

Qy        186 ProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSer 205
              ||||||||||||:::||||||||||:::||||||||||||||||||||||||||||||
Db        456 CCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACCAGCAGC 397

Qy        206 PhePheIleArgAspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeu 225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 TTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTA 337

Qy        226 LysAsnSerArgHisValGluValSerTrpGluTyrProAspThrTrpSerThrProHis 245
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db        336 AAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACAT 277

Qy        246 SerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLys 265
              ||||||||||||||||||   ||||||||||||||||:::   ||||||||||||
Db        276 TCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGCAAGAGAGAAAAGAAA 217

Qy        266 AspArgLeuSerValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIle 285
              ||||||:::      ||||||||||||||   |||:::|||   |||:::|||   |||
Db        216 GATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGCAAAAATGCCAGCATT 157

Qy        286 ArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSer 305
                  |||:::|||:::|||||||||||||||||||||||||||   ||||||||||||
Db        156 AGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAATGGGCATCTGTGCCC 97

Qy        306 CysSer 307
              ||||||
Db         96 TGCAGT 91
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RESULT 13
CD559452/c

LOCUS	CD559452	754 bp	mRNA	linear	EST 19-NOV-2003

DEFINITION AGENCOURT_14496548 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971870 5', mRNA sequence.
ACCESSION CD559452
VERSION CD559452.2 GI:38453473
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 754)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585520.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: h column: 01
High quality sequence start: 130
High quality sequence stop: 572.

FEATURES Location/Qualifiers

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	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/clone="IMAGE:6971870"
	/tissue_type="mixed"
	/lab_host="DH5A (T1 phage-resistant)"
	/clone_lib="NIH_MGC_195"
	/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	4.04e-89	Length:	754
Score:	890.50	Matches:	171
Percent Similarity:	85.8%	Conservative:	17
Best Local Similarity:	78.1%	Mismatches:	30
Query Match:	54.1%	Indels:	2
DB:	5	Gaps:	1

US-10-821-670A-27 (1-307) x CD559452 (1-754)

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Qy         89 IleTrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLys 108
              |||||||||   |||   |||:::::|||||||||   |||||||||   ||||||:::
Db        750 ATTTGGTCCAATGATAT-TTAAAGGACCAGAAAGAACCCAAAAATAAGACCTTTCTAAGA 692

Qy        109 CysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThr 128
              ||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db        691 TGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGACAATCAGTACT 632

Qy        129 AspLeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGluValThrCys 148
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Db        631 GATTTGACATTCAGTGTCAAGAGCAGCAGAGGCTTTTTTGACCCCCAAGGGGTGACGTGC 572

Qy        149 GlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyr 168
              ||||||||||||||||   ||||||:::||||||   ||||||::::::|||   :::|||
Db        571 GGAGCTGCTACACTCTTTGCAGAGAGAGTCAGAGGGGACAACAAGGAGTAT---GAGTAC 515

Qy        169 ThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGlu 188
              :::||||||||||||||   ||||||||||||||   ||||||||||||||||||||||
Db        514 TCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGGTGAGGAGAGTTTGCCCATTGAG 455

Qy        189 ValValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIle 208
              |||:::|||||||||:::|||||||||||||||||||||||||||||   |||||||||
Db        454 GTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACCAGCAGGTTTTTCATC 395

Qy        209 ArgAspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSer 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 AGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCT 335

Qy        229 ArgHisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPhe 248
              ||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        334 TGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACATTCCTAATTT 275

Qy        249 SerLeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeu 268
              ||||||||||||   ||||||||||||||:::   ||||||||||||||||||:::
Db        274 TCCCTGACATTTTGCGTTCAGGTTCAGGGCAAGAGCAAGAGAGAAAAGAAAGATAGAGTT 215

Qy        269 SerValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGln 288
              |||||||||   |||   |||:::|||   |||:::|||   |||   |||:::
Db        214 TTCACGGACAAGACCTTAGCCACGGTCATTTGCCGCAAAAATGCCAGCATTAGCGTGCGG 155

Qy        289 AlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSer 307
              |||:::||||||||||||||||   ||||||   ||||||   |||   ||||||
Db        154 GCCCAGGACCGGTACTATAGCTCATTTTGGAGCGAATGGGCATTTGTGCCCTGCAGT 98

RESULT 14
CD559454/c
LOCUS       CD559454                725 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14497089 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971868 5', mRNA sequence.
ACCESSION   CD559454
VERSION     CD559454.2  GI:38453478
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 725)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585522.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: g  column: 11
            High quality sequence start: 13
            High quality sequence stop: 573.
FEATURES             Location/Qualifiers
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                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:                  9.21e-81        Length:          725
Score:                      816.00          Matches:         164
Percent Similarity:         85.6%           Conservative:    15
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US-10-821-670A-27 (1-307) x CD559454 (1-725)

Qy         99 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 118
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Qy        139 GlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 158
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Db        606 GGTTCCTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 547

Qy        159 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 178
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Qy        179 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 198
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Qy        199 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 218
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Qy        219 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 238
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Qy        259 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 278
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Qy        279 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 298
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Qy        299 SerAsnTrpAlaSerValSerCysSer 307
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RESULT 15
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DEFINITION  AGENCOURT_14496630 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971873 5', mRNA sequence.
ACCESSION   CD559603
VERSION     CD559603.2  GI:38558932
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 724)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585671.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
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                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

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Best Local Similarity:  88.2%           Mismatches:     8
Query Match:            42.5%           Indels:         0
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US-10-821-670A-27 (1-307) x CD559603 (1-724)
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Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
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Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
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Qy        141 SerAspProGln 144
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 10, 2006, 01:16:39 ; Search time 158.55 Seconds
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Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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	37	1418.5	86.2	1018	2	US-08-458-356-194	Sequence 194, App
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	42	1418.5	86.2	1399	2	US-08-751-767A-3	Sequence 3, Appli
	43	1418.5	86.2	1560	2	US-08-751-767A-11	Sequence 11, Appl
	44	1418.5	86.2	1623	2	US-08-751-767A-9	Sequence 9, Appli
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ALIGNMENTS

RESULT 1
US-09-917-265A-26
; Sequence 26, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(921)
US-09-917-265A-26

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Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
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RESULT 2
US-09-917-265A-28/c
; Sequence 28, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265A-28

Alignment Scores:

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Score:	1646.00	Matches:	307
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Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
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US-10-821-670A-27 (1-307) x US-09-917-265A-28 (1-921)

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Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202
```

```
Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCAGT 1

RESULT 3
US-09-917-265A-43
; Sequence 43, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-09-917-265A-43

Alignment Scores:
Pred. No.:              1.21e-182       Length:         1533
Score:                  1646.00         Matches:        307
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-27 (1-307) x US-09-917-265A-43 (1-1533)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 4
US-09-917-265A-45/c
; Sequence 45, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-45

Alignment Scores:
Pred. No.:              1.21e-182       Length:         1533
Score:                  1646.00         Matches:        307
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0
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US-10-821-670A-27 (1-307) x US-09-917-265A-45 (1-1533)

```
Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613
```

RESULT 5
US-09-917-265A-38
; Sequence 38, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1599)
US-09-917-265A-38

Alignment Scores:

Pred. No.:	1.29e-182	Length:	1599
Score:	1646.00	Matches:	307
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-821-670A-27 (1-307) x US-09-917-265A-38 (1-1599)

```
Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        301 TrpAlaSerValSerCysSer 307
                |||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987

RESULT 6
US-09-917-265A-40/c
; Sequence 40, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-40

Alignment Scores:
Pred. No.:              1.29e-182       Length:         1599
Score:                  1646.00         Matches:        307
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-27 (1-307) x US-09-917-265A-40 (1-1599)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        301 TrpAlaSerValSerCysSer 307
                |||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613

RESULT 7
US-09-011-143-6
; Sequence 6, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
```

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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  921 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-6

Alignment Scores:
Pred. No.:              3.68e-182      Length:         921
Score:                  1639.00        Matches:        306
Percent Similarity:     99.7%          Conservative:   0
Best Local Similarity:  99.7%          Mismatches:     1
Query Match:            99.6%          Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-27 (1-307) x US-09-011-143-6 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
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Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 8
US-09-011-143-7
; Sequence 7, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  921 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-7

Alignment Scores:
Pred. No.:              3.68e-182      Length:         921
Score:                  1639.00        Matches:        306
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Percent Similarity:     99.7%          Conservative:  0
Best Local Similarity:  99.7%          Mismatches:    1
Query Match:            99.6%          Indels:        0
DB:                     3              Gaps:          0

US-10-821-670A-27 (1-307) x US-09-011-143-7 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||    ||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
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Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 9
US-09-302-495-6
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; Sequence 6, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-302-495-6

Alignment Scores:
Pred. No.:              3.68e-182      Length:        921
Score:                  1639.00        Matches:       306
Percent Similarity:     99.7%          Conservative:  0
Best Local Similarity:  99.7%          Mismatches:    1
Query Match:            99.6%          Indels:        0
DB:                     3              Gaps:          0

US-10-821-670A-27 (1-307) x US-09-302-495-6 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
                ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
                |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 10
US-09-302-495-7
; Sequence 7, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;    INFORMATION FOR SEQ ID NO: 7:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-302-495-7

Alignment Scores:
Pred. No.:                3.68e-182       Length:          921
Score:                    1639.00         Matches:         306
Percent Similarity:       99.7%           Conservative:    0
Best Local Similarity:    99.7%           Mismatches:      1
Query Match:              99.6%           Indels:          0
DB:                       3               Gaps:            0

US-10-821-670A-27 (1-307) x US-09-302-495-7 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
                ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
                |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 11
US-10-079-616-6
; Sequence 6, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-079-616-6

Alignment Scores:
Pred. No.:                3.68e-182      Length:          921
Score:                    1639.00        Matches:         306
Percent Similarity:       99.7%          Conservative:    0
Best Local Similarity:    99.7%          Mismatches:      1
Query Match:              99.6%          Indels:          0
DB:                       3              Gaps:            0

US-10-821-670A-27 (1-307) x US-10-079-616-6 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
                ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
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Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 12
US-10-079-616-7
; Sequence 7, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 7:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-079-616-7

Alignment Scores:
Pred. No.:              3.68e-182      Length:         921
Score:                  1639.00        Matches:        306
Percent Similarity:     99.7%          Conservative:   0
Best Local Similarity:  99.7%          Mismatches:     1
Query Match:            99.6%          Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-27 (1-307) x US-10-079-616-7 (1-921)
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Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 13
US-09-917-265A-29
; Sequence 29, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
```

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;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
US-09-917-265A-29

Alignment Scores:
Pred. No.:              4.09e-182       Length:         987
Score:                  1639.00         Matches:        306
Percent Similarity:     99.7%           Conservative:   0
Best Local Similarity:  99.7%           Mismatches:     1
Query Match:            99.6%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-27 (1-307) x US-09-917-265A-29 (1-987)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
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Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
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Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
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Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
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Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
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Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
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Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
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Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
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Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
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Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
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Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
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Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
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Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
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Qy        301 TrpAlaSerValSerCysSer 307
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RESULT 14
US-09-917-265A-31/c
; Sequence 31, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-31

Alignment Scores:
Pred. No.:              4.09e-182       Length:         987
Score:                  1639.00         Matches:        306
Percent Similarity:     99.7%           Conservative:   0
Best Local Similarity:  99.7%           Mismatches:     1
Query Match:            99.6%           Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-27 (1-307) x US-09-917-265A-31 (1-987)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
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Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
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Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
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Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
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Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
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Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
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Db        501 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
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Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
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Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
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Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
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Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
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Qy        301 TrpAlaSerValSerCysSer 307
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Db         21 TGGGCATCCGTGTCCTGCAGT 1
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RESULT 15
US-09-011-143-5
; Sequence 5, Application US/09011143
; Patent No. 6472509
; GENERAL INFORMATION:
; APPLICANT: IMAMURA, Takayuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: FUJIYASU, Takeshi
; APPLICANT: IMAGAWA, Yoshitaka
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011,143
; FILING DATE: 04-FEB-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP97/01824
; FILING DATE: 29-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 165249/1996
; FILING DATE: 04-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: IMAMURA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2193 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-011-143-5

Alignment Scores:

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Score:	1639.00	Matches:	306
Percent Similarity:	99.7%	Conservative:	0
Best Local Similarity:	99.7%	Mismatches:	1
Query Match:	99.6%	Indels:	0
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US-10-821-670A-27 (1-307) x US-09-011-143-5 (1-2193)

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Db        130 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 189

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
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Db        190 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 249

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
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Db        250 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 309

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 369

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
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Db        370 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 429

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Db        430 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 489

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
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Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
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Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
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Db        670 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 729

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
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Db        730 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 789

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
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Db        790 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 849

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
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Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 969

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
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Qy        301 TrpAlaSerValSerCysSer 307
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GenCore version 5.1.9
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SUMMARIES

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5	1646	100.0	1533	3	US-09-917-265-43	Sequence 43, Appl
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9	1646	100.0	1599	3	US-09-917-265-38	Sequence 38, Appl
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14	1639	99.6	921	6	US-10-079-616-7	Sequence 7, Appli
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17	1639	99.6	987	9	US-10-821-670-29	Sequence 29, Appl
c 18	1639	99.6	987	9	US-10-821-670-31	Sequence 31, Appl
19	1639	99.6	990	7	US-10-041-672C-1	Sequence 1, Appli
20	1639	99.6	2193	6	US-10-079-616-5	Sequence 5, Appli
21	1639	99.6	4522	7	US-10-041-672C-10	Sequence 10, Appl
22	1635	99.3	985	3	US-09-917-265-55	Sequence 55, Appl
c 23	1635	99.3	985	3	US-09-917-265-57	Sequence 57, Appl
24	1635	99.3	985	9	US-10-821-670-55	Sequence 55, Appl
c 25	1635	99.3	985	9	US-10-821-670-57	Sequence 57, Appl
26	1546	93.9	921	3	US-09-917-265-52	Sequence 52, Appl
c 27	1546	93.9	921	3	US-09-917-265-54	Sequence 54, Appl
28	1546	93.9	921	9	US-10-821-670-52	Sequence 52, Appl
c 29	1546	93.9	921	9	US-10-821-670-54	Sequence 54, Appl
30	1546	93.9	987	3	US-09-917-265-58	Sequence 58, Appl
c 31	1546	93.9	987	3	US-09-917-265-60	Sequence 60, Appl
32	1546	93.9	987	9	US-10-821-670-58	Sequence 58, Appl
c 33	1546	93.9	987	9	US-10-821-670-60	Sequence 60, Appl
34	1546	93.9	1533	3	US-09-917-265-66	Sequence 66, Appl
c 35	1546	93.9	1533	3	US-09-917-265-68	Sequence 68, Appl
36	1546	93.9	1533	9	US-10-821-670-66	Sequence 66, Appl
c 37	1546	93.9	1533	9	US-10-821-670-68	Sequence 68, Appl
38	1546	93.9	1599	3	US-09-917-265-61	Sequence 61, Appl
c 39	1546	93.9	1599	3	US-09-917-265-63	Sequence 63, Appl
40	1546	93.9	1599	9	US-10-821-670-61	Sequence 61, Appl
c 41	1546	93.9	1599	9	US-10-821-670-63	Sequence 63, Appl
42	1546	93.9	2267	3	US-09-917-265-107	Sequence 107, App
c 43	1546	93.9	2267	3	US-09-917-265-109	Sequence 109, App
44	1546	93.9	2267	9	US-10-821-670-107	Sequence 107, App
c 45	1546	93.9	2267	9	US-10-821-670-109	Sequence 109, App

ALIGNMENTS

RESULT 1
US-09-917-265-26
; Sequence 26, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(921)
; OTHER INFORMATION:
US-09-917-265-26

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Alignment Scores:
Pred. No.:              1.9e-190        Length:         921
Score:                  1646.00         Matches:        307
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-27 (1-307) x US-09-917-265-26 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
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Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
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Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
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Db        901 TGGGCATCCGTGTCCTGCAGT 921
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RESULT 2
US-09-917-265-28/c
; Sequence 28, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-28

Alignment Scores:
Pred. No.:              1.9e-190        Length:         921
Score:                  1646.00         Matches:        307
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-27 (1-307) x US-09-917-265-28 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
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Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        301 TrpAlaSerValSerCysSer 307
                |||||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCAGT 1

RESULT 3
US-10-821-670-26
; Sequence 26, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(921)
US-10-821-670-26

Alignment Scores:
Pred. No.:              1.9e-190        Length:         921
Score:                  1646.00         Matches:        307
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-27 (1-307) x US-10-821-670-26 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
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Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
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Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
                |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 4
US-10-821-670-28/c
; Sequence 28, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-28

Alignment Scores:
Pred. No.:              1.9e-190        Length:         921
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Score:                 1646.00       Matches:       307
Percent Similarity:    100.0%        Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:           100.0%        Indels:        0
DB:                    9             Gaps:          0

US-10-821-670A-27 (1-307) x US-10-821-670-28 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
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Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
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Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCAGT 1

RESULT 5
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US-09-917-265-43
; Sequence 43, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
;   OTHER INFORMATION:
US-09-917-265-43

Alignment Scores:
Pred. No.:             4.03e-190     Length:        1533
Score:                 1646.00       Matches:       307
Percent Similarity:    100.0%        Conservative:  0
Best Local Similarity: 100.0%        Mismatches:    0
Query Match:           100.0%        Indels:        0
DB:                    3             Gaps:          0

US-10-821-670A-27 (1-307) x US-09-917-265-43 (1-1533)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 6
US-09-917-265-45/c
; Sequence 45, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-45

Alignment Scores:
Pred. No.:              4.03e-190     Length:          1533
Score:                  1646.00       Matches:         307
Percent Similarity:     100.0%        Conservative:    0
Best Local Similarity:  100.0%        Mismatches:      0
Query Match:            100.0%        Indels:          0
DB:                     3             Gaps:            0

US-10-821-670A-27 (1-307) x US-09-917-265-45 (1-1533)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613

RESULT 7
US-10-821-670-43
; Sequence 43, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-10-821-670-43

Alignment Scores:
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Pred. No.:              4.03e-190       Length:         1533
Score:                  1646.00         Matches:        307
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-27 (1-307) x US-10-821-670-43 (1-1533)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921
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RESULT 8
US-10-821-670-45/c
; Sequence 45, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-45

Alignment Scores:
Pred. No.:              4.03e-190       Length:         1533
Score:                  1646.00         Matches:        307
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-27 (1-307) x US-10-821-670-45 (1-1533)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        301 TrpAlaSerValSerCysSer 307
                 |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613

RESULT 9
US-09-917-265-38
; Sequence 38, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
US-09-917-265-38

Alignment Scores:
Pred. No.:              4.28e-190       Length:         1599
Score:                  1646.00         Matches:        307
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

US-10-821-670A-27 (1-307) x US-09-917-265-38 (1-1599)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        301 TrpAlaSerValSerCysSer 307
                 |||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987

RESULT 10
US-09-917-265-40/c
; Sequence 40, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-40

Alignment Scores:
Pred. No.:              4.28e-190       Length:         1599
Score:                  1646.00         Matches:        307
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Percent Similarity:     100.0%          Conservative:  0
Best Local Similarity:  100.0%          Mismatches:    0
Query Match:            100.0%          Indels:        0
DB:                     3               Gaps:          0

US-10-821-670A-27 (1-307) x US-09-917-265-40 (1-1599)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613

RESULT 11
US-10-821-670-38
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; Sequence 38, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-10-821-670-38

Alignment Scores:
Pred. No.:              4.28e-190       Length:        1599
Score:                  1646.00         Matches:       307
Percent Similarity:     100.0%          Conservative:  0
Best Local Similarity:  100.0%          Mismatches:    0
Query Match:            100.0%          Indels:        0
DB:                     9               Gaps:          0

US-10-821-670A-27 (1-307) x US-10-821-670-38 (1-1599)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
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Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987

RESULT 12
US-10-821-670-40/c
; Sequence 40, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-40

Alignment Scores:
Pred. No.:              4.28e-190       Length:         1599
Score:                  1646.00         Matches:        307
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     9               Gaps:           0

US-10-821-670A-27 (1-307) x US-10-821-670-40 (1-1599)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613

RESULT 13
US-10-079-616-6
; Sequence 6, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
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;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;    INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-079-616-6

Alignment Scores:
Pred. No.:                1.36e-189      Length:          921
Score:                    1639.00        Matches:         306
Percent Similarity:       99.7%          Conservative:    0
Best Local Similarity:    99.7%          Mismatches:      1
Query Match:              99.6%          Indels:          0
DB:                       6              Gaps:            0

US-10-821-670A-27 (1-307) x US-10-079-616-6 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 14
US-10-079-616-7
; Sequence 7, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;    INFORMATION FOR SEQ ID NO: 7:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
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;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-079-616-7

Alignment Scores:
Pred. No.:              1.36e-189      Length:         921
Score:                  1639.00        Matches:        306
Percent Similarity:     99.7%          Conservative:   0
Best Local Similarity:  99.7%          Mismatches:     1
Query Match:            99.6%          Indels:         0
DB:                     6              Gaps:           0

US-10-821-670A-27 (1-307) x US-10-079-616-7 (1-921)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921

RESULT 15
US-09-917-265-29
; Sequence 29, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
;   OTHER INFORMATION:
US-09-917-265-29

Alignment Scores:
Pred. No.:              1.51e-189      Length:         987
Score:                  1639.00        Matches:        306
Percent Similarity:     99.7%          Conservative:   0
Best Local Similarity:  99.7%          Mismatches:     1
Query Match:            99.6%          Indels:         0
DB:                     3              Gaps:           0

US-10-821-670A-27 (1-307) x US-09-917-265-29 (1-987)

Qy          1 IleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaPro 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSer 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186

Qy         41 AspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPhe 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246

Qy         61 AlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306

Qy         81 LeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366

Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
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Qy        161 AspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAla 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606

Qy        181 AlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666

Qy        201 AsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726

Qy        221 GlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786

Qy        241 TrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846

Qy        261 AsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHis 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906

Qy        281 LysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsn 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966

Qy        301 TrpAlaSerValSerCysSer 307
              |||||||||||||||||||||
Db        967 TGGGCATCCGTGTCCTGCAGT 987
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Search completed: June 10, 2006, 04:33:55
Job time : 1207.22 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 10, 2006, 01:18:36 ; Search time 15.9725 Seconds
(without alignments)
3659.318 Million cell updates/sec

Title: US-10-821-670A-27
Perfect score: 1646
Sequence: 1 IWELEKNVYVVELDWHPDAP.....QARDRYYSSSWSNWASVSCS 307

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 253354 seqs, 63461778 residues

Total number of hits satisfying chosen parameters: 506708

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/abss/ABSSWEB_spool/US10821670/runat_07062006_110114_26355/app_query.fasta_1
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss05h
-USER=US10821670_@CGN_1_1_80_@runat_07062006_110114_26355 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	178	10.8	1363	6	US-10-827-684B-6	Sequence 6, Appli
2	178	10.8	1369	6	US-10-827-684B-5	Sequence 5, Appli
3	176	10.7	1923	7	US-11-145-307A-52	Sequence 52, Appl
4	132.5	8.0	1161	7	US-11-297-134-9	Sequence 9, Appli
5	105.5	6.4	2534	7	US-11-293-697-1946	Sequence 1946, Ap
6	99.5	6.0	2341	6	US-10-511-937-349	Sequence 349, App
7	96.5	5.9	3646	6	US-10-511-937-358	Sequence 358, App
8	93.5	5.7	3597	6	US-10-505-928-651	Sequence 651, App
9	93.5	5.7	3597	6	US-10-511-937-2802	Sequence 2802, Ap
10	92	5.6	2582	7	US-11-293-697-2331	Sequence 2331, Ap
11	91	5.5	5997	7	US-11-313-450-1	Sequence 1, Appli
12	91	5.5	8370	7	US-11-263-326-90	Sequence 90, Appl
13	91	5.5	8377	7	US-11-263-326-95	Sequence 95, Appl
14	91	5.5	8380	7	US-11-263-326-89	Sequence 89, Appl
15	91	5.5	8381	7	US-11-263-326-1	Sequence 1, Appli
16	91	5.5	8381	7	US-11-263-326-3	Sequence 3, Appli
17	91	5.5	8381	7	US-11-263-326-5	Sequence 5, Appli
18	91	5.5	8381	7	US-11-263-326-7	Sequence 7, Appli
19	91	5.5	8381	7	US-11-263-326-8	Sequence 8, Appli
20	91	5.5	8381	7	US-11-263-326-11	Sequence 11, Appl
21	91	5.5	8381	7	US-11-263-326-91	Sequence 91, Appl
22	91	5.5	8381	7	US-11-263-326-92	Sequence 92, Appl
23	91	5.5	8381	7	US-11-263-326-93	Sequence 93, Appl
24	91	5.5	8381	7	US-11-263-326-96	Sequence 96, Appl
25	91	5.5	8381	7	US-11-263-326-97	Sequence 97, Appl
26	91	5.5	8381	7	US-11-263-326-108	Sequence 108, App
27	91	5.5	8381	7	US-11-263-326-136	Sequence 136, App
28	91	5.5	8381	7	US-11-263-326-137	Sequence 137, App
29	91	5.5	8381	7	US-11-263-326-138	Sequence 138, App
30	91	5.5	8381	7	US-11-263-326-139	Sequence 139, App
31	91	5.5	8381	7	US-11-263-326-140	Sequence 140, App
32	91	5.5	8381	7	US-11-263-326-141	Sequence 141, App
33	91	5.5	8381	7	US-11-263-326-142	Sequence 142, App
34	91	5.5	8381	7	US-11-263-326-143	Sequence 143, App
35	91	5.5	8381	7	US-11-263-326-144	Sequence 144, App
36	91	5.5	8388	7	US-11-263-326-94	Sequence 94, Appl
37	89.5	5.4	3084	6	US-10-511-937-448	Sequence 448, App
38	89.5	5.4	5193	7	US-11-270-040-5	Sequence 5, Appli
39	89	5.4	1152	7	US-11-217-529-1932	Sequence 1932, Ap
40	87.5	5.3	1219	6	US-10-953-349-15072	Sequence 15072, A
41	87	5.3	1216	6	US-10-953-349-26426	Sequence 26426, A
42	86.5	5.3	1301	7	US-11-274-375-7	Sequence 7, Appli
43	86.5	5.3	1479	7	US-11-274-375-3	Sequence 3, Appli
44	86.5	5.3	1784	7	US-11-274-375-1	Sequence 1, Appli
45	86.5	5.3	1910	7	US-11-274-375-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-10-827-684B-6
; Sequence 6, Application US/10827684B
; Publication No. US20060115807A1
; GENERAL INFORMATION:
; APPLICANT: Chambers, Ian P
; TITLE OF INVENTION: Improved episomal expression system
; FILE REFERENCE: 78870/00003
; CURRENT APPLICATION NUMBER: US/10/827,684B
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 09/359,672
; PRIOR FILING DATE: 1999-07-23
; PRIOR APPLICATION NUMBER: GB 9701492.2
; PRIOR FILING DATE: 1997-01-24
; PRIOR APPLICATION NUMBER: PCT/GB98/00216
; PRIOR FILING DATE: 1998-01-26
; PRIOR APPLICATION NUMBER: GB 0407043.9
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1363
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-827-684B-6

Alignment Scores:

Pred. No.:	1.85e-10	Length:	1363
Score:	178.00	Matches:	76
Percent Similarity:	40.5%	Conservative:	50
Best Local Similarity:	24.4%	Mismatches:	125

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Query Match:            10.8%          Indels:        61
DB:                     6              Gaps:          13

US-10-821-670A-27 (1-307) x US-10-827-684B-6 (1-1363)

Qy         15 TrpHisProAsp-Ala---ProGlyGluMetValValLeuThrCysAsnThrProGlu-- 32
              ||||||   ||| :::   ||||||      |||   |||   |||          |||
Db         76 TGGCACAGTGACAAGCCTGCCAGGGGCCACCGTTACCCTGATTTGCCCCGGGAAGGAAGC 135

Qy         33 -GluAspAspIleThr-----------TrpThrSerAspGlnSerSerGluValLeuGl 48
                    ::::::|||           ::::::      |||:::   |||
Db        136 AGCAGGCAATGTTACCATTCACTGGGTGTACTCTGGCTCACAAAACAGAGAATGGACTAC 195

Qy         48 ySerGlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCy 68
               :::|||   ||||||   ::::::      :::   :::|||   |||   |||   ||
Db        196 CACAGGAAACACACTGGTTCTGAGGGACGTGCAGCTCAGCGACACTGGGGACTATTTATG 255

Qy         68 sHisLysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGl 88
              |               ::::::           ||||||:::
Db        256 CTCCCTGAATGATCACCTGGTGGGGACTGTGCCCTTGCTGGTG---------------- 298

Qy         88 yIleTrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLy 108
                        |||:::     |||:::  :::                  |||
Db        299 ------------GATGTTCCCCCAGAGGAGCCCAAG-----------------CTCTC 327

Qy        108 sCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerTh 128
               |||      ||||||           |||   |||
Db        328 CTGCTTCCGGAAGAACCCCCTTGTCAACGCCATCTGTGAGTGG---------------- 370

Qy        128 rAspLeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGluValThrCy 148
                                       |||   ||||||   |||          |||
Db        371 ---------------------------CGTCCGAGCAGCACCCCCTCTCCAACCACG-- 400

Qy        148 sGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTy 168
                  |||   |||   |||:::|||:::          |||                ::
Db        401 ----AAGGCTGTGCTGTTTGCAAAGAAAATCAACACCACCAAC---GGGAAGAGTGACTT 453

Qy        168 rThrValGluCysGlnGluGlySerAlaCys---------------------------Pr 179
               :   |||   ||||||      ||||||                            ||
Db        454 CCAGGTGCCCTGCCAGTATTC-TCAGCAGCTGAAAAGCTTCTCCTGCCAGGTGGAGATCC 512

Qy        179 oAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTy 199
              |          :::|||:::|||       |||   |||                 |||
Db        513 TGGAGGGTGACAAAGTATACCACATAGTGTCACTGTGCGTTGCAAACAGTGTGGGAAGCA 572

Qy        199 r-GluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysA 219
                 ::::::      :::|||           :::::::::||||||||||||    |
Db        573 AGTCCAGCCACAACGAAGCGTTTCACAGCTTAAAAATGGTGCAGCCGGATCCACCTGCCA 632

Qy        219 snLeuGlnLeuLysProLeuLys---AsnSerArgHisValGluValSerTrpGluTyrP 238
              |||||   :::      :::          |||   ::::::||||||||::::::|
Db        633 ACCTTGTGGTATCAGCCATACCTGGAAGGCCGCGCTGGCTCAAAGTCAGCTGGCAGCACC 692

Qy        238 roAspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnG 258
              ||:::||||||           ||||||:::   |||   |||   ::::::   :::
Db        693 CTGAGACCTGGGACCCG------AGTTACTACTTGCTGCAGTTCCAGCTTCGATACCGAC 746

Qy        258 lyLysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValV 278
                    ::::::|||           |||  :::                 :::   |
Db        747 CTGTATGGTCAAAGGAG---TTCACGGTGTTGCTGCTCCCGGTGGCCCAGTACCAATGCG 803

Qy        278 alCysHisLysAspAlaLys--------------IleArgValGlnAlaArgAspArgT 293
              ||   |||      :::              ::::::|||:::   ::::::
Db        804 TCATCCATGATGCCTTGCGAGGAGTGAAGCACGTGGTCCAGGTCCGTGGGAAGGAGGAGC 863

Qy        293 yrTyrSerSerSerTrpSerAsnTrpAla 302
                         ||||||   |||:::
Db        864 TTGACCTTGGCCAGTGGAGTGAATGGTCC 892

RESULT 2
US-10-827-684B-5
; Sequence 5, Application US/10827684B
; Publication No. US20060115807A1
; GENERAL INFORMATION:
;  APPLICANT: Chambers, Ian P
;  TITLE OF INVENTION: Improved episomal expression system
;  FILE REFERENCE: 78870/00003
;  CURRENT APPLICATION NUMBER: US/10/827,684B
;  CURRENT FILING DATE:  2004-04-19
;  PRIOR APPLICATION NUMBER: US 09/359,672
;  PRIOR FILING DATE: 1999-07-23
;  PRIOR APPLICATION NUMBER: GB 9701492.2
;  PRIOR FILING DATE: 1997-01-24
;  PRIOR APPLICATION NUMBER: PCT/GB98/00216
;  PRIOR FILING DATE: 1998-01-26
;  PRIOR APPLICATION NUMBER: GB 0407043.9
;  PRIOR FILING DATE: 2004-03-29
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 1369
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-827-684B-5

Alignment Scores:
Pred. No.:              1.86e-10       Length:        1369
Score:                  178.00         Matches:       76
Percent Similarity:     40.5%          Conservative:  50
Best Local Similarity:  24.4%          Mismatches:    125
Query Match:            10.8%          Indels:        61
DB:                     6              Gaps:          13

US-10-821-670A-27 (1-307) x US-10-827-684B-5 (1-1369)

Qy         15 TrpHisProAsp-Ala---ProGlyGluMetValValLeuThrCysAsnThrProGlu-- 32
              ||||||   ||| :::   ||||||      |||   |||   |||          |||
Db         82 TGGCACAGTGACAAGCCTGCCAGGGGCCACCGTTACCCTGATTTGCCCCGGGAAGGAAGC 141

Qy         33 -GluAspAspIleThr-----------TrpThrSerAspGlnSerSerGluValLeuGl 48
                    ::::::|||           ::::::      |||:::   |||
Db        142 AGCAGGCAATGTTACCATTCACTGGGTGTACTCTGGCTCACAAAACAGAGAATGGACTAC 201

Qy         48 ySerGlyLysThrLeuThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCy 68
               :::|||   ||||||   ::::::      :::   :::|||   |||   |||   ||
Db        202 CACAGGAAACACACTGGTTCTGAGGGACGTGCAGCTCAGCGACACTGGGGACTATTTATG 261

Qy         68 sHisLysGlyGlyGluValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGl 88
              |               ::::::           ||||||:::
Db        262 CTCCCTGAATGATCACCTGGTGGGGACTGTGCCCTTGCTGGTG---------------- 304

Qy         88 yIleTrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLy 108
                        |||:::     |||:::  :::                  |||
Db        305 ------------GATGTTCCCCCAGAGGAGCCCAAG-----------------CTCTC 333

Qy        108 sCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerTh 128
               |||      ||||||           |||   |||
Db        334 CTGCTTCCGGAAGAACCCCCTTGTCAACGCCATCTGTGAGTGG---------------- 376

Qy        128 rAspLeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGluValThrCy 148
                                       |||   ||||||   |||          |||
Db        377 ---------------------------CGTCCGAGCAGCACCCCCTCTCCAACCACG-- 406

Qy        148 sGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTy 168
                  |||   |||   |||:::|||:::          |||                ::
Db        407 ----AAGGCTGTGCTGTTTGCAAAGAAAATCAACACCACCAAC---GGGAAGAGTGACTT 459

Qy        168 rThrValGluCysGlnGluGlySerAlaCys---------------------------Pr 179
               :   |||   ||||||      ||||||                            ||
Db        460 CCAGGTGCCCTGCCAGTATTC-TCAGCAGCTGAAAAGCTTCTCCTGCCAGGTGGAGATCC 518

Qy        179 oAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTy 199
              |          :::|||:::|||       |||   |||                 |||
Db        519 TGGAGGGTGACAAAGTATACCACATAGTGTCACTGTGCGTTGCAAACAGTGTGGGAAGCA 578
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Qy        199 r-GluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysA 219
Db        579 AGTCCAGCCACAACGAAGCGTTTCACAGCTTAAAAATGGTGCAGCCGGATCCACCTGCCA 638

Qy        219 snLeuGlnLeuLysProLeuLys---AsnSerArgHisValGluValSerTrpGluTyrP 238
Db        639 ACCTTGTGGTATCAGCCATACCTGGAAGGCCGCGCTGGCTCAAAGTCAGCTGGCAGCACC 698

Qy        238 roAspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnG 258
Db        699 CTGAGACCTGGGACCCG------AGTTACTACTTGCTGCAGTTCCAGCTTCGATACCGAC 752

Qy        258 lyLysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValV 278
Db        753 CTGTATGGTCAAAGGAG---TTCACGGTGTTGCTGCTCCCGGTGGCCCAGTACCAATGCG 809

Qy        278 alCysHisLysAspAlaLys--------------IleArgValGlnAlaArgAspArgT 293
Db        810 TCATCCATGATGCCTTGCGAGGAGTGAAGCACGTGGTCCAGGTCCGTGGGAAGGAGGAGC 869

Qy        293 yrTyrSerSerSerTrpSerAsnTrpAla 302
Db        870 TTGACCTTGGCCAGTGGAGTGAATGGTCC 898

RESULT 3
US-11-145-307A-52
; Sequence 52, Application US/11145307A
; Publication No. US20060094035A1
; GENERAL INFORMATION:
;  APPLICANT: Arcturus Bioscience, Inc.
;  APPLICANT:  Erlander, Mark G.
;  APPLICANT:  Ma, Xiao-Jun
;  TITLE OF INVENTION: Identification of Tumors
;  FILE REFERENCE: 022041-002020US
;  CURRENT APPLICATION NUMBER: US/11/145,307A
;  CURRENT FILING DATE:  2005-06-03
;  PRIOR APPLICATION NUMBER: US 60/577,084
;  PRIOR FILING DATE: 2004-06-04
;  NUMBER OF SEQ ID NOS: 268
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
;   LENGTH: 1923
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-145-307A-52

Alignment Scores:
Pred. No.:              5.06e-10      Length:         1923
Score:                  176.00        Matches:        79
Percent Similarity:     37.8%         Conservative:   40
Best Local Similarity:  25.1%         Mismatches:     105
Query Match:            10.7%         Indels:         93
DB:                     7             Gaps:           17

US-10-821-670A-27 (1-307) x US-11-145-307A-52 (1-1923)

Qy         21 GlyGluMetValValLeuThrCysAsnThrProGluGluAsp---AspIleThrTrpThr 39
Db        264 GGCTCTGACGTGACACTGCCATGTGGGACAGCAAACTGGGATGCTGCGGTGACGTGGCGG 323

Qy         40 ---------SerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGln 56
Db        324 GTAAATGGGACAGACCTGGCCCCTGACCTGCTC---AACGGCTCTCAGCTGGTGCTCCAT 380

Qy         57 ValLysGluPheAlaAspAlaGlyGlnTyrThrCys---HisLysGlyGlyGluValLeu 75
Db        381 GGCCTGGAACTGGGCCACAGTGGCCTCTACGCCTGCTTCCACCGTGACTCCTGGCACCTG 440

Qy         76 SerHisSerPheLeuLeu---------IleHisLysLysGluAspGlyIleTrpSerThr 92
Db        441 CGCCACCAAGTCCTGCTGCATGTGGGCTTGCCGCCGCGGGAGCCT-------------- 485

Qy         93 AspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLys 112
Db        486 ------------------------------------GTGCTCAGCTGCCGCTCCAAC 506

Qy        113 AsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPhe 132
Db        507 ACTTACCCCAAGGGCTTCTACTGCAGCTGGCATCTGCCCACCCCCACCTACATT------ 560

Qy        133 ThrValLysSerSerArgGlySerSerAspProGlnGluValThrCysGlyAlaAlaThr 152
Db        561 ----------------------------CCCAAC------ACCTTCAATGTGACTGTG 584

Qy        153 LeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrValGluCys 172
Db        585 CTGCATGGCTCCAAAATTATGGTC--------------------------------TGT 611

Qy        173 GlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValValValAsp 192
Db        612 GA-GAAGGA---------CCCAGCCCTCAAGAACCGCTGCCACATTCGCTACATGCACCT 661

Qy        193 AlaIleHisLysLeuLysTyrGlu--------------------------------Asn 201
Db        662 GTTCTCCACC--ATCAAGTACAAGGTCTCCATAAGTGTCAGCAATGCCCTGGGCCACAAT 719

Qy        202 TyrThrSerSerPhePheIleArg---AspIleIleLysProAspProProLysAsnLeu 220
Db        720 GCCACAGCTATCACCTTTGACGAGTTCACCATTGTGAAGCCTGATCCTCCAGAAAATGTG 779

Qy        221 GlnLeuLysProLeu---LysAsnSerArgHisValGluValSerTrpGluTyrProAsp 239
Db        780 GTAGCCCGGCCAGTGCCCAGCAACCCTCGCCGGCTGGAGGTGACGTGGCAGACCCCCTCG 839

Qy        240 ThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLys 259
Db        840 ACCTGGCCTGACCCTGAGTCT---TTTCCTCTCAAGTTCTTTCTGCGCTACCGA------ 890

Qy        260 AsnAsnArgGluLysLysAspArgLeuSerValAspLys---------------------- 272
Db        891 ----------------------CCCCTCATCCTGGACCAGTGGCAGCATGTGGAGCTGTCC 929

Qy        273 ---------------ThrSerAlaLysValValCysHisLysAspAlaLysIleArgVal 287
Db        930 GACGGCACAGCACACACCATCACAGATGCCTACGCCGGGAAGGAGTACATTATCCAGGTG 989

Qy        288 GlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAla 302
Db        990 GCAGCCAAGGACAATGAGATT---GGGACATGGAGTGACTGGAGC 1031

RESULT 4
US-11-297-134-9
; Sequence 9, Application US/11297134
; Publication No. US20060111297A1
; GENERAL INFORMATION:
;  APPLICANT: Genzyme Corporation
;  APPLICANT:  Roberts, Bruce
;  TITLE OF INVENTION: BLOOD FACTOR DOMAINS
;  FILE REFERENCE: 5270C
;  CURRENT APPLICATION NUMBER: US/11/297,134
;  CURRENT FILING DATE:  2005-12-08
;  PRIOR APPLICATION NUMBER: PCT/US2005/018461
;  PRIOR FILING DATE: 2004-06-09
;  PRIOR APPLICATION NUMBER: US 60/477,291
;  PRIOR FILING DATE: 2003-06-09
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
;   LENGTH: 1161
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-297-134-9

Alignment Scores:
Pred. No.:              1.49e-05      Length:         1161
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Score:                 132.50        Matches:       52
Percent Similarity:    38.9%         Conservative:  36
Best Local Similarity: 23.0%         Mismatches:    81
Query Match:           8.0%          Indels:        57
DB:                    7             Gaps:          9

US-10-821-670A-27 (1-307) x US-11-297-134-9 (1-1161)

Qy        107 LeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIle 126
              ::::::|||   |||      |||                |||   |||
Db        110 GTGCAATGCCGAGCCTCTCGGTACCCGATCGCCGTGGATTGCTCCTGGACCCTGCCGCCT 169

Qy        127 SerThrAspLeuLysPheThrValLys--------------------------SerSer 137
              :::   :::            |||                          ::::::
Db        170 GCTCCAAACTCCACCAGCCCCGTGTCCTTCATTGCCACGTACAGGCTCGGCATGGCTGCC 229

Qy        138 ArgGlySerSerAspPro---------GlnGluValThrCysGlyAlaAlaThrLeuSer 154
              ||||||  |||  |||          |||      |||      :::   |||::::::
Db        230 CGGGGCCACAGCTGGCCCTGCCTGCAGCAGACGCCAACGTCCACCAGCTGCACCATCACG 289

Qy        155 AlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGlu 174
                                     |||   :::   :::::::::
Db        290 --------------------------GATGTCCAGCTGTTCTCCATG------------ 310

Qy        175 GlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIle 194
                                                |||      :::   |||  |||:::
Db        311 ----------------------------GCTCCCTACGTGCTCAATGTCACCGCCGTC 340

Qy        195 HisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysPro 214
              |||             :::          |||                ||||||||||||
Db        341 CACCCCTGGGGCTCCAGCAGCAGCTTCGTGCCTTTCATAACAGAGCACATCATCAAGCCC 400

Qy        215 AspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSer 234
              |||||||||:::   ::::::|||  ||||||        ||||||||:::|||
Db        401 GACCCTCCAGAAGGCGTGCGCCTAAGCCCCCTCGCT---GAGCGCCACGTACAGGTGCAG 457

Qy        235 TrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyVal 254
              ||||||  |||  :::|||      |||          |||||||||   :::   :::
Db        458 TGGGAGCCTCCCGGGTCCTGGCCCTTCCCA---GAGATCTTCTCACTGAAGTACTGGATC 514

Qy        255 GlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSer 274
              :::   :::   :::          :::      |||:::      :::   :::
Db        515 CGTTACAAG---CGTCAGGGAGCTGCGCGCTTCCACCGGGTGGGGCCCATTGAAGCCACG 571

Qy        275 AlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyr 294
              :::   ::::::                        |||:::   |||  |||||||||
Db        572 TCCTTCATCCTC-----------------AGGGCTGTGCGGCCCCGAGCCAGGTACTAC 613

Qy        295 ---------------------------------------SerSerSerTrpSerAsnTrp 301
                                                    |||   ||||||
Db        614 GTCCAAGTGGCGGCTCAGGACCTCACAGACTACGGGGAACTGAGTGACTGGAGTCTCCCC 673

Qy        302 AlaSerValSerCysSer 307
              |||:::   :::   |||
Db        674 GCCACTGCCACAATGAGC 691

RESULT 5
US-11-293-697-1946
; Sequence 1946, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1946
;   LENGTH: 2534
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1946

Alignment Scores:
Pred. No.:             0.0433        Length:        2534
Score:                 105.50        Matches:       62
Percent Similarity:    35.6%         Conservative:  33
Best Local Similarity: 23.2%         Mismatches:    107
Query Match:           6.4%          Indels:        65
DB:                    7             Gaps:          13

US-10-821-670A-27 (1-307) x US-11-293-697-1946 (1-2534)

Qy         24 ValValLeuThrCysAsnThrProGlu---GluAspAspIleThrTrpThrSerAsp--- 41
              :::   |||  |||       :::   |||      :::   |||      |||
Db        298 CTGGCCCTGCAGTGTGAAGTCTCTGACCCCGAGGCCCATGTGGTGTGGCGCAAAGATGGC 357

Qy         42 -----------------GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIle 55
                                        :::   |||   :::       |||      :::
Db        358 GTGCAGCTGGGCCCCAGTGACAAGTATGACTTCCTGCACACGGCGGGCACGCGGGGGCTC 417

Qy         56 GlnValLysGluPheAla------AspAlaGlyGlnTyrThrCysHisLysGlyGlyGlu 73
                 |||   :::   :::      |||||||||   ||||||||||||   |||   |||
Db        418 GTGGTGCATGACGTGAGCCCTGAAGACGCCGGCCTGTACACCTGCCACGTGGGCTCCGAG 477

Qy         74 ValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAsp 93
                  :::   :::   :::   :::|||              ||||||
Db        478 GAG---ACCCGGGCCCGGGTCCGCGTGCACGATCTGCACGTGGGCATC------------ 522

Qy         94 IleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsn 113
                        |||      |||           |||:::   |||
Db        523 -----------ACCAAGAGGCTGAAGACAATGGAGGTGCTGGAAGGGGAA--------- 561

Qy        114 TyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThr 133
                 |||      |||   |||
Db        562 ---AGCTGCAGCTTTGAGTGC-------------------------------------- 579

Qy        134 ValLysSerSerArgGlySerSerAspProGlnGluValThrCysGlyAlaAlaThrLeu 153
              |||  |||       :::|||||||||          |||   |||      |||:::
Db        580 GTCCTGTCCCACGAGAGTGCCAGCGACCCGGCCATGTGGACAGTCGGTGGGAAGACAGTG 639

Qy        154 SerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGln 173
                 :::                      |||      :::||||||   :::      :::
Db        640 GGCAGCTCCAGCCGCTTCCAGGCCACACGTCAGGGCCGAAAATACATCCTGGTGGTCCGG 699

Qy        174 GluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValValValAspAla 193
              |||   :::          |||   |||                        ||||||   :::
Db        700 GAGGCTGCACCAAGTGATGCCGGGGAG--------------------GTGGTCTTCTCT 738

Qy        194 IleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLys 213
                 :::      |||      :::      :::|||      :::|||
Db        739 GTGCGGGGCCTCACCTCCAAG---------GCCTCACTCATTGTCAGA------------ 777

Qy        214 ProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluVal 233
                 :::   |||      :::   :::|||||||||:::
Db        778 ---GAGAGGCCGGCCACCATC---ATCAAGCCCCTGGAA-------------------- 810

Qy        234 SerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGly 253
                       |||   |||      |||                |||
Db        811 --------------GACCAGTGGGTGGCGCCAGGGGAGGACGTGGAGCTGCGCTGTGAG 855

Qy        254 ValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThr 273
                 :::         |||                    |||||||||   ::::::   |||:::
Db        856 CTGTCACGGGCGGGAACGCCCGTGCACTGGCTGAAGGACAGGAAGGCCATCCGCAAGAGC 915

Qy        274 SerAla---LysValValCys 279
                       |||||||||
Db        916 CAGAAGTATGATGTGGTCTGC 936

RESULT 6
US-10-511-937-349
; Sequence 349, Application US/10511937
; Publication No. US20060088836A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: EXPRESSION DIAGNOSTICS, INC.
;  APPLICANT:  Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  APPLICANT:  Prentice, James
;  APPLICANT:  Morris, MacDonald
;  APPLICANT:  Rosenberg, Steven
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
;  TITLE OF INVENTION:  AND MONITORING TRANSPLANT REJECTION
;  FILE REFERENCE: 506612000104
;  CURRENT APPLICATION NUMBER: US/10/511,937
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: PCT/US2003/012946
;  PRIOR FILING DATE: 2003-04-24
;  PRIOR APPLICATION NUMBER: US 10/131,831
;  PRIOR FILING DATE: 2002-04-24
;  PRIOR APPLICATION NUMBER: US 10/325,899
;  PRIOR FILING DATE: 2002-12-20
;  NUMBER OF SEQ ID NOS: 3117
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 349
;   LENGTH: 2341
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-511-937-349

Alignment Scores:
Pred. No.:                0.177          Length:          2341
Score:                    99.50          Matches:           69
Percent Similarity:       31.8%          Conservative:      37
Best Local Similarity:    20.7%          Mismatches:        89
Query Match:              6.0%           Indels:           139
DB:                       6              Gaps:              14

US-10-821-670A-27 (1-307) x US-10-511-937-349 (1-2341)

Qy          3 GluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaProGlyGlu 22
              :::|||   |||   |||     :::|||     |||:::           :::
Db        356 GATCTCCCAAAGGCTGTGGTGTTCCTGGAGCCTCAATGGTACAGGGTGCTCGAGAAGGAC 415

Qy         23 MetValValLeuThrCysAsn---------ThrProGluGluAspAspIleThrTrpThr 39
                |||   |||   |||           :::||||||:::::         |||
Db        416 AGTGTGACTCTGAAGTGCCAGGGAGCCTACTCCCCTGAGGACAATTCCACACAGTGGTTT 475

Qy         40 SerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGlu 59
                ::::::|||     :::               :::      |||
Db        476 CACAATGAGAGCCTC---ATCTCAAGCCAGGCCTCGAGCTACTTCATTGACGCTGCCACA 532

Qy         60 PheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPhe 79
                |||:::|||:::|||   |||                    ||||||
Db        533 GTCGACGACAGTGGAGAGTACAGGTGCCAGACAAACCTCTCCACCCTCAGTGACCCGGTG 592

Qy         80 LeuLeu-----------------------------------------IleHisLysLys 85
                |||                                        :::   |||:::
Db        593 CAGCTAGAAGTCCATATCGGCTGGCTGTTGCTCCAGGCCCCTCGGTGGGTGTTCAAGGAG 652

Qy         86 GluAspGlyIle-----------------TrpSerThrAspIleLeu------------ 95
              ||||||   |||                 |||          |||
Db        653 GAAGACCCTATTCACCTGAGGTGTCACAGCTGGAAGAACACTGCTCTGCATAAGGTCACA 712

Qy         95 ------------------------------------------------------------ 95

Db        713 TATTTACAGAATGGCAAAGGCAGGAAGTATTTTCATCATAATTCTGACTTCTACATTCCA 772

Qy         96 ----------------------------------ArgGluGlnLysGluSerLysAsn 103
                                                 |||          |||||||||
Db        773 AAAGCCACACTCAAAGACAGCGGCTCCTACTTCTGCAGGGGGCTTGTTGGGAGTAAAAAT 832

Qy        104 LysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe--------------- 118
                :::|||     ||||||     :::::|||   ||||||
Db        833 GT-GTCTTCAGAGACTGTGAACATCACCATCACTCA---AGGTTTGGCAGTGTCAACCAT 888

Qy        119 ------------ThrCysTrp-Trp------------------------------LeuTh 124
                         :::   ||| :::                              |||
Db        889 CTCATCATTCTTTCCACCTGGGTACCAAGTCTCTTTCTGCTTGGTGATGGTACTCCTTTT 948

Qy        124 rAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSer-------- 141
               |||:::   |||   |||   |||:::||||||::::::      ||||||
Db        949 TGCAGTGGACACAGGACTATATTTCTCTGTGAAGACAAACATTCGAAGCTCAACAAGAGA 1008

Qy        142 -------------------------------AspProGln--------------------- 144
                                            |||||||||
Db       1009 CTGGAAGGACCATAAATTTAAATGGAGAAAGGACCCTCAAGACAAATGACCCCCATCCCA 1068

Qy        145 ---------------------------------GluValThrCysGlyAlaAlaThrLe 153
                                               |||         |||   ||||||||
Db       1069 TGGGGGTAATAAGAGCAGTAGCAGCAGCATCTCTGAACATTTCTCTGGATTTGCAACCCT 1128

Qy        153 uSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGl 173
               ||||:::      :::          :::|||   ::::::                ||
Db       1129 ATCATCCTCAGGCCTCTCTACAAGCAGCAGGAAACATAGA--------------ACTCA 1173

Qy        173 nGluGlySerAlaCysProAlaAlaGluGluSerLeu---------------------- 185
               |              |||       :::   ||||||
Db       1174 GAGCCAGATCCCTTATCCAACTCTCGACTTTTCCTTGGTCTCCAGTGGAAGGGAAAAGCC 1233

Qy        186 ----------------------ProIleGluValValValAspAlaIleHis------Ly 196
                                   |||   |||                 :::|||      ||
Db       1234 CATGATCTTCAAGCAGGGAAGCCCCAGTGAG------------TAGCTGCATTCCTAGAA 1281

Qy        196 sLeuLysTyrGluAsnTyrThrSerSerPhePheIle 208
               |||||||:::::::::||||||::::::|||   :::
Db       1282 ATTGAAGTTTCAGAGCTACACAAACACTTTTTCTGTC 1318

RESULT 7
US-10-511-937-358
; Sequence 358, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
;  APPLICANT: EXPRESSION DIAGNOSTICS, INC.
;  APPLICANT:  Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  APPLICANT:  Prentice, James
;  APPLICANT:  Morris, MacDonald
;  APPLICANT:  Rosenberg, Steven
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
;  TITLE OF INVENTION:  AND MONITORING TRANSPLANT REJECTION
;  FILE REFERENCE: 506612000104
;  CURRENT APPLICATION NUMBER: US/10/511,937
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: PCT/US2003/012946
;  PRIOR FILING DATE: 2003-04-24
;  PRIOR APPLICATION NUMBER: US 10/131,831
;  PRIOR FILING DATE: 2002-04-24
;  PRIOR APPLICATION NUMBER: US 10/325,899
;  PRIOR FILING DATE: 2002-12-20
;  NUMBER OF SEQ ID NOS: 3117
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 358
;   LENGTH: 3646
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-511-937-358

Alignment Scores:
Pred. No.:                0.718          Length:          3646
Score:                    96.50          Matches:           66
Percent Similarity:       37.4%          Conservative:      54
Best Local Similarity:    20.6%          Mismatches:       137
Query Match:              5.9%           Indels:            65
DB:                       6              Gaps:              13
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US-10-821-670A-27 (1-307) x US-10-511-937-358 (1-3646)

Qy         17 ProAspAlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIle 36
Db        611 CCACAGAAACCTGCTGCCCTGCTCTGCAGAGGCCTCACTCAGCCT-----------CTG 658

Qy         37 ThrTrpThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGln 56
Db        659 CTCTGGACCAGTCTCCATGTGCTCAGCCCACAATGCCCTGGCAAGATGGA-CCAAAGCAG 717

Qy         57 ValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSer 76
Db        718 ACCTCCCCAAGTAGAGAAGCTTCAGCTCTGACAGCAGAGGGTGGAAGCTGCCTCATCTCA 777

Qy         77 ----------------HisSerPheLeuLeuIleHisLysLysGluAspGlyIle--- 89
Db        778 GGACTCCAGCCTGGCAACTCCTACTGGCTGCAGCTGCGCAGCGAACCTGATGGGATCTCC 837

Qy         90 --------------------TrpSerThrAspIleLeuArgGluGlnLysGluSerLys 102
Db        838 CTCGGTGGCTCCTGGGGATCCTGGTCCCTCCCTGTGACTGTGGACCTGCCTGGAGATGCA 897

Qy        103 AsnLysIlePheLeuLysCys---------GluAlaLysAsnTyrSerGlyArgPheThr 119
Db        898 GTGGCACTTGGACTGCAATGCTTTACCTTGGACCTGAAGAAT-----------GTTACC 945

Qy        120 CysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGly 139
Db        946 TGTCAATGGCAGCAACAGGACCATGCTAGCTCCCAAGGCTTCTTCTACCACAGCAGGGCA 1005

Qy        140 -SerSerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValAr 159
Db       1006 CGGTGCTGCCCCAGAGACAGGTACCCCATCTGGGAGAACT------GCGAAGAGGAAGAG 1059

Qy        159 gValAspAsnArgAspTyrLysLysTyrThr-ValGluCysGlnGluGlySerAlaCysP 179
Db       1060 AAAACAAATCCAGGACTACAGACCCCACAGTTCTC------------------------- 1094

Qy        179 roAlaAlaGluGluSerLeuProIleGluValValVal-AspAlaIleHisLysLeuLys 198
Db       1095 -------------TCGCTGCCACTTCAAGTCACGAAATGACAGCATTATTCACATCCTT 1140

Qy        199 TyrGluAsnTyrThr----------------------------SerSerPhePheIle 208
Db       1141 GTGGAGGTGACCACAGCCCCGGGTACTGTTCACAGCTACCTGGGCTCCCCTTTCTGGATC 1200

Qy        209 ArgAspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSer 228
Db       1201 CACCAGGCTGTGCGCCTC---CCCACCCCAAACTTGCACTGGAGGGAGATC---TCCAGT 1254

Qy        229 ArgHisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPhe 248
Db       1255 GGGCATCTGGAATTGGAGTGGCAGCACCCATCGTCCTGGGCAGCCCAAGAGACCTGTTAT 1314

Qy        249 SerLeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGlu---LysLysAspArg 267
Db       1315 CAACTCCGATAC------------ACAGGAGAAGGCCATCAGGACTGGAAGGTGCTGGAG 1362

Qy        268 LeuSerValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgVal 287
Db       1363 CCGCCTCTCGGGGCCCGAGGAGGGACCCTGGAGCTGCGCCCGCGATCTCGCTACCGTTTA 1422

Qy        288 GlnAlaArgAspArgTyr------------TyrSerSerSerTrpSerAsnTrpAla 302
Db       1423 CAGCTGCGCGCCAGGCTCAACGGCCCCACCTACCAAGGTCCCTGGAGCTCGTGGTCG 1479

RESULT 8
US-10-505-928-651
; Sequence 651, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
;  APPLICANT: Ludwig Institute for Cancer Research et al.
;  TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
;  FILE REFERENCE: 28967/39178
;  CURRENT APPLICATION NUMBER: US/10/505,928
;  CURRENT FILING DATE:  2004-08-27
;  PRIOR APPLICATION NUMBER: US 60/363,019
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: PatentIn 3.2
; SEQ ID NO 651
;   LENGTH: 3597
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-505-928-651

Alignment Scores:
Pred. No.:                1.51          Length:          3597
Score:                    93.50         Matches:         55
Percent Similarity:       34.0%         Conservative:    28
Best Local Similarity:    22.5%         Mismatches:      73
Query Match:              5.7%          Indels:          89
DB:                       6             Gaps:            11

US-10-821-670A-27 (1-307) x US-10-505-928-651 (1-3597)

Qy        113 AsnTyrSerGlyArgPheThrCysTrpTrpLeu-----------ThrAlaIleSerThr 128
Db        284 GACTACATGAGCATCTCTACTTGCGAGTGGAAGATGAATGGTCCCACCAATTGCAGCACC 343

Qy        129 AspLeuLysPheThrValLys--------------SerSerArgGlySerSerAspPro 143
Db        344 GAGCTCCGCCTGTTGTACCAGCTGGTTTTTCTGCTCTCCGAAGCCCACACGTGTATCCCT 403

Qy        144 GlnGlu---------ValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
Db        404 GAGAACAACGGAGGCGCGGGGTGCGTGTGCCACCTGCTCATGGATGACGTGGTCAGTGCG 463

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGlu-CysGlnGluGlySerAlaCysProAl 180
Db        464 GATAAC---------------TATACACTGGACCTGTGGGCTGGGCAGCAGCTGCTGTGG 508

Qy        180 aAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGl 200
Db        509 AAGGGCTCCTTCAAG-CCCAGCGAG-----------------CAT-------------- 535

Qy        200 uAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLe 220
Db        536 --------------------------------GTGAAACCCAGGGCCCCAGGAAACCT 561

Qy        220 uGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspTh 240
Db        562 GACAGTT--------------------CACACCAATGTCTCCGACACTCTGCTGCTGAC 600

Qy        240 rTrpSerThrProHisSer--------------TyrPheSerLeuThrPheGlyValGl 255
Db        601 CTGGAGCAACCCGTATCCCCCTGACAATTACCTGTATAATCATCTCACCTATGCAGTCAA 660

Qy        255 nValGlnGlyLysAsnAsn--------------------------------ArgGluLy 264
Db        661 CATTTGGAGTGAAAACGACCCGGCAGATTTCAGAATCTATAACGTGACCTACCTAGAACC 720

Qy        264 sLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHisLysAspAlaLy 284
Db        721 CTCCCTCCGCATCGCAGCCAGCACCCTGAAGTCTGGGATT------------TCCTACAG 768

Qy        284 sIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAla----- 302
Db        769 GGCACGGGTGAGGGCCTGGGCTCAGTGCTATAACACCACCTGGAGTGAGTGGAGCCCCAG 828

Qy        303 ----------------------------------------------------------Se 303
Db        829 CACCAAGTGGCACAACTCCTACAGGGAGCCCTTCGAGCAGCACCTCCTGCTGGGCGTCAG 888

Qy        303 rValSerCys 306
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```
Db        889 CGTTTCCTGC 898

RESULT 9
US-10-511-937-2802
; Sequence 2802, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
;  APPLICANT: EXPRESSION DIAGNOSTICS, INC.
;  APPLICANT:  Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  APPLICANT:  Prentice, James
;  APPLICANT:  Morris, MacDonald
;  APPLICANT:  Rosenberg, Steven
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
;  TITLE OF INVENTION:  AND MONITORING TRANSPLANT REJECTION
;  FILE REFERENCE: 506612000104
;  CURRENT APPLICATION NUMBER: US/10/511,937
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: PCT/US2003/012946
;  PRIOR FILING DATE: 2003-04-24
;  PRIOR APPLICATION NUMBER: US 10/131,831
;  PRIOR FILING DATE: 2002-04-24
;  PRIOR APPLICATION NUMBER: US 10/325,899
;  PRIOR FILING DATE: 2002-12-20
;  NUMBER OF SEQ ID NOS: 3117
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2802
;   LENGTH: 3597
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-511-937-2802

Alignment Scores:
Pred. No.:              1.51          Length:        3597
Score:                  93.50         Matches:       55
Percent Similarity:     34.0%         Conservative:  28
Best Local Similarity:  22.5%         Mismatches:    73
Query Match:            5.7%          Indels:        89
DB:                     6             Gaps:          11

US-10-821-670A-27 (1-307) x US-10-511-937-2802 (1-3597)

Qy        113 AsnTyrSerGlyArgPheThrCysTrpTrpLeu------------ThrAlaIleSerThr 128
              :::|||          ||||||   |||             |||       ||||||
Db        284 GACTACATGAGCATCTCTACTTGCGAGTGGAAGATGAATGGTCCCACCAATTGCAGCACC 343

Qy        129 AspLeuLysPheThrValLys---------------SerSerArgGlySerSerAspPro 143
              :::|||:::        :::               |||         :::      |||
Db        344 GAGCTCCGCCTGTTGTACCAGCTGGTTTTTCTGCTCTCCGAAGCCCACACGTGTATCCCT 403

Qy        144 GlnGlu---------ValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
              :::              |||           |||       :::   |||
Db        404 GAGAACAACGGAGGCGCGGGGTGCGTGTGCCACCTGCTCATGGATGACGTGGTCAGTGCG 463

Qy        161 AspAsnArgAspTyrLysLysTyrThrValGlu-CysGlnGluGlySerAlaCysProAl 180
              ||||||              ||||||:::::: |||     ||||||:::|||
Db        464 GATAAC--------------TATACACTGGACCTGTGGGCTGGGCAGCAGCTGCTGTGG 508

Qy        180 aAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGl 200
                  |||   |||   |||                 |||
Db        509 AAGGGCTCCTTCAAG-CCCAGCGAG-----------------CAT-------------- 535

Qy        200 uAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLe 220
                                          :::||||||      |||   |||||
Db        536 --------------------------------GTGAAACCCAGGGCCCCAGGAAACCT 561

Qy        220 uGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspTh 240
              |   :::                   |||      ||||||                ||
Db        562 GACAGTT-------------------CACACCAATGTCTCCGACACTCTGCTGCTGAC 600

Qy        240 rTrpSerThrProHisSer--------------TyrPheSerLeuThrPheGlyValGl 255
              |||||||   |||:::                  |||      ||||||:::   |||
Db        601 CTGGAGCAACCCGTATCCCCCTGACAATTACCTGTATAATCATCTCACCTATGCAGTCAA 660

Qy        255 nValGlnGlyLysAsnAsn--------------------------------ArgGluLy 264
               :::      :::|||:::                                  |||
Db        661 CATTTGGAGTGAAAACGACCCGGCAGATTTCAGAATCTATAACGTGACCTACCTAGAACC 720

Qy        264 sLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHisLysAspAlaLy 284
                  |||::::::                 :::   :::              ::
Db        721 CTCCCTCCGCATCGCAGCCAGCACCCTGAAGTCTGGGATT------------TCCTACAG 768

Qy        284 sIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAla----- 302
              :   ||||||:::|||      :::   |||:::::::::||||||   |||:::
Db        769 GGCACGGGTGAGGGCCTGGGCTCAGTGCTATAACACCACCTGGAGTGAGTGGAGCCCCAG 828

Qy        303 ----------------------------------------------------------Se 303
                                                                         ||
Db        829 CACCAAGTGGCACAACTCCTACAGGGAGCCCTTCGAGCAGCACCTCCTGCTGGGCGTCAG 888

Qy        303 rValSerCys 306
              |||||||||
Db        889 CGTTTCCTGC 898

RESULT 10
US-11-293-697-2331
; Sequence 2331, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2331
;   LENGTH: 2582
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-2331

Alignment Scores:
Pred. No.:              1.36          Length:        2582
Score:                  92.00         Matches:       64
Percent Similarity:     35.1%         Conservative:  40
Best Local Similarity:  21.6%         Mismatches:    123
Query Match:            5.6%          Indels:        69
DB:                     7             Gaps:          14

US-10-821-670A-27 (1-307) x US-11-293-697-2331 (1-2582)

Qy          6 LysAsnValTyrValValGluLeuAspTrpHisProAspAlaProGlyGluMetValVal 25
              |||   |||  ::::::          |||             ||||||   |||
Db        286 AAAGCTGTACTTCTCCTCAATCCTCCATGGTCCACAGCCTTCAAAGGAGAAAAAGTGGCT 345

Qy         26 LeuThrCysAsnThrProGlu------------GluAspAspIleThrTrpThrSerAsp 41
              |||   |||::::::                :::   |||      |||      |||
Db        346 CTCATATGCAGCAGCATATCACATTCCCTAGCCCAGGGAGACACATATTGGTATCACGAT 405

Qy         42 GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheAla 61
              :::             :::         |||         ||||||:::   |||
Db        406 GAGAAGTTGTTGAAAATAAAACATGACAAG---------ATCCAAATTACAGAG------ 450

Qy         62 AspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeuLeu 81
                 |||   |||   |||          |||       ||||||   :::
Db        451 ---CCTGGAAATTACCAATGTAAGACCCGAGGATCCTCCCTCAGTGATGCC--------- 498

Qy         82 IleHisLysLysGluAspGlyIleTrp---SerThrAspIleLeuArgGluGlnLysGlu 100
              :::|||   :::             |||               |||       |||
Db        499 GTGCATGTGGAAATTTTCACCTGACTGGCTGATCCTGCAGGCTTTACATCCTGTCTTTGAA 558
```

```
Qy        101 SerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCys 120
Db        559 GGAGACAAT---GTCATTCTGAGATGTCAGGGGAAAGACAACAAA-------------- 600

Qy        121 TrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySer 140
Db        601 ------------------AACACTCATCAAAAGGTTTACTACAAGGAT------GGAAAA 636

Qy        141 SerAspProGlnGluValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgVal 160
Db        637 CAGCTTCCTAAT--------------------AGTTATAATTTAGAGAAGATCACAGTG 675

Qy        161 Asp------AsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 178
Db        676 AATTCAGTCTCCAGGGATAATAGCAAATAT-----------------------CATTGT 711

Qy        179 ProAlaAlaGluGlu------SerLeuProIleGluValValValAspAlaIleHisLys 196
Db        712 ACTGCTTATAGGAAGTTTTACATACTTGACATTGAAGTAACTTCAAAACCCCTAAATATC 771

Qy        197 LeuLysTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspPro 216
Db        772 CAAGTTCAAGAG--------------CTGTTTCTACATCCTGTGCTGAGAGCCAGCTCT 816

Qy        217 ProLysAsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGlu 236
Db        817 TCCACGCCCATAGAGGGGAGTCCCATGACCCTGACCTGTGAGACCCAGCTCTCTCCACAG 876

Qy        237 TyrProAspThr---------------------------------------------- 240
Db        877 AGGCCAGATGTCCAGCTGCAATTCTCCCTCTTCAGAGATAGCCAGACCCTCGGATTGGGC 936

Qy        241 TrpSerThr-ProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAs 260
Db        937 TGGAGCAGGTCCCCCAAACTCCAGATCCCTGCCATGTGGACTGAAGACTCAGGGTCTTAC 996

Qy        260 nAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAla 275
Db        997 TGGTGTGAGGTGGAGACAGTGACTCACAGCATCAAAAAAAGGAGCC 1042
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RESULT 11
US-11-313-450-1
; Sequence 1, Application US/11313450
; Publication No. US20060110778A1
; GENERAL INFORMATION:
; APPLICANT: Adorante, Joeseph S.
; APPLICANT: Ehring, George R.
; TITLE OF INVENTION: High-Throughput Screens For Identifying
; TITLE OF INVENTION: Selective Persistent Sodium Channels Channel Blockers
; FILE REFERENCE: 17407 CIP (AP)
; CURRENT APPLICATION NUMBER: US/11/313,450
; CURRENT FILING DATE: 2005-12-19
; PRIOR APPLICATION NUMBER: 09/989797
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252771
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 5997
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-313-450-1

Alignment Scores:

Pred. No.:	5.96	Length:	5997
Score:	91.00	Matches:	45
Percent Similarity:	34.7%	Conservative:	22
Best Local Similarity:	23.3%	Mismatches:	89
Query Match:	5.5%	Indels:	37
DB:	7	Gaps:	6

US-10-821-670A-27 (1-307) x US-11-313-450-1 (1-5997)

```
Qy         14 AspTrpHisProAspAlaProGlyGluMet-ValValLeuThrCysAsnThrProGluGl 33
Db       2898 GATTGGAAACCTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTCTGAGCTCATTTAGTGC 2957

Qy         33 uAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLe 53
Db       2958 AGACAACCTTGCAGCCACTGATGATGATAATGAAATG---------------AATAATCT 3002

Qy         53 uThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGl 73
Db       3003 CCAAATTGCTGTGGATAGGATGCACAAAGGAGTAGCTTATGTGAAAAGAAAAATATATGA 3062

Qy         73 uValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAs 93
Db       3063 ATTTATTCAACAGTCCTTCATTAGGAAACAAAAGATTTTAGATGAAATTAAACCACTTGA 3122

Qy         93 pIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAs 113
Db       3123 TGATCTAAACAACAAGAAAGACAGT--------------------TGTATGTCCAATCA 3161

Qy        113 nTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheTh 133
Db       3162 T--------------------------ACAACAGAAATTGGGAAAGATCTTGACTATCT 3194

Qy        133 rValLysSerSerArgGlySerSerAspProGlnGluValThrCysGlyAlaAlaThr-- 152
Db       3195 T--------------------AAAGATGTAAATGGAACTACAAGTGGTATAGGAACTGG 3233

Qy        153 -LeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrValGluCy 172
Db       3234 CAGCAGTGTTGAAAAATACATTATTGATGAAAGTGATTACATGTCATTCATAAACAAC-- 3291

Qy        172 sGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValValValAs 192
Db       3292 ------------------CCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGAGAATC 3332

Qy        192 pAlaIleHisLysLeuLysTyrGluAsnTyrThrSer 204
Db       3333 TGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGT 3369
```

RESULT 12
US-11-263-326-90
; Sequence 90, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulley, John C
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT APPLICATION NUMBER: US/11/263,326
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US 10/482,834
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 90
; LENGTH: 8370
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-263-326-90

Alignment Scores:

Pred. No.:	9.66	Length:	8370
Score:	91.00	Matches:	45
Percent Similarity:	34.7%	Conservative:	22
Best Local Similarity:	23.3%	Mismatches:	89
Query Match:	5.5%	Indels:	37

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DB:                    7             Gaps:          6

US-10-821-670A-27 (1-307) x US-11-263-326-90 (1-8370)

Qy         14 AspTrpHisProAspAlaProGlyGluMet-ValValLeuThrCysAsnThrProGluGl 33
              ||||||   |||      |||      ::: :::   |||      ::::::
Db       3186 GATTGGAAACCTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTCTGAGCTCATTTAGTGC 3245

Qy         33 uAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLe 53
              |||::::::      |||   |||   :::                            ||
Db       3246 AGACAACCTTGCAGCCACTGATGATGATAATGAAATG--------------AATAATCT 3290

Qy         53 uThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGl 73
              |   |||   |||                     |||         |||       ||
Db       3291 CCAAATTGCTGTGGATAGGATGCACAAAGGAGTAGCTTATGTGAAAAGAAAAATATATGA 3350

Qy         73 uValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAs 93
              |   :::      ||||||:::         |||      |||   |||         ||
Db       3351 ATTTATTCAACAGTCCTTCATTAGGAAACAAAAGATTTTAGATGAAATTAAACCACTTGA 3410

Qy         93 pIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAs 113
              |   |||      :::|||:::|||                    |||   :::   ::
Db       3411 TGATCTAAACAACAAGAAAGACAGT--------------------TGTATGTCCAATCA 3449

Qy        113 nTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheTh 133
              :                              |||   |||      ||||||   :::
Db       3450 T--------------------------ACAACAGAAATTGGGAAAGATCTTGACTATCT 3482

Qy        133 rValLysSerSerArgGlySerSerAspProGlnGluValThrCysGlyAlaAlaThr-- 152
                                        |||          |||   |||      |||
Db       3483 T--------------------AAAGATGTAAATGGAACTACAAGTGGTATAGGAACTGG 3521

Qy        153 -LeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrValGluCy 172
               |||   ||||||     :::|||      ||||||     :::
Db       3522 CAGCAGTGTTGAAAAATACATTATTGATGAAAGTGATTACATGTCATTCATAAACAAC-- 3579

Qy        172 sGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValValValAs 192
                                 |||:::        ::::::||||||   |||
Db       3580 ------------------CCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGAGAATC 3620

Qy        192 pAlaIleHisLysLeuLysTyrGluAsnTyrThrSer 204
                       |||      |||:::::::::|||
Db       3621 TGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGT 3657

RESULT 13
US-11-263-326-95
; Sequence 95, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
;  APPLICANT: Wallace, Robyn H
;  APPLICANT:  Mulley, John C
;  APPLICANT:  Berkovic, Samuel F
;  TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
;  FILE REFERENCE: 1386/13/3
;  CURRENT APPLICATION NUMBER: US/11/263,326
;  CURRENT FILING DATE:  2005-10-31
;  PRIOR APPLICATION NUMBER: US 10/482,834
;  PRIOR FILING DATE: 2004-10-12
;  PRIOR APPLICATION NUMBER: PCT/AU2004/001051
;  PRIOR FILING DATE: 2004-08-06
;  PRIOR APPLICATION NUMBER: US 10/451,126
;  PRIOR FILING DATE: 2003-10-08
;  NUMBER OF SEQ ID NOS: 179
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 95
;   LENGTH: 8377
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-263-326-95

Alignment Scores:
Pred. No.:          9.67          Length:       8377
Score:             91.00          Matches:        45
Percent Similarity:     34.7%          Conservative:  22
Best Local Similarity:  23.3%          Mismatches:    89
Query Match:            5.5%           Indels:        37
DB:                     7              Gaps:          6

US-10-821-670A-27 (1-307) x US-11-263-326-95 (1-8377)

Qy         14 AspTrpHisProAspAlaProGlyGluMet-ValValLeuThrCysAsnThrProGluGl 33
              ||||||   |||      |||      ::: :::   |||      ::::::
Db       3197 GATTGGAAACCTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTCTGAGCTCATTTAGTGC 3256

Qy         33 uAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLe 53
              |||::::::      |||   |||   :::                            ||
Db       3257 AGACAACCTTGCAGCCACTGATGATGATAATGAAATG--------------AATAATCT 3301

Qy         53 uThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGl 73
              |   |||   |||                     |||         |||       ||
Db       3302 CCAAATTGCTGTGGATAGGATGCACAAAGGAGTAGCTTATGTGAAAAGAAAAATATATGA 3361

Qy         73 uValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAs 93
              |   :::      ||||||:::         |||      |||   |||         ||
Db       3362 ATTTATTCAACAGTCCTTCATTAGGAAACAAAAGATTTTAGATGAAATTAAACCACTTGA 3421

Qy         93 pIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAs 113
              |   |||      :::|||:::|||                    |||   :::   ::
Db       3422 TGATCTAAACAACAAGAAAGACAGT--------------------TGTATGTCCAATCA 3460

Qy        113 nTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheTh 133
              :                              |||   |||      ||||||   :::
Db       3461 T--------------------------ACAACAGAAATTGGGAAAGATCTTGACTATCT 3493

Qy        133 rValLysSerSerArgGlySerSerAspProGlnGluValThrCysGlyAlaAlaThr-- 152
                                        |||          |||   |||      |||
Db       3494 T--------------------AAAGATGTAAATGGAACTACAAGTGGTATAGGAACTGG 3532

Qy        153 -LeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrValGluCy 172
               |||   ||||||     :::|||      ||||||     :::
Db       3533 CAGCAGTGTTGAAAAATACATTATTGATGAAAGTGATTACATGTCATTCATAAACAAC-- 3590

Qy        172 sGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValValValAs 192
                                 |||:::        ::::::||||||   |||
Db       3591 ------------------CCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGAGAATC 3631

Qy        192 pAlaIleHisLysLeuLysTyrGluAsnTyrThrSer 204
                       |||      |||:::::::::|||
Db       3632 TGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGT 3668

RESULT 14
US-11-263-326-89
; Sequence 89, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
;  APPLICANT: Wallace, Robyn H
;  APPLICANT:  Mulley, John C
;  APPLICANT:  Berkovic, Samuel F
;  TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
;  FILE REFERENCE: 1386/13/3
;  CURRENT APPLICATION NUMBER: US/11/263,326
;  CURRENT FILING DATE:  2005-10-31
;  PRIOR APPLICATION NUMBER: US 10/482,834
;  PRIOR FILING DATE: 2004-10-12
;  PRIOR APPLICATION NUMBER: PCT/AU2004/001051
;  PRIOR FILING DATE: 2004-08-06
;  PRIOR APPLICATION NUMBER: US 10/451,126
;  PRIOR FILING DATE: 2003-10-08
;  NUMBER OF SEQ ID NOS: 179
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 89
;   LENGTH: 8380
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-263-326-89
```

```
Alignment Scores:
Pred. No.:              9.68          Length:         8380
Score:                  91.00         Matches:        45
Percent Similarity:     34.7%         Conservative:   22
Best Local Similarity:  23.3%         Mismatches:     89
Query Match:            5.5%          Indels:         37
DB:                     7             Gaps:           6

US-10-821-670A-27 (1-307) x US-11-263-326-89 (1-8380)

Qy         14 AspTrpHisProAspAlaProGlyGluMet-ValValLeuThrCysAsnThrProGluGl 33
              ||||||   |||      |||      ::: :::   |||      ::::::
Db       3196 GATTGGAAACCTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTCTGAGCTCATTTAGTGC 3255

Qy         33 uAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLe 53
              |||::::::      |||   |||   :::                            ||
Db       3256 AGACAACCTTGCAGCCACTGATGATGATAATGAAATG--------------AATAATCT 3300

Qy         53 uThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGl 73
              |   |||   |||                    |||          |||       ||
Db       3301 CCAAATTGCTGTGGATAGGATGCACAAAGGAGTAGCTTATGTGAAAAGAAAAATATATGA 3360

Qy         73 uValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAs 93
              |   :::      ||||||:::          |||      |||   |||          ||
Db       3361 ATTTATTCAACAGTCCTTCATTAGGAAACAAAAGATTTTAGATGAAATTAAACCACTTGA 3420

Qy         93 pIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAs 113
              |   |||      :::|||:::|||                        |||   :::   ::
Db       3421 TGATCTAAACAACAAGAAAGACAGT--------------------TGTATGTCCAATCA 3459

Qy        113 nTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheTh 133
              :                                  |||   |||      ||||||   :::
Db       3460 T--------------------------ACAACAGAAATTGGGAAAGATCTTGACTATCT 3492

Qy        133 rValLysSerSerArgGlySerSerAspProGlnGluValThrCysGlyAlaAlaThr-- 152
                                    |||          |||   |||      |||
Db       3493 T--------------------AAAGATGTAAATGGAACTACAAGTGGTATAGGAACTGG 3531

Qy        153 -LeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrValGluCy 172
               |||   ||||||      :::|||      ||||||      :::
Db       3532 CAGCAGTGTTGAAAAATACATTATTGATGAAAGTGATTACATGTCATTCATAAACAAC-- 3589

Qy        172 sGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValValValAs 192
                                 |||:::         ::::::||||||   |||
Db       3590 ------------------CCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGAGAATC 3630

Qy        192 pAlaIleHisLysLeuLysTyrGluAsnTyrThrSer 204
                     |||      |||:::::::::|||
Db       3631 TGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGT 3667

RESULT 15
US-11-263-326-1
; Sequence 1, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
;  APPLICANT: Wallace, Robyn H
;  APPLICANT:  Mulley, John C
;  APPLICANT:  Berkovic, Samuel F
;  TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
;  FILE REFERENCE: 1386/13/3
;  CURRENT APPLICATION NUMBER: US/11/263,326
;  CURRENT FILING DATE:  2005-10-31
;  PRIOR APPLICATION NUMBER: US 10/482,834
;  PRIOR FILING DATE: 2004-10-12
;  PRIOR APPLICATION NUMBER: PCT/AU2004/001051
;  PRIOR FILING DATE: 2004-08-06
;  PRIOR APPLICATION NUMBER: US 10/451,126
;  PRIOR FILING DATE: 2003-10-08
;  NUMBER OF SEQ ID NOS: 179
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
;   LENGTH: 8381
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-263-326-1

Alignment Scores:
Pred. No.:              9.68          Length:         8381
Score:                  91.00         Matches:        45
Percent Similarity:     34.7%         Conservative:   22
Best Local Similarity:  23.3%         Mismatches:     89
Query Match:            5.5%          Indels:         37
DB:                     7             Gaps:           6

US-10-821-670A-27 (1-307) x US-11-263-326-1 (1-8381)

Qy         14 AspTrpHisProAspAlaProGlyGluMet-ValValLeuThrCysAsnThrProGluGl 33
              ||||||   |||      |||      ::: :::   |||      ::::::
Db       3197 GATTGGAAACCTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTCTGAGCTCATTTAGTGC 3256

Qy         33 uAspAspIleThrTrpThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLe 53
              |||::::::      |||   |||   :::                          , ||
Db       3257 AGACAACCTTGCAGCCACTGATGATGATAATGAAATG--------------AATAATCT 3301

Qy         53 uThrIleGlnValLysGluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGl 73
              |   |||   |||                    |||          |||       ||
Db       3302 CCAAATTGCTGTGGATAGGATGCACAAAGGAGTAGCTTATGTGAAAAGAAAAATATATGA 3361

Qy         73 uValLeuSerHisSerPheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAs 93
              |   :::      ||||||:::          |||      |||   |||          ||
Db       3362 ATTTATTCAACAGTCCTTCATTAGGAAACAAAAGATTTTAGATGAAATTAAACCACTTGA 3421

Qy         93 pIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAs 113
              |   |||      :::|||:::|||                        |||   :::   ::
Db       3422 TGATCTAAACAACAAGAAAGACAGT--------------------TGTATGTCCAATCA 3460

Qy        113 nTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheTh 133
              :                                  |||   |||      ||||||   :::
Db       3461 T--------------------------ACAACAGAAATTGGGAAAGATCTTGACTATCT 3493

Qy        133 rValLysSerSerArgGlySerSerAspProGlnGluValThrCysGlyAlaAlaThr-- 152
                                    |||          |||   |||      |||
Db       3494 T--------------------AAAGATGTAAATGGAACTACAAGTGGTATAGGAACTGG 3532

Qy        153 -LeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThrValGluCy 172
               |||   ||||||      :::|||      ||||||      :::
Db       3533 CAGCAGTGTTGAAAAATACATTATTGATGAAAGTGATTACATGTCATTCATAAACAAC-- 3590

Qy        172 sGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluValValValAs 192
                                 |||:::         ::::::||||||   |||
Db       3591 ------------------CCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGAGAATC 3631

Qy        192 pAlaIleHisLysLeuLysTyrGluAsnTyrThrSer 204
                     |||      |||:::::::::|||
Db       3632 TGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGT 3668


Search completed: June 10, 2006, 01:22:18
Job time : 30.9725 secs
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OM nucleic - nucleic search, using sw model

Run on: June 10, 2006, 03:13:25 ; Search time 4065.4 Seconds
(without alignments)
15525.205 Million cell updates/sec

Title: US-10-821-670A-29
Perfect score: 987
Sequence: 1 atgcatcctcagcagttggt.....gggcatccgtgtcctgcagt 987

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	987	100.0	987	2	AR595950	AR595950 Sequence
c	2	987	100.0	987	2	AR595951	AR595951 Sequence
	3	985	99.8	985	2	AR595967	AR595967 Sequence
c	4	985	99.8	985	2	AR595968	AR595968 Sequence
	5	983.8	99.7	990	2	AX076200	AX076200 Sequence
	6	983.8	99.7	990	2	AX076482	AX076482 Sequence
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c	9	983.8	99.7	1599	2	AR595957	AR595957 Sequence
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	13	982.2	99.5	2193	2	AR280203	AR280203 Sequence
	14	982.2	99.5	2193	2	AR322418	AR322418 Sequence
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	18	921	93.3	921	2	AR322419	AR322419 Sequence
	19	919.4	93.2	921	2	AR242437	AR242437 Sequence
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	26	886.2	89.8	990	2	AR151071	AR151071 Sequence
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	28	886.2	89.8	990	2	E15017	E15017 Canine mRNA
	29	886.2	89.8	990	2	AR316470	AR316470 Sequence
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c	31	886.2	89.8	2267	2	AR596012	AR596012 Sequence
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c	33	883	89.5	987	2	AR595970	AR595970 Sequence
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	35	883	89.5	1599	2	AR595971	AR595971 Sequence
c	36	883	89.5	1599	2	AR595972	AR595972 Sequence
	37	875	88.7	990	2	BD014653	BD014653 Process f
	38	871.8	88.3	990	2	AR151061	AR151061 Sequence
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c	43	826.6	83.7	921	2	AR595966	AR595966 Sequence
	44	825	83.6	1533	2	AR595973	AR595973 Sequence
c	45	825	83.6	1533	2	AR595974	AR595974 Sequence

ALIGNMENTS

RESULT 1
AR595950
LOCUS AR595950 987 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 29 from patent US 6818444.
ACCESSION AR595950
VERSION AR595950.1 GI:56646931
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 987)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 29 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .987
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 100.0%; Score 987; DB 2; Length 987;
Best Local Similarity 100.0%; Pred. No. 1.6e-288;
Matches 987; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
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Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
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Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
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Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
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Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
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Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
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Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
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RESULT 2
AR595951/c
LOCUS       AR595951                 987 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 31 from patent US 6818444.
ACCESSION   AR595951
VERSION     AR595951.1  GI:56646932
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 31 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
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 Query Match           100.0%;  Score 987;  DB 2;  Length 987;
 Best Local Similarity  100.0%;  Pred. No. 1.6e-288;
 Matches  987;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
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Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
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Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
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Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
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Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

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Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
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Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
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Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

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Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
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Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
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Db         27 AGCAACTGGGCATCCGTGTCCTGCAGT 1
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RESULT 3
AR595967
LOCUS       AR595967                985 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 55 from patent US 6818444.
ACCESSION   AR595967
VERSION     AR595967.1  GI:56646948
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 985)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 55 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .985
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 6.5e-288;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
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Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
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Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
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Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
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Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
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Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
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RESULT 4
AR595968/c
LOCUS       AR595968                985 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 57 from patent US 6818444.
ACCESSION   AR595968
VERSION     AR595968.1  GI:56646949
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 985)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 57 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .985
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ORIGIN

  Query Match             99.8%;  Score 985;  DB 2;  Length 985;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-288;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
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Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
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Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
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Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
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Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
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Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
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Db         25 AGCAACTGGGCATCCGTGTCCTGCA 1


RESULT 5
AX076200
LOCUS       AX076200                990 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 1 from Patent WO0104155.
ACCESSION   AX076200
VERSION     AX076200.1  GI:12710825
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 1 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="feline IL-12 p40"
ORIGIN

  Query Match             99.7%;  Score 983.8;  DB 2;  Length 990;
  Best Local Similarity   99.8%;  Pred. No. 1.5e-287;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
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Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
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Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
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Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
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Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

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Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
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Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
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Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
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Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987


RESULT 6
AX076482
LOCUS       AX076482                990 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 8 from Patent WO0104280.
ACCESSION   AX076482
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VERSION     AX076482.1  GI:12711034
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 8 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Sequence coding for SEQ ID NO 2, IL-12 p40"
ORIGIN

  Query Match             99.7%;  Score 983.8;  DB 2;  Length 990;
  Best Local Similarity   99.8%;  Pred. No. 1.5e-287;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
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Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
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Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

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Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
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Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987


RESULT 7
FCIL12P40
LOCUS       FCIL12P40               1006 bp    mRNA    linear   MAM 18-APR-2005
DEFINITION  Felis catus mRNA for interleukin-12 p40 chain.
ACCESSION   Y07762
VERSION     Y07762.1  GI:2102664
KEYWORDS    interleukin-12 p40.
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1
  AUTHORS   Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
  TITLE     Molecular cloning of cat interleukin-12
  JOURNAL   Immunogenetics 45 (6), 462-463 (1997)
   PUBMED   9089110
REFERENCE   2  (bases 1 to 1006)
  AUTHORS   Schijns,V.E.C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
            Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
            Utrecht, NETHERLANDS
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ORIGIN
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  Query Match             99.7%;  Score 983.8;  DB 14;  Length 1006;
  Best Local Similarity   99.8%;  Pred. No. 1.5e-287;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
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Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
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Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
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Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

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Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
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Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
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Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
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RESULT 8
AR595956
LOCUS       AR595956               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 38 from patent US 6818444.
ACCESSION   AR595956
VERSION     AR595956.1  GI:56646937
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 38 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             99.7%;  Score 983.8;  DB 2;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 1.7e-287;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
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Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
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Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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RESULT 9
AR595957/c
LOCUS       AR595957               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 40 from patent US 6818444.
ACCESSION   AR595957
VERSION     AR595957.1  GI:56646938
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 40 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             99.7%;  Score 983.8;  DB 2;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 1.7e-287;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
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Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
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Db       1419 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

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Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db       1119 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 1060

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Db        999 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 940

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
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Db        879 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 820

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
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Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 760

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
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Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
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RESULT 10
AX076209
LOCUS       AX076209               4522 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 10 from Patent WO0104155.
ACCESSION   AX076209
VERSION     AX076209.1  GI:12710834
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 10 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             99.7%;  Score 983.8;  DB 2;  Length 4522;
  Best Local Similarity   99.8%;  Pred. No. 2.2e-287;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
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Db       3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
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Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
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Db       3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
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Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

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Db       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db       3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Db       3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

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Db       3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
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Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
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Db       3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
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Db       4007 AGCAACTGGGCATCCGTGTCCTGCAGT 4033


RESULT 11
AX076476
LOCUS       AX076476                4522 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 2 from Patent WO0104280.
ACCESSION   AX076476
VERSION     AX076476.1  GI:12711028
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 2 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             99.7%;  Score 983.8;  DB 2;  Length 4522;
  Best Local Similarity   99.8%;  Pred. No. 2.2e-287;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
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Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

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Db       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db       3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Db       3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
                ||||||||||||||||||||||||||
Db       4007 AGCAACTGGGCATCCGTGTCCTGCAGT 4033


RESULT 12
AR242435
LOCUS       AR242435               2193 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 5 from patent US 6472509.
ACCESSION   AR242435
VERSION     AR242435.1  GI:27288852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2193)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 5 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .2193
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match            99.5%;  Score 982.2;  DB 2;  Length 2193;
  Best Local Similarity  99.7%;  Pred. No. 5.6e-287;
  Matches  984;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||| |||||||||||||||||| |||||||||||||||||||| |||
Db         64 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTACCTGGTTTTGCTGGCACCTCCTCTC 123

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 183

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 243

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 303

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 363

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 423

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        424 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 483

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 543

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 603

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 663

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 723

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 783

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 843

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 903

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 963

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 1023

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||
Db       1024 AGCAACTGGGCATCCGTGTCCTGCAGT 1050


RESULT 13
AR280203
LOCUS       AR280203               2193 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 5 from patent US 6518045.
ACCESSION   AR280203
VERSION     AR280203.1  GI:29715593
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2193)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 5 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .2193
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match            99.5%;  Score 982.2;  DB 2;  Length 2193;
  Best Local Similarity  99.7%;  Pred. No. 5.6e-287;
  Matches  984;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||| |||||||||||||||||| |||||||||||||||||||| |||
Db         64 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTACCTGGTTTTGCTGGCACCTCCTCTC 123
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Qy          61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         124 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 183

Qy         121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         184 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 243

Qy         181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         244 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 303

Qy         241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         304 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 363

Qy         301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         364 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 423

Qy         361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         424 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 483

Qy         421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         484 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 543

Qy         481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         544 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 603

Qy         541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         604 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 663

Qy         601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         664 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 723

Qy         661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         724 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 783

Qy         721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         784 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 843

Qy         781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         844 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 903

Qy         841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         904 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 963

Qy         901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         964 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 1023

Qy         961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
               ||||||||||||||||||||||||||||
Db        1024 AGCAACTGGGCATCCGTGTCCTGCAGT 1050
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RESULT 14
AR322418
LOCUS       AR322418                2193 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 5 from patent US 6566097.
ACCESSION   AR322418
VERSION     AR322418.1  GI:33708171
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2193)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 5 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .2193
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             99.5%;  Score 982.2;  DB 2;  Length 2193;
  Best Local Similarity   99.7%;  Pred. No. 5.6e-287;
  Matches  984;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy           1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
               ||||||||||||||| |||||||||||||||||| |||||||||||||||||||||| |||
Db          64 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTACCTGGTTTTGCTGGCACCTCCTCTC 123

Qy          61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         124 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 183

Qy         121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         184 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 243

Qy         181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         244 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 303

Qy         241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         304 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 363

Qy         301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         364 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 423

Qy         361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         424 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 483

Qy         421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         484 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 543

Qy         481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         544 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 603

Qy         541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         604 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 663

Qy         601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         664 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 723

Qy         661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         724 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 783

Qy         721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         784 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 843

Qy         781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 903

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 963

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 1023

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
                ||||||||||||||||||||||||||||
Db       1024 AGCAACTGGGCATCCGTGTCCTGCAGT 1050


RESULT 15
FCU83184
LOCUS       FCU83184                990 bp    mRNA    linear   MAM 16-JUL-1999
DEFINITION  Felis catus interleukin-12 p40 subunit (IL-12) mRNA, complete cds.
ACCESSION   U83184
VERSION     U83184.1  GI:2735050
KEYWORDS    .
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Nucleotide and predicted peptide sequence of feline interleukin-12
            (IL-12)
  JOURNAL   DNA Seq. 8 (1-2), 77-82 (1997)
   PUBMED   9522125
REFERENCE   2  (bases 1 to 990)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal
            Veterinary Medicine, University of Zurich, Winterthurerstrasse 260,
            Zurich, ZH 8057, Switzerland
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="Felis catus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
     CDS             1. .990
                     /note="cytokine"
                     /codon_start=1
                     /product="interleukin-12 p40 subunit"
                     /protein_id="AAB93835.1"
                     /db_xref="GI:2735051"
                     /translation="MHPQQLVIAWFSLVLLAPPLMAIWELEKNVYVVELDWHPDAPGE
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                     LIHKKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFTVKSSR
                     GSSDPQGVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPAAEESLPIEVVVDAIHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFGV
                     QVQGKNNREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSNWASVSCS"
ORIGIN

  Query Match             99.2%;  Score 979;  DB 14;  Length 990;
  Best Local Similarity   99.5%;  Pred. No. 4.3e-286;
  Matches  982;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||||||||||||| | || ||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGTGACACGCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
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Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987


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Job time : 4067.4 secs
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 10, 2006, 03:13:22 ; Search time 729.104 Seconds
(without alignments)
9438.451 Million cell updates/sec

Title: US-10-821-670A-29
Perfect score: 987
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: geneseqn1990s:*
3: geneseqn2000s:*
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15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	987	100.0	987	6	ABK98944	Abk98944 Feline in
c	2	987	100.0	987	6	ABK98945	Abk98945 Feline in
	3	987	100.0	987	14	ADV34682	Adv34682 Feline si
c	4	987	100.0	987	14	ADV34684	Adv34684 Feline si
c	5	985	99.8	985	6	ABK98962	Abk98962 Feline in
	6	985	99.8	985	6	ABK98961	Abk98961 Feline in
	7	985	99.8	985	14	ADV34707	Adv34707 Feline N-
c	8	985	99.8	985	14	ADV34709	Adv34709 Feline N-
	9	983.8	99.7	990	4	AAF26082	Aaf26082 Feline IL
	10	983.8	99.7	990	4	AAF26085	Aaf26085 Feline IL
	11	983.8	99.7	1599	6	ABK98950	Abk98950 Feline in
c	12	983.8	99.7	1599	6	ABK98951	Abk98951 Feline in
	13	983.8	99.7	1599	14	ADV34691	Adv34691 Feline si
c	14	983.8	99.7	1599	14	ADV34693	Adv34693 Feline si
	15	983.8	99.7	4522	4	AAF26076	Aaf26076 Feline IL
	16	983.8	99.7	4522	4	AAF26094	Aaf26094 Plasmid p
	17	982.2	99.5	2193	2	AAV56625	Aav56625 Feline FL
	18	921	93.3	921	2	AAV56626	Aav56626 Feline FL
	19	919.4	93.2	921	2	AAV56627	Aav56627 Feline FL
	20	919.4	93.2	921	6	ABK98942	Abk98942 Feline in
c	21	919.4	93.2	921	6	ABK98943	Abk98943 Feline in
c	22	919.4	93.2	921	14	ADV34681	Adv34681 Feline si
	23	919.4	93.2	921	14	ADV34679	Adv34679 Feline si
c	24	919.4	93.2	1533	6	ABK98954	Abk98954 Feline in
	25	919.4	93.2	1533	6	ABK98953	Abk98953 Feline in
c	26	919.4	93.2	1533	14	ADV34697	Adv34697 Feline si
	27	919.4	93.2	1533	14	ADV34695	Adv34695 Feline si
	28	886.2	89.8	990	2	AAV13817	Aav13817 Canine IL
	29	886.2	89.8	990	2	AAX03162	Aax03162 Nucleic a
	30	886.2	89.8	990	2	AAX35625	Aax35625 Nucleic a
	31	886.2	89.8	990	4	AAI64388	Aai64388 Canine co
c	32	886.2	89.8	2267	6	ABK99006	Abk99006 Canine in
	33	886.2	89.8	2267	6	ABK99005	Abk99005 Canine in
	34	886.2	89.8	2267	14	ADV34757	Adv34757 Canine si
c	35	886.2	89.8	2267	14	ADV34759	Adv34759 Canine si
	36	883	89.5	987	6	ABK98963	Abk98963 Canine in
c	37	883	89.5	987	6	ABK98964	Abk98964 Canine in
c	38	883	89.5	987	14	ADV34712	Adv34712 Canine si
	39	883	89.5	987	14	ADV34710	Adv34710 Canine si
	40	883	89.5	1015	13	ADT04849	Adt04849 Canine in
	41	883	89.5	1599	6	ABK98965	Abk98965 Canine in
c	42	883	89.5	1599	6	ABK98966	Abk98966 Canine in
c	43	883	89.5	1599	14	ADV34715	Adv34715 Canine si
	44	883	89.5	1599	14	ADV34713	Adv34713 Canine si
	45	875	88.7	990	2	AAV13816	Aav13816 Canine IL

ALIGNMENTS

RESULT 1
ABK98944
ID ABK98944 standard; cDNA; 987 BP.
XX
AC ABK98944;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p40-987 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69303.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 1; Page 51-53; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain

```
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 987 BP; 283 A; 250 C; 246 G; 208 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 987;  DB 6;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-298;
  Matches  987;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987


RESULT 2
ABK98945/c
ID   ABK98945 standard; cDNA; 987 BP.
XX
AC   ABK98945;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p40-987 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 3; Page 54; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 987 BP; 208 A; 246 C; 250 G; 283 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 987;  DB 6;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-298;
  Matches  987;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928
```

```
Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGCAGT 1
```

RESULT 3
ADV34682
ID ADV34682 standard; cDNA; 987 BP.
XX
AC ADV34682;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain IL-12p40 full-length cDNA, nFeIL-12p40 987.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; gene; ss.
XX
OS Felis catus.
XX
FH Key Location/Qualifiers
FT CDS 1. .987
FT /*tag= a
FT /product= "PFeIL-12p40 329 protein "
FT /partial
FT /note= "No stop codon"
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
DR P-PSDB; ADV34683.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Claim 23; SEQ ID NO 29; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain IL-12p40 subunit protein
CC encoding full-length cDNA.
XX
SQ Sequence 987 BP; 283 A; 250 C; 246 G; 208 T; 0 U; 0 Other;

Query Match 100.0%; Score 987; DB 14; Length 987;
Best Local Similarity 100.0%; Pred. No. 1.7e-298;
Matches 987; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
```

```
Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
```

RESULT 4
ADV34684/c
ID ADV34684 standard; DNA; 987 BP.
XX
AC ADV34684;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain IL-12p40 complementary DNA, nFeIL-12p40 987.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Felis catus.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX

PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 3; SEQ ID NO 31; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain IL-12p40 subunit full-length
CC complementary DNA.
XX
SQ Sequence 987 BP; 208 A; 246 C; 250 G; 283 T; 0 U; 0 Other;

Query Match 100.0%; Score 987; DB 14; Length 987;
Best Local Similarity 100.0%; Pred. No. 1.7e-298;
Matches 987; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
                |||||||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGCAGT 1
```

RESULT 5
ABK98962/c
ID ABK98962 standard; cDNA; 985 BP.
XX
AC ABK98962;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p40-N985 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Example 3; Page 75-76; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 985 BP; 207 A; 245 C; 250 G; 283 T; 0 U; 0 Other;

Query Match 99.8%; Score 985; DB 6; Length 985;
Best Local Similarity 100.0%; Pred. No. 7.3e-298;
Matches 985; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        361 AAAGAATCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
```

```
                    ||||||||||||||||||||||||
Db          25 AGCAACTGGGCATCCGTGTCCTGCA 1


RESULT 6
ABK98961
ID   ABK98961 standard; cDNA; 985 BP.
XX
AC   ABK98961;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p40-N985 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69311.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 3; Page 73-74; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 985 BP; 283 A; 250 C; 245 G; 207 T; 0 U; 0 Other;

  Query Match             99.8%;  Score 985;  DB 6;  Length 985;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-298;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 7
ADV34707
ID   ADV34707 standard; cDNA; 985 BP.
XX
AC   ADV34707;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline N-terminal IL-12p40 protein encoding cDNA, nFeIL-12p40-N985.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
```

```
FH   Key             Location/Qualifiers
FT   CDS             1. .984
FT                   /*tag= a
FT                   /product= "PCaIL-12P40-N328 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34708.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 55; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline N-terminal single chain IL-12p40 protein
CC   encoding cDNA.
XX
SQ   Sequence 985 BP; 283 A; 250 C; 245 G; 207 T; 0 U; 0 Other;

  Query Match             99.8%;  Score 985;  DB 14;  Length 985;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-298;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 8
ADV34709/c
ID   ADV34709 standard; DNA; 985 BP.
XX
AC   ADV34709;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline N-terminal IL-12p40 protein complementary DNA, nFeIL-12p40-N985.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
```

```
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 57; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline N-terminal single chain IL-12p40
CC   complementary DNA.
XX
SQ   Sequence 985 BP; 207 A; 245 C; 250 G; 283 T; 0 U; 0 Other;

  Query Match             99.8%;  Score 985;  DB 14;  Length 985;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-298;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGCA 1


RESULT 9
AAF26082
ID   AAF26082 standard; DNA; 990 BP.
XX
AC   AAF26082;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p40 encoding DNA SEQ ID 8.
XX
KW   Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW   interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS   Felis sp.
XX
PN   WO200104280-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002262.
XX
PR   08-JUL-1999;   99CH-00001258.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
XX
PI   Leutenegger C,  Schroff M,  Wittig B,  Lutz H;
XX
DR   WPI; 2001-147190/15.
XX
PT   Vaccine for treating or preventing lentivirus infection in cats, contains
PT   nucleic acid sequence encoding viral protein under control of eukaryotic
PT   promoter.
XX
PS   Claim 14; Page 36; 37pp; German.
XX
CC   This invention describes a novel vaccine (A) for prevention or treatment
CC   of lentivirus infection in felines which comprises an immunizing nucleic
CC   acid sequence (I) that contains, or comprises, at least part of a gene
CC   encoding a protein (II) of the virus, under control of a eukaryotic
CC   promoter functional in the relevant animal. (II) is especially the
CC   envelope (env) protein. The invention also describes (1) vaccine (A)
CC   containing an immunizing protein, or fragment, from a lentivirus plus at
CC   least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC   lentivirus protein, or fragment, especially derived from feline immune
CC   deficiency virus (FIV), by expressing the corresponding nucleic acid
CC   sequence in a host cell. The products of the invention have antiviral
CC   activity. The vaccine (A) and related protein-based vaccines, are
CC   particularly used to treat or prevent lentivirus infections in domestic
CC   cats, especially feline immune deficiency virus (FIV). Vaccination with
CC   (A) allows differentiation between vaccinated and infected animals, from
CC   the antibody status. The vaccines may be formulated with an adjuvant
CC   (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC   immune response, particularly a Th1 response
XX
SQ   Sequence 990 BP; 283 A; 249 C; 248 G; 210 T; 0 U; 0 Other;
```

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  Query Match             99.7%;  Score 983.8;  DB 4;  Length 990;
  Best Local Similarity   99.8%;  Pred. No. 1.7e-297;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
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RESULT 10
AAF26085
ID   AAF26085 standard; DNA; 990 BP.
XX
AC   AAF26085;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p40 encoding DNA.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS   Felis sp.
XX
PN   WO200104155-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002263.
XX
PR   08-JUL-1999;   99CH-00001259.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Lutz H,  Leutenegger C,  Pedersen N,  Schroff M,  Wittig B;
XX
DR   WPI; 2001-147178/15.
XX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs.
XX
PS   Claim 3; Page 30; 35pp; German.
XX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
CC   following: (i) as immunostimulant, for preventative or therapeutic use;
CC   and (ii) treating tumors and autoimmune diseases, or diseases associated
CC   with a Th1 defect, especially pre-existing infections by feline immune
CC   deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ   Sequence 990 BP; 283 A; 249 C; 248 G; 210 T; 0 U; 0 Other;

  Query Match             99.7%;  Score 983.8;  DB 4;  Length 990;
  Best Local Similarity   99.8%;  Pred. No. 1.7e-297;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
```

```
Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987


RESULT 11
ABK98950
ID   ABK98950 standard; cDNA; 1599 BP.
XX
AC   ABK98950;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1599 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69306.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 58-60; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

  Query Match            99.7%;  Score 983.8;  DB 6;  Length 1599;
  Best Local Similarity  99.8%;  Pred. No. 2.3e-297;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987


RESULT 12
ABK98951/c
ID   ABK98951 standard; cDNA; 1599 BP.
XX
AC   ABK98951;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1599 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 61-62; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

  Query Match             99.7%;  Score 983.8;  DB 6;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 2.3e-297;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1599 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 1540

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 1420

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1359 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 1300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1299 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 1240

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1179 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 1120

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1119 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 1060

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        999 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 940

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        939 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 880

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        879 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 820

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 760

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        759 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 640

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||||||||
Db        639 AGCAACTGGGCATCCGTGTCCTGCAGT 613


RESULT 13
ADV34691
ID   ADV34691 standard; cDNA; 1599 BP.
XX
AC   ADV34691;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1599
FT                   /*tag=  a
FT                   /product= "PFeIL-12p533 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34692.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 38; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

  Query Match             99.7%;  Score 983.8;  DB 14;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 2.3e-297;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Db        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
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Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
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Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
```

```
Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987


RESULT 14
ADV34693/c
ID   ADV34693 standard; DNA; 1599 BP.
XX
AC   ADV34693;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 complementary DNA, nFeIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 40; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 complementary DNA.
XX
SQ   Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

  Query Match             99.7%;  Score 983.8;  DB 14;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 2.3e-297;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
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Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 1420

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1359 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 1300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
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Db       1299 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 1240

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Db       1239 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db       1179 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 1120

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Db       1119 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 1060

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
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Db        999 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 940

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
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Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
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Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 760

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        759 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 640

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||||
Db        639 AGCAACTGGGCATCCGTGTCCTGCAGT 613


RESULT 15
AAF26076
ID   AAF26076 standard; DNA; 4522 BP.
XX
AC   AAF26076;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p40 encoding DNA SEQ ID 2.
XX
KW   Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW   interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS   Felis sp.
XX
PN   WO200104280-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002262.
XX
```

PR 08-JUL-1999; 99CH-00001258.
XX
PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA (UYZU-) UNIV ZUERICH.
XX
PI Leutenegger C, Schroff M, Wittig B, Lutz H;
XX
DR WPI; 2001-147190/15.
XX
PT Vaccine for treating or preventing lentivirus infection in cats, contains
PT nucleic acid sequence encoding viral protein under control of eukaryotic
PT promoter.
XX
PS Disclosure; Page 29-31; 37pp; German.
XX
CC This invention describes a novel vaccine (A) for prevention or treatment
CC of lentivirus infection in felines which comprises an immunizing nucleic
CC acid sequence (I) that contains, or comprises, at least part of a gene
CC encoding a protein (II) of the virus, under control of a eukaryotic
CC promoter functional in the relevant animal. (II) is especially the
CC envelope (env) protein. The invention also describes (1) vaccine (A)
CC containing an immunizing protein, or fragment, from a lentivirus plus at
CC least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC lentivirus protein, or fragment, especially derived from feline immune
CC deficiency virus (FIV), by expressing the corresponding nucleic acid
CC sequence in a host cell. The products of the invention have antiviral
CC activity. The vaccine (A) and related protein-based vaccines, are
CC particularly used to treat or prevent lentivirus infections in domestic
CC cats, especially feline immune deficiency virus (FIV). Vaccination with
CC (A) allows differentiation between vaccinated and infected animals, from
CC the antibody status. The vaccines may be formulated with an adjuvant
CC (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC immune response, particularly a Th1 response
XX
SQ Sequence 4522 BP; 1180 A; 1126 C; 1106 G; 1110 T; 0 U; 0 Other;

Query Match 99.7%; Score 983.8; DB 4; Length 4522;
Best Local Similarity 99.8%; Pred. No. 4.2e-297;
Matches 985; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
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Db       3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
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Db       3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Db       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
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Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
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Db       3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Db       3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
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Db       3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
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Db       4007 AGCAACTGGGCATCCGTGTCCTGCAGT 4033
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Job time : 730.104 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 10, 2006, 03:16:38 ; Search time 5764.02 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	579.6	58.7	735	5	CD559605	CD559605 AGENCOURT
	3	570	57.8	747	5	CD559607	CD559607 AGENCOURT
	4	568.6	57.6	772	5	CD559604	CD559604 AGENCOURT
	5	512.8	52.0	745	5	CD559602	CD559602 AGENCOURT
	6	509.6	51.6	1839	6	AK162981	AK162981 Mus muscu
c	7	509.2	51.6	785	5	CD559448	CD559448 AGENCOURT
c	8	508	51.5	772	5	CD559450	CD559450 AGENCOURT
c	9	503	51.0	736	5	CD559453	CD559453 AGENCOURT
c	10	501.4	50.8	762	5	CD559451	CD559451 AGENCOURT
	11	498.6	50.5	2908	6	AK155593	AK155593 Mus muscu
c	12	479	48.5	754	5	CD559452	CD559452 AGENCOURT
c	13	473.4	48.0	766	5	CD559449	CD559449 AGENCOURT
c	14	437.6	44.3	725	5	CD559454	CD559454 AGENCOURT
	15	418.8	42.4	724	5	CD559603	CD559603 AGENCOURT
	16	401.4	40.7	1042	5	CD559606	CD559606 AGENCOURT
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	18	265.8	26.9	475	7	BF704417	BF704417 MI-P-E6-a
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	22	217.4	22.0	432	4	BY154173	BY154173 BY154173
	23	210	21.3	375	4	BY222535	BY222535 BY222535
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	25	202.8	20.5	355	4	BY221814	BY221814 BY221814
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	37	47.8	4.8	657	13	CL344592	CL344592 RPCI44_27
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c	39	42.8	4.3	581	11	AQ394113	AQ394113 CITBI-E1-
c	40	42.2	4.3	801	2	BI661062	BI661062 603304362
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	44	40.2	4.1	862	12	CG277764	CG277764 OG5BA27TC
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ALIGNMENTS

RESULT 1
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DEFINITION AGENCOURT_14496566 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971871 5', mRNA sequence.
ACCESSION CK130264
VERSION CK130264.1 GI:38622200
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 756)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: h column: 02
High quality sequence start: 5
High quality sequence stop: 731.
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/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:

loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 58.9%; Score 581.6; DB 5; Length 756;
Best Local Similarity 88.6%; Pred. No. 1e-158;
Matches 642; Conservative 0; Mismatches 80; Indels 3; Gaps 1;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              |||  ||  |||||||||||||||| | ||||||||||||||||||| |||||| ||||||||
Db         34 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 93

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
               |||||||||||||||||| ||||| | |||||||| ||||| ||||| ||| | || |||
Db         94 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 153

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||| |||||||||||||||||||||||  | || ||||||||||||||  |||||||||
Db        154 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 213

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||  |||||||||||||| ||| |||||||||| ||||| ||||||||||||||||||
Db        214 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 273

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              || |||| |||||||||||||||| |||||||| |||||||||||||||||| |||||||||
Db        274 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 333

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              |||| ||| | ||||||||||||||||||||||||||||||||||| |||| ||| |||
Db        334 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 393

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||| |||||||||||| |||||||| ||| ||||| ||||||||||||||||||||||
Db        394 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 453

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              |||||||||||||||||| |||||||||| ||||||| ||||| ||||||||||||||||
Db        454 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 513

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||| |||||||||||||||||||| || ||||| || |||||||| |||||||  |||
Db        514 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 573

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||| |||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||
Db        574 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 630

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              || ||||| |||||||| || |||||||| ||| ||||||| ||  ||||||||||||||
Db        631 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 690

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              || ||||||||||||||||||||||||||||||||||||||||| |||| ||||||||||
Db        691 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCNAACCTGACCCACCCAAG 750

Qy        721 AACCT 725
              ||| |
Db        751 AACTT 755
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RESULT 2
CD559605

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LOCUS       CD559605                735 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496534 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971870 5', mRNA sequence.
ACCESSION   CD559605
VERSION     CD559605.2  GI:38558937
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 735)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585673.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 01
            High quality sequence stop: 709.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971870"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN
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Query Match 58.7%; Score 579.6; DB 5; Length 735;
Best Local Similarity 88.6%; Pred. No. 3.9e-158;
Matches 640; Conservative 0; Mismatches 79; Indels 3; Gaps 1;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              |||  ||  |||||||||||||||| | ||||||||||||||||||| |||||| ||||||||
Db         17 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 76

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
               |||||||||||||||||| ||||| | |||||||| ||||| ||||| ||| | || |||
Db         77 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 136
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Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||| |||||||||||||||||||||||  | || ||||||||||||  |||||||||
Db        137 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 196

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||  |||||||||||||| ||| |||||||||| ||||| ||||||||||||||||||
Db        197 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 256

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              || |||| |||||||||||||| |||||||| |||||||||||||||| |||||||||
Db        257 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 316

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
               |||| ||| | |||||||||||||||||||||||||||||||||| |||| ||| |||
Db        317 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 376

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||| |||||||||||| |||||||| ||| ||||| ||||||||||||||||||||
Db        377 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 436

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db        437 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAGAGCAGCAGA 496

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Db        497 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 556

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Db        557 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 613

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              || ||||| |||||||| || |||||||| ||| ||||||| ||  ||||||||||||||
Db        614 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 673

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              || ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        674 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 733

Qy        721 AA 722
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Db        734 AA 735
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RESULT 3
CD559607
LOCUS       CD559607                747 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14497061 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971868 5', mRNA sequence.
ACCESSION   CD559607
VERSION     CD559607.2  GI:38558941
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 747)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585675.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: g  column: 11
            High quality sequence start: 14
            High quality sequence stop: 671.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971868"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN
```

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  Query Match           57.8%;  Score 570;  DB 5;  Length 747;
  Best Local Similarity   88.4%;  Pred. No. 2.6e-155;
  Matches  631;  Conservative    0;  Mismatches   80;  Indels    3;  Gaps    1;

Qy          8 CTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCA 67
              | |||||||||||||| | |||||||||||||||| |||||| |||||||| ||||||
Db         36 CCCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTCGTGGCCA 95

Qy         68 TATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCG 127
              |||||||||| ||||| | |||||||| ||||| ||||| ||| | || ||||||| |
Db         96 TATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCTG 155

Qy        128 GAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCTG 187
              |||||||||||||||||||||  | || ||||||||||||  ||||||||||||  |
Db        156 GAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTGG 215

Qy        188 ACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTG 247
              |||||||||||| ||| |||||||||| ||||| |||||||||||||||||||| ||||
Db        216 ACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTTG 275

Qy        248 CAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCC 307
              |||||||||||||||| |||||||| |||||||||||||||| ||||||||| |||| |
Db        276 GAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTGC 335

Qy        308 TGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAAT 367
              || | ||||||||||||||||||||||||||||||||||||||| |||| ||| |||||||||
Db        336 TGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAAC 395

Qy        368 CCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCT 427
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Db        396 CCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCT 455

Qy        428 GGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCT 487
              |||||||||| |||||||| ||||||| ||||| ||||||||||||||||||||| |
Db        456 GGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTT 515

Qy        488 CTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGG 547
              |||||||||||||||||| || ||||| || |||||||| |||||||  ||||||| ||
Db        516 CTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGG 575
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Qy        548 ACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTG 607
              |||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||||  ||||
Db        576 ACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTG 632

Qy        608 CCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAA 667
              | |||||||| || |||||||| ||| |||||||     |||||||||| |||| ||||
Db        633 CTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATTGCGTTCACAAGCTCCAGTATGAAA 692

Qy        668 ACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGA 721
              |||||||| |||||||||||||||||||||||||||||| |||||||||| |
Db        693 ACTACACCCGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAAA 746


RESULT 4
CD559604
LOCUS       CD559604                772 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496598 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971872 5', mRNA sequence.
ACCESSION   CD559604
VERSION     CD559604.2  GI:38558934
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 772)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585672.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 03
            High quality sequence start: 13
            High quality sequence stop: 750.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:6971872"
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                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match           57.6%;  Score 568.6;  DB 5;  Length 772;
  Best Local Similarity   87.9%;  Pred. No. 6.7e-155;
  Matches  632;  Conservative    0;  Mismatches   84;  Indels    3;  Gaps    1;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
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Db         38 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 97

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||| ||||| | |||||||| ||||| ||||| ||| | || |||
Db         98 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 157

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
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Db        158 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 217

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||  |||||||||||||| |||||||||||||| ||||| |||||||||||||||||
Db        218 ACCTTGGACCAGAGCAGTGAGGTCCTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 277

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
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Db        278 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 337

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              |||| ||| | |||||||||||||||||||||||||||||||||| |||| ||| |||
Db        338 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 397

Qy        361 AAAGAATCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Db        398 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 457

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db        458 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 517

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Db        518 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 577

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||| |||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||
Db        578 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 634

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              || ||||| |||||||| || |||||||| ||| ||||||| ||  ||||||||||||||
Db        635 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 694

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAA 719
              || |||||||||||||||||||||||||||||||||||||| | |  |   || ||
Db        695 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAACCTGACCAACCCAAA 753


RESULT 5
CD559602
LOCUS       CD559602                745 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496684 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971874 5', mRNA sequence.
ACCESSION   CD559602
VERSION     CD559602.2  GI:38558930
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 745)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585670.
```

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            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 05
            High quality sequence start: 2
            High quality sequence stop: 644.
FEATURES              Location/Qualifiers
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                      /clone="IMAGE:6971874"
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                      /lab_host="DH5A (T1 phage-resistant)"
                      /clone_lib="NIH_MGC_195"
                      /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                      loxP-HindIII; Clones from this library have been
                      PCR-amplified using gene-specific primers to contain the
                      complete open reading frame (based on known gene sequences
                      available from NCBI's RefSeq). Template for PCR is cDNA
                      derived from either pooled cytoplasmic polyA RNA from 30
                      cells lines or pooled total RNA from 10 different tissues
                      (from BD Biosciences/Clontech and Washington University).
                      PCR products are directionally cloned into the loxP sites
                      of the pDNR-Dual vector. Library constructed by Dr.
                      Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                      Expression Laboratory, Research Technology Program, SAIC
                      Frederick, NCI-Frederick, Frederick, MD 21702). For
                      information on which gene each clone represents, please
                      visit our anonymous ftp site at
                      ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                      a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             52.0%;  Score 512.8;  DB 5;  Length 745;
  Best Local Similarity   86.6%;  Pred. No. 1.6e-138;
  Matches  589;  Conservative    0;  Mismatches   87;  Indels    4;  Gaps    2;

Qy          8 CTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCA 67
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Db         13 CCCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTCGTGGCCA 72

Qy         68 TATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCG 127
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Qy        128 GAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCTG 187
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Qy        248 CAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCC 307
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Qy        308 TGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAAT 367
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Qy        368 CCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCT 427
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Db        373 CCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCT 432

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Db        433 GGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTT 492

Qy        488 CTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGG 547
              |||||||||||||||||| || ||||| || |||||||| |||||||  ||||||| ||
Db        493 CTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGG 552

Qy        548 ACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTG 607
              |||||| ||| |||    ||||| |||||||||| ||||||| |||||||||||| ||||
Db        553 ACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTG 609

Qy        608 CCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAA 667
              | |||||||| || |||||||| ||| ||||||| ||    |||||||||| ||   |||
Db        610 CTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGC-CGTCACAAGCTCATGTTGAAAA 668

Qy        668 ACTACACCAGCAGCTTCTTC 687
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Db        669 TACACCACGGCTTCTTTCTC 688


RESULT 6
AK162981
LOCUS       AK162981               1839 bp    mRNA    linear   HTC 21-SEP-2005
DEFINITION  Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched
            library, clone:A430014H12 product:interleukin 12b, full insert
            sequence.
ACCESSION   AK162981
VERSION     AK162981.1  GI:74188061
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
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            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
            Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
            Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
            Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
            Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
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Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
CONSRTM RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
PUBMED 11217851
REFERENCE 5
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
CONSRTM FANTOM Consortium
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420 (6915), 563-573 (2002)
PUBMED 12466851
REFERENCE 6
AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.
CONSRTM FANTOM Consortium
TITLE The transcriptional landscape of the mammalian genome
JOURNAL Science 309 (5740), 1559-1563 (2005)
PUBMED 16141072
REFERENCE 7
AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.
CONSRTM RIKEN Genome Exploration Research Group
TITLE Antisense transcription in the mammalian transcriptome
JOURNAL Science 309 (5740), 1564-1566 (2005)
PUBMED 16141073
REFERENCE 8 (bases 1 to 1839)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
FEATURES Location/Qualifiers
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LLHKKENGIWSTEILKNFKNKTFLKCEAPNYSGRFTCSWLVQRNMDLKFNIKSSSSSP
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ORIGIN

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Db        238 ACCTCAGACCAGAGACATGGAGTCATAGGCTCTGGAAAGACCCTGACCATCACTGTCAAA 297

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
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Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
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Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Db        529 AGTTCCCCTGACTCTCGGGCAGTGACATGTGGAATGGCGTCTCTGTCTGCAGAGAAGGTC 588

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Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
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Qy        841 AAGAACAACA----------------------GAGAAAAGAAAGACAGACTCTCCGTG 876
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Db        886 AAGAAAGAAAAGATGAAGGAGACAGAGGAGGGGGTGTAACCAGAAAGGTGCGTTCCTCGTA 945

Qy        877 GACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGA 936
              || ||||| ||  || | |||   ||   ||| |  |  ||  || ||||||||||
Db        946 GAGAAGACATCTACCGAAGTCCAATG---CAAAGGCGGGAATGTCTGCGTGCAAGCTCAG 1002

Qy        937 GACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAG 986
              || ||||| || |  || || || ||||| |||||||  ||  |||||||
Db       1003 GATCGCTATTACAATTCCTCATGCAGCAAGTGGGCATGTGTTCCCTGCAG 1052


RESULT 7
CD559448/c
LOCUS       CD559448                 785 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496712 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971874 5', mRNA sequence.
ACCESSION   CD559448
VERSION     CD559448.2  GI:38453466
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 785)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585516.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 05
            High quality sequence stop: 696.
FEATURES             Location/Qualifiers
     source          1. .785
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971874"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match           51.6%;  Score 509.2;  DB 5;  Length 785;
  Best Local Similarity  85.9%;  Pred. No. 1.8e-137;
  Matches  589;  Conservative    0;  Mismatches   93;  Indels    4;  Gaps    2;

Qy        302 TCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGA 361
              ||   ||| | | || ||| | |    | | ||||||||||||||| |||| ||| ||||
Db        774 TCGCTCTGCTGCTCACAAAAGGAAGATGGAATTGGTCCACTGATAT-TTAAAGGACCAGA 716
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Qy        362 AAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCA 421
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Db        715 AAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCA 656

Qy        422 CCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAG 481
              |||||||||||||||| |||||||||| ||||||| ||||| ||||||||||||||||||
Db        655 CCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAG 596

Qy        482 GCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCA 541
              |||| ||||||||||||||||||| || ||||| || |||||||| |||||||  ||||
Db        595 GCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCA 536

Qy        542 GAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCC 601
              ||| |||||||| ||| |||     ||||| |||||||||| ||||||| ||||||||||
Db        535 GAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCC 479

Qy        602 CGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGT 661
              | ||||| |||||||| || |||||||| ||| ||||||| ||  ||||||||||||||
Db        478 CAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGT 419

Qy        662 ACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGA 721
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Db        418 ATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGA 359

Qy        722 ACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTG 781
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Db        358 ACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTG 299

Qy        782 ACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCA 841
              |||||||||| || |||||||||||||||||| | |||||  |||| ||||||||||||
Db        298 ACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCA 239

Qy        842 AGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGT 901
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Db        238 AGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCT 179

Qy        902 GCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGA 961
              ||| |||  |||||| ||  |||||| |||  ||||||||||||||||||| ||||
Db        178 GCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGA 119

Qy        962 GCAACTGGGCATCCGTGTCCTGCAGT 987
              || | |||||||| ||| ||||||||
Db        118 GCGAATGGGCATCTGTGCCCTGCAGT 93


RESULT 8
CD559450/c
LOCUS       CD559450                772 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496612 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971872 5', mRNA sequence.
ACCESSION   CD559450
VERSION     CD559450.2  GI:38453469
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 772)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585518.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 03
            High quality sequence start: 2
            High quality sequence stop: 753.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /clone="IMAGE:6971872"
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                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match           51.5%;  Score 508;  DB 5;  Length 772;
  Best Local Similarity   86.6%;  Pred. No. 4.1e-137;
  Matches  583;  Conservative    0;  Mismatches   86;  Indels    4;  Gaps    2;

Qy        315 CAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAA 374
              || ||| | |    ||||| |||||||||||| |||| ||| ||||||||| |||||||
Db        770 CACAAAAGGAAGATGAATTNGGTCCACTGATAT-TTAAAGGACCAGAAAGAACCCAAAAA 712

Qy        375 TAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCT 434
              ||||| |||||||| ||| ||||| ||||||||||||||||||||||||||||||||||
Db        711 TAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCT 652

Qy        435 GACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCC 494
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Db        651 GACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCTGACCC 592

Qy        495 CCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAG 554
              |||||||||||| || ||||| || |||||||| |||||||  ||||||| ||||||||
Db        591 CCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAACAA 532

Qy        555 GGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGA 614
              ||| |||    ||||| |||||||||| ||||||| |||||||||||| ||||| |||||
Db        531 GGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCTGAGGA 475

Qy        615 GAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACAC 674
              ||| || |||||||| ||| ||||||| || |||||||||||||||| ||||||||||
Db        474 GAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACAC 415

Qy        675 CAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAA 734
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Db        414 CAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAA 355

Qy        735 GCCATTAAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCAC 794
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Db        354 GCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTAC 295

Qy        795 CCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGA 854
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Db        294 TCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGCAAGAGAGA 235
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Qy        855 AAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGC 914
              |||||||||| ||| ||| |  ||||||||||||||||||| |||| | |||| ||| ||||
Db        234 AAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGCAAAAATGC 175

Qy        915 CAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATC 974
              ||  ||  ||||||  |||   |||||||||||||||||||| |||||| | ||||||||
Db        174 CAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAATGGGCATC 115

Qy        975 CGTGTCCTGCAGT 987
              |||  ||||||||
Db        114 TGTGCCCTGCAGT 102


RESULT 9
CD559453/c
LOCUS       CD559453                736 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14497154 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971869 5', mRNA sequence.
ACCESSION   CD559453
VERSION     CD559453.2  GI:38453475
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 736)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585521.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: g  column: 12
            High quality sequence stop: 683.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
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                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN
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  Query Match           51.0%;  Score 503;  DB 5;  Length 736;
  Best Local Similarity  87.3%;  Pred. No. 1.2e-135;
  Matches  575;  Conservative    0;  Mismatches   80;  Indels    4;  Gaps    2;

Qy        329 GAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAA 388
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Db        732 GGAATTGGTCCACTGATAT-TTAAAGGACCAGAAAGAACCCAAAAATAAGACCTTTCTAA 674

Qy        389 AATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTA 448
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Db        673 GATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGACAATCAGTA 614

Qy        449 CCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTT 508
              | ||||||| ||||| |||||||||||||||||||||| |||||||||||||||||| |
Db        613 CTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGT 554

Qy        509 GTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGT 568
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Db        553 GCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAACAAGGAGTAT---GAGT 497

Qy        569 ACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTG 628
              || |||||||||| ||||||| |||||||||||  ||||| |||||||| || |||||||
Db        496 ACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCTGAGGAGAGTCTGCCCATTG 437

Qy        629 AAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCA 688
              | ||| ||||||| ||  |||||||||||||||| ||||||||||||||||||||||||
Db        436 AGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCA 377

Qy        689 TCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATT 748
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Db        376 TCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATT 317

Qy        749 CTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACT 808
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Qy        809 TCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGAC 868
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Db        256 TCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGCAAGAGAGAAAAGAAAGATAGAG 197

Qy        869 TCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGC 928
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Db        196 TCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGCAAAAATGCCAGCATTAGCGTGC 137

Qy        929 AAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987
              |||  |||||||||||||||||| |||||| | |||||||| ||| ||||||||
Db        136 GGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAATGGGCATCTGTGCCCTGCAGT 78


RESULT 10
CD559451/c
LOCUS       CD559451                762 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496580 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971871 5', mRNA sequence.
ACCESSION   CD559451
VERSION     CD559451.2  GI:38453471
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585519.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
```

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            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: IRBK2  row: h  column: 02
           High quality sequence start: 38
           High quality sequence stop: 761.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971871"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             50.8%;  Score 501.4;  DB 5;  Length 762;
  Best Local Similarity   87.1%;  Pred. No. 3.5e-135;
  Matches  574;  Conservative    0;  Mismatches   81;  Indels    4;  Gaps    2;

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Db        753 GGAATTGGTCCACTGATAT-TTAAAGGACCAGAAAGAACCCAAAAATAAGACCTCTCTAA 695

Qy        389 AATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTA 448
              ||| ||||| ||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        694 GATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGACAATCAGTA 635

Qy        449 CCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTT 508
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Db        634 CTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGT 575

Qy        509 GTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGT 568
              | ||||| || |||||||| ||||||| ||||||| |||||||| ||| |||    |||
Db        574 GCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAACAAGGAGTAT---GAGT 518

Qy        569 ACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTG 628
              || |||||||||| ||||||| |||||||||||| ||||| |||||||| || |||||||
Db        517 ACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCTGAGGAGAGTCTGCCCATTG 458

Qy        629 AAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCA 688
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Db        457 AGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCA 398

Qy        689 TCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATT 748
              |||||||||||||||||| |||||||||||||| |||| |||||||||||||| ||||
Db        397 TCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATT 338

Qy        749 CTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACT 808
              ||||||| ||||| || |||||||| |||||||||||||||| || ||||||||||||
Db        337 CTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACATTCCTACT 278

Qy        809 TCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGAC 868
              ||||| | |||||  |||| |||||||||||||||| ||| |||||||||||||| |||
Db        277 TCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGCAAGAGAGAAAAGAAAGATAGAG 218

Qy        869 TCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGC 928
              ||| |  ||||||||||||||||| |||| | |||| ||| ||||||  ||  ||||||
Db        217 TCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGCAAAAATGCCAGCATTAGCGTGC 158

Qy        929 AAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987
                |||   |||||||||||||||||||| |||||| | ||||||| ||| ||||||||
Db        157 GGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAATGGGCATCTGTGCCCTGCAGT 99
```

RESULT 11
AK155593

LOCUS	AK155593 2908 bp mRNA linear HTC 21-SEP-2005
DEFINITION	Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F730005O03 product:interleukin 12b, full insert sequence.
ACCESSION	AK155593
VERSION	AK155593.1 GI:74212721
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE	1
AUTHORS	Carninci,P. and Hayashizaki,Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
PUBMED	10349636
REFERENCE	2
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
PUBMED	11042159
REFERENCE	3
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
PUBMED	11076861
REFERENCE	4
AUTHORS	Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
CONSRTM	RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium

```
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
   PUBMED   11217851
REFERENCE   5
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
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            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
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            Rogers,J., Birney,E. and Hayashizaki,Y.
  CONSRTM   FANTOM Consortium
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420 (6915), 563-573 (2002)
   PUBMED   12466851
REFERENCE   6
  AUTHORS   Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C.,
            Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R.,
            Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R.,
            Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E.,
            Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L.,
            Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M.,
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            di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G.,
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            Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H.,
            Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K.,
            Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J.,
            Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L.,
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            Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G.,
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            Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D.,
            Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R.,
            Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S.,
            Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R.,
            Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A.,
            Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T.,
            Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A.,
            Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M.,
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            Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K.,
            Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.
  CONSRTM   FANTOM Consortium
  TITLE     The transcriptional landscape of the mammalian genome
  JOURNAL   Science 309 (5740), 1559-1563 (2005)
   PUBMED   16141072
REFERENCE   7
  AUTHORS   Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M.,
            Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H.,
            Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T.,
            Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L.,
            Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A.,
            Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and
            Wahlestedt,C.
  CONSRTM   RIKEN Genome Exploration Research Group
  TITLE     Antisense transcription in the mammalian transcriptome
  JOURNAL   Science 309 (5740), 1564-1566 (2005)
   PUBMED   16141073
REFERENCE   8  (bases 1 to 2908)
  AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K.,
            Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S.,
            Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N.,
            Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D.,
            Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
            Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
            Trust/MRC building Addenbrookes Hospital Cambridge) whose
            assistance we gratefully acknowledge.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
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ORIGIN

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Qy        360 GAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTT 419

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Qy        420 CACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAG 479

Db        872 CACGTGCTCATGGCTGGTGCAAAGAAACATGGACTTGAAGTTCAACATCAAGAGCAGTAG 931

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Db        932 CAGTTCCCCTGACTCTCGGGCAGTGACATGTGGAATGGCGTCTCTGTCTGCAGAGAAGGT 991

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Qy        660 GTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAA 719

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RESULT 12
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LOCUS       CD559452                754 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496548 NIH_MGC_195 Homo sapiens cDNA clone
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ACCESSION   CD559452
VERSION     CD559452.2  GI:38453473
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 754)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585520.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 01
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                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match           48.5%;  Score 479;  DB 5;  Length 754;
  Best Local Similarity   85.0%;  Pred. No. 1.3e-128;
  Matches  560;  Conservative    0;  Mismatches   95;  Indels    4;  Gaps    2;

Qy        329 GAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAA 388

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Db        276 TTTCCCTGACATTTTGCGTTCAGGTTCAGGGCAAGAGCAAGAGAGAAAAGAAAGATAGAG 217

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Db        216 TTTTCACGGACAAGACCTTAGCCACGGTCATTTGCCGCAAAAATGCCAGCATTAGCGTGC 157

Qy        929 AAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987

Db        156 GGGCCCAGGACCGGTACTATAGCTCATTTTGGAGCGAATGGGCATTTGTGCCCTGCAGT 98
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RESULT 13
CD559449/c

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LOCUS       CD559449                766 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496649 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971873 5', mRNA sequence.
ACCESSION   CD559449
VERSION     CD559449.2  GI:38453467
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 766)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585517.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 04
            High quality sequence stop: 641.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971873"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN
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  Query Match           48.0%;  Score 473.4;  DB 5;  Length 766;
  Best Local Similarity  85.8%;  Pred. No. 5.8e-127;
  Matches  538;  Conservative    0;  Mismatches   86;  Indels    3;  Gaps    1;

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Db        714 AGAAGAACCCAGAAATAGTACTTTCTAAGATGCGAGGCCAAGAAGTATTCTGGACGTTTC 655

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Db        654 ACCTGGTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 595

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Db        594 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 535

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Db        534 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 478

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Db        477 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 418

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Db        417 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 358

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Db        357 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 298

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Db        297 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 238

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Db        237 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 178

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Db        177 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 118

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987

Db        117 AGCGAATGGGCATCTGTGCCCTGCAGT 91
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RESULT 14
CD559454/c

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LOCUS       CD559454                725 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14497089 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971868 5', mRNA sequence.
ACCESSION   CD559454
VERSION     CD559454.2  GI:38453478
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
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REFERENCE   1  (bases 1 to 725)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585522.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: g  column: 11
            High quality sequence start: 13
            High quality sequence stop: 573.
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                     /clone="IMAGE:6971868"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match           44.3%;  Score 437.6;  DB 5;  Length 725;
  Best Local Similarity   84.1%;  Pred. No. 1.8e-116;
  Matches  518;  Conservative    0;  Mismatches   94;  Indels    4;  Gaps    2;

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Db        714 AAAAATAAAGCTTTTTAAGATGGGGGCCAAGAAGTATTTGGGAAGTTTCCCTCGCTGTCG 655

Qy        432 GCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGA 491
              |||||||  ||||||||||  ||  |||||  ||||  ||||||||||||||||||  ||||||||
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Qy        492 CCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAA 551
              ||||||||||||||  ||  |||||  ||  ||||||||  |||||||   |||||||  ||||||
Db        595 CCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAA 536

Qy        552 CAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGA 611
              ||  |||  |||     |||||  ||||||||||  |||||||  ||||||||||||  |||||  ||
Db        535 CAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCTGA 479

Qy        612 GGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTA 671
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Db        478 GGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTA 419

Qy        672 CACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACT 731
              ||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||  ||||  ||
Db        418 CACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCT 359

Qy        732 GAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAG 791
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Db        358 GAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAG 299

Qy        792 CACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAG 851
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Db        178 TGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAATGGGC 119

Qy        972 ATCCGTGTCCTGCAGT 987
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RESULT 15
CD559603
LOCUS       CD559603                724 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496630 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971873 5', mRNA sequence.
ACCESSION   CD559603
VERSION     CD559603.2  GI:38558932
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 724)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585671.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 04
            High quality sequence stop: 525.
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                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
```

PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 42.4%; Score 418.8; DB 5; Length 724;
Best Local Similarity 89.6%; Pred. No. 6e-111;
Matches 450; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              |||  ||  |||||||||||||||| | |||||||||||||||||| |||||| ||||||||
Db         14 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 73

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||| ||||| | |||||||| ||||| ||||| ||| | || |||
Db         74 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 133

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
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Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
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Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
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Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Qy        481 GGCTCCTCTGACCCCCAAGGGG 502
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
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Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	3	985	99.8	985	3	US-09-917-265A-55	Sequence 55, Appl
c	4	985	99.8	985	3	US-09-917-265A-57	Sequence 57, Appl
	5	983.8	99.7	1599	3	US-09-917-265A-38	Sequence 38, Appl
c	6	983.8	99.7	1599	3	US-09-917-265A-40	Sequence 40, Appl
	7	982.2	99.5	2193	3	US-09-011-143-5	Sequence 5, Appli
	8	982.2	99.5	2193	3	US-09-302-495-5	Sequence 5, Appli
	9	982.2	99.5	2193	3	US-10-079-616-5	Sequence 5, Appli
	10	921	93.3	921	3	US-09-011-143-6	Sequence 6, Appli
	11	921	93.3	921	3	US-09-302-495-6	Sequence 6, Appli
	12	921	93.3	921	3	US-10-079-616-6	Sequence 6, Appli
	13	919.4	93.2	921	3	US-09-011-143-7	Sequence 7, Appli
	14	919.4	93.2	921	3	US-09-302-495-7	Sequence 7, Appli
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	18	919.4	93.2	1533	3	US-09-917-265A-43	Sequence 43, Appl
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	20	886.2	89.8	990	3	US-09-079-984A-11	Sequence 11, Appl
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	24	883	89.5	987	3	US-09-917-265A-58	Sequence 58, Appl
c	25	883	89.5	987	3	US-09-917-265A-60	Sequence 60, Appl
	26	883	89.5	1599	3	US-09-917-265A-61	Sequence 61, Appl
c	27	883	89.5	1599	3	US-09-917-265A-63	Sequence 63, Appl
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	29	871.8	88.3	990	3	US-09-390-729-1	Sequence 1, Appli
	30	826.6	83.7	921	3	US-09-917-265A-52	Sequence 52, Appl
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	32	825	83.6	1533	3	US-09-917-265A-66	Sequence 66, Appl
c	33	825	83.6	1533	3	US-09-917-265A-68	Sequence 68, Appl
	34	780.6	79.1	987	2	US-08-186-529-1	Sequence 1, Appli
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	36	780.6	79.1	1018	2	US-08-184-009-194	Sequence 194, App
	37	780.6	79.1	1018	2	US-08-458-356-194	Sequence 194, App
	38	780.6	79.1	1018	3	US-08-460-736-194	Sequence 194, App
	39	780.6	79.1	1018	3	US-09-535-370-194	Sequence 194, App
	40	780.6	79.1	1018	3	US-09-663-667-194	Sequence 194, App
	41	780.6	79.1	1389	3	US-09-634-368-4	Sequence 4, Appli
	42	780.6	79.1	1399	2	US-08-751-767A-3	Sequence 3, Appli
	43	780.6	79.1	1623	2	US-08-751-767A-9	Sequence 9, Appli
	44	780.6	79.1	2362	2	US-08-265-087-1	Sequence 1, Appli
	45	780.6	79.1	2362	2	US-08-621-493-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
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; Sequence 29, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(987)
US-09-917-265A-29

Query Match 100.0%; Score 987; DB 3; Length 987;
Best Local Similarity 100.0%; Pred. No. 5.1e-311;
Matches 987; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
```

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Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987

Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987


RESULT 2
US-09-917-265A-31/c
; Sequence 31, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-31
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  Query Match           100.0%;  Score 987;  DB 3;  Length 987;
  Best Local Similarity  100.0%;  Pred. No. 5.1e-311;
  Matches  987;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987

Db         27 AGCAACTGGGCATCCGTGTCCTGCAGT 1
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RESULT 3
US-09-917-265A-55
; Sequence 55, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(984)
US-09-917-265A-55

  Query Match             99.8%;  Score 985;  DB 3;  Length 985;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-310;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
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Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 4
US-09-917-265A-57/c
; Sequence 57, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-57

  Query Match             99.8%;  Score 985;  DB 3;  Length 985;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-310;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
                |||||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGCA 1
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RESULT 5
US-09-917-265A-38
; Sequence 38, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-09-917-265A-38
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  Query Match           99.7%;  Score 983.8;  DB 3;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 7.8e-310;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
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RESULT 6
US-09-917-265A-40/c
; Sequence 40, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-40

  Query Match             99.7%;  Score 983.8;  DB 3;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 7.8e-310;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1599 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 1540

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 1420

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1359 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 1300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1299 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 1240

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1179 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 1120

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1119 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 1060

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        999 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 940

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        939 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 880

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        879 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 820

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 760

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        759 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 640

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
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Db        639 AGCAACTGGGCATCCGTGTCCTGCAGT 613


RESULT 7
US-09-011-143-5
; Sequence 5, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2193 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-5

  Query Match             99.5%;  Score 982.2;  DB 3;  Length 2193;
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  Best Local Similarity   99.7%;  Pred. No. 3.2e-309;
  Matches  984;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||| |||||||||||||||| |||||||||||||||||||| |||
Db         64 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTACCTGGTTTTGCTGGCACCTCCTCTC 123

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 183

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 243

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 303

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 363

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 423

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 483

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 543

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 603

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 663

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 723

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 783

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 843

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 903

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 963

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 1023

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||
Db       1024 AGCAACTGGGCATCCGTGTCCTGCAGT 1050
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RESULT 8

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US-09-302-495-5
; Sequence 5, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2193 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-302-495-5
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  Query Match            99.5%;  Score 982.2;  DB 3;  Length 2193;
  Best Local Similarity   99.7%;  Pred. No. 3.2e-309;
  Matches  984;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||| |||||||||||||||| |||||||||||||||||||| |||
Db         64 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTACCTGGTTTTGCTGGCACCTCCTCTC 123

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 183

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 243

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 303

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
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Db        304 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 363

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 423

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 483

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db        484 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 543

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 603

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 663

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 723

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 783

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 843

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 903

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 963

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 1023

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||||
Db       1024 AGCAACTGGGCATCCGTGTCCTGCAGT 1050


RESULT 9
US-10-079-616-5
; Sequence 5, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2193 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-079-616-5

  Query Match           99.5%;  Score 982.2;  DB 3;  Length 2193;
  Best Local Similarity  99.7%;  Pred. No. 3.2e-309;
  Matches  984;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
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Db         64 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTACCTGGTTTTGCTGGCACCTCCTCTC 123

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 183

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 243

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Db        244 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 303

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
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Db        304 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 363

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
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Db        364 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 423

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 483

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 543

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 603

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 663
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Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 723

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 783

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 843

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 903

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 963

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
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Db        964 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 1023

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
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Db       1024 AGCAACTGGGCATCCGTGTCCTGCAGT 1050
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RESULT 10
US-09-011-143-6
; Sequence 6, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  921 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-6

  Query Match            93.3%;  Score 921;  DB 3;  Length 921;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-289;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
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Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
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Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
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Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
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Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
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Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
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Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
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Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
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Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
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Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
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Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
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Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

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Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

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Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

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Qy        967 TGGGCATCCGTGTCCTGCAGT 987
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Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 11
US-09-302-495-6
; Sequence 6, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-302-495-6

  Query Match             93.3%;  Score 921;  DB 3;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-289;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
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Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

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Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
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Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

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Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

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Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

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Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
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Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
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Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
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Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
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Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
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Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 12
US-10-079-616-6
; Sequence 6, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
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;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;          CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;          PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;          ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;          TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;       INFORMATION FOR SEQ ID NO: 6:
;          SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;          MOLECULE TYPE: cDNA
;          SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-079-616-6

  Query Match             93.3%;  Score 921;  DB 3;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-289;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
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Db          61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
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Db         121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
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Db         181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
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Db         241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy         367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
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Db         361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy         487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy         547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy         607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
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Db         541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy         667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
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Db         601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy         727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
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               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
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Db         781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy         907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
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Db         841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

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Db         901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 13
US-09-011-143-7
; Sequence 7, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  921 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
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;    MOLECULE TYPE:  cDNA
US-09-011-143-7

  Query Match            93.2%;  Score 919.4;  DB 3;  Length 921;
  Best Local Similarity  99.9%;  Pred. No. 5.5e-289;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
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Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

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Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
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Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
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Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
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Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
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Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
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Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
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Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
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Qy        967 TGGGCATCCGTGTCCTGCAGT 987
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Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 14
US-09-302-495-7
; Sequence 7, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 7:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-302-495-7

  Query Match            93.2%;  Score 919.4;  DB 3;  Length 921;
  Best Local Similarity  99.9%;  Pred. No. 5.5e-289;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
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Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
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Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
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Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
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Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
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Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
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Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
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Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
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Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

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Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
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Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
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Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
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Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 15
US-10-079-616-7
; Sequence 7, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 7:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-079-616-7

  Query Match             93.2%;  Score 919.4;  DB 3;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 5.5e-289;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
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Db           1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
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Db         121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
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Db         481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

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Db         541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy         667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
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Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
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Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
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Db        901 TGGGCATCCGTGTCCTGCAGT 921
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16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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c	2	987	100.0	987	3	US-09-917-265-31	Sequence 31, Appl
	3	987	100.0	987	9	US-10-821-670-29	Sequence 29, Appl
c	4	987	100.0	987	9	US-10-821-670-31	Sequence 31, Appl
	5	985	99.8	985	3	US-09-917-265-55	Sequence 55, Appl
c	6	985	99.8	985	3	US-09-917-265-57	Sequence 57, Appl
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c	35	883	89.5	1599	3	US-09-917-265-63	Sequence 63, Appl
	36	883	89.5	1599	9	US-10-821-670-61	Sequence 61, Appl
c	37	883	89.5	1599	9	US-10-821-670-63	Sequence 63, Appl
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c	43	825	83.6	1533	3	US-09-917-265-68	Sequence 68, Appl
	44	825	83.6	1533	9	US-10-821-670-66	Sequence 66, Appl
c	45	825	83.6	1533	9	US-10-821-670-68	Sequence 68, Appl

ALIGNMENTS

RESULT 1
US-09-917-265-29
; Sequence 29, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(987)
; OTHER INFORMATION:
US-09-917-265-29

Query Match 100.0%; Score 987; DB 3; Length 987;
Best Local Similarity 100.0%; Pred. No. 2.9e-308;
Matches 987; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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; Sequence 31, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
;
; SEQ ID NO 31
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-31

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  Best Local Similarity  100.0%;  Pred. No. 2.9e-308;
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RESULT 3
US-10-821-670-29
; Sequence 29, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(987)
US-10-821-670-29

Query Match 100.0%; Score 987; DB 9; Length 987;
Best Local Similarity 100.0%; Pred. No. 2.9e-308;
Matches 987; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

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Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

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Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
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Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
```

RESULT 4
US-10-821-670-31/c
; Sequence 31, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Felis catus
US-10-821-670-31

Query Match 100.0%; Score 987; DB 9; Length 987;
Best Local Similarity 100.0%; Pred. No. 2.9e-308;
Matches 987; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748
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Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGCAGT 1
```

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RESULT 5
US-09-917-265-55
; Sequence 55, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(984)
;   OTHER INFORMATION:
US-09-917-265-55

  Query Match             99.8%;  Score 985;  DB 3;  Length 985;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-307;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
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Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985
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RESULT 6
US-09-917-265-57/c
; Sequence 57, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
; LENGTH: 985
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265-57

Query Match 99.8%; Score 985; DB 3; Length 985;
Best Local Similarity 100.0%; Pred. No. 1.3e-307;
Matches 985; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326
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Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGCA 1
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RESULT 7
US-10-821-670-55
; Sequence 55, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
; LENGTH: 985
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(984)
US-10-821-670-55

Query Match 99.8%; Score 985; DB 9; Length 985;
Best Local Similarity 100.0%; Pred. No. 1.3e-307;
Matches 985; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985
```

RESULT 8
US-10-821-670-57/c
; Sequence 57, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/10/821,670
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 985
; TYPE: DNA
; ORGANISM: Felis catus
US-10-821-670-57

Query Match 99.8%; Score 985; DB 9; Length 985;
Best Local Similarity 100.0%; Pred. No. 1.3e-307;
Matches 985; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
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Db         25 AGCAACTGGGCATCCGTGTCCTGCA 1
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RESULT 9
US-10-041-672C-1
; Sequence 1, Application US/10041672C
; Publication No. US20030157059A1
; GENERAL INFORMATION:
;  APPLICANT: Mologen Forschungs-, Entwicklungs- und Vetriebs GmbH
;  APPLICANT:  Universitat Zurich
;  TITLE OF INVENTION: FELINE INTERLEUKIN-12 AS IMMUNOSTIMULANT
;  FILE REFERENCE: NHL-NP-36
;  CURRENT APPLICATION NUMBER: US/10/041,672C
;  CURRENT FILING DATE:  2002-01-08
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 990
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: feline IL-12 p40
US-10-041-672C-1

  Query Match             99.7%;  Score 983.8;  DB 7;  Length 990;
  Best Local Similarity   99.8%;  Pred. No. 3.1e-307;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987


RESULT 10
US-09-917-265-38
; Sequence 38, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
US-09-917-265-38

  Query Match             99.7%;  Score 983.8;  DB 3;  Length 1599;
  Best Local Similarity   99.8%;  Pred. No. 4.1e-307;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
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Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
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RESULT 11
US-09-917-265-40/c
; Sequence 40, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265-40

Query Match 99.7%; Score 983.8; DB 3; Length 1599;
Best Local Similarity 99.8%; Pred. No. 4.1e-307;
Matches 985; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1599 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 1540

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 1420

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1359 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 1300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1299 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 1240

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1179 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 1120

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       1119 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 1060

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        999 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 940

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        939 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 880

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        879 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 820

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 760

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        759 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 640

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||||
Db        639 AGCAACTGGGCATCCGTGTCCTGCAGT 613
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RESULT 12
US-10-821-670-38
; Sequence 38, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.

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;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-10-821-670-38

  Query Match            99.7%;  Score 983.8;  DB 9;  Length 1599;
  Best Local Similarity  99.8%;  Pred. No. 4.1e-307;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987


RESULT 13
US-10-821-670-40/c
; Sequence 40, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-40

  Query Match            99.7%;  Score 983.8;  DB 9;  Length 1599;
  Best Local Similarity  99.8%;  Pred. No. 4.1e-307;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1599 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 1540

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 1420

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1359 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 1300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1299 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 1240

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180
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Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1179 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 1120

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       1119 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 1060

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        999 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 940

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        939 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 880

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        879 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 820

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 760

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        759 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 640

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
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Db        639 AGCAACTGGGCATCCGTGTCCTGCAGT 613
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RESULT 14
US-10-041-672C-10
; Sequence 10, Application US/10041672C
; Publication No. US20030157059A1
; GENERAL INFORMATION:
; APPLICANT: Mologen Forschungs-, Entwicklungs- und Vetriebs GmbH
; APPLICANT: Universitat Zurich
; TITLE OF INVENTION: FELINE INTERLEUKIN-12 AS IMMUNOSTIMULANT
; FILE REFERENCE: NHL-NP-36
; CURRENT APPLICATION NUMBER: US/10/041,672C
; CURRENT FILING DATE: 2002-01-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 4522
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pMol-fil12p40
US-10-041-672C-10

Query Match 99.7%; Score 983.8; DB 7; Length 4522;
Best Local Similarity 99.8%; Pred. No. 7.2e-307;
Matches 985; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
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Db       3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166
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Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db       3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||
Db       4007 AGCAACTGGGCATCCGTGTCCTGCAGT 4033
```

RESULT 15
US-10-079-616-5
; Sequence 5, Application US/10079616
; Publication No. US20020107366A1
; GENERAL INFORMATION:
; APPLICANT: IMAMURA, Takayuki
; MAEDA, Hiroaki
; FUJIYASU, Takeshi
; IMAGAWA, Yoshitaka
; TOKIYOSHI, Sachio
; TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN

```
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 5:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 2193 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-079-616-5

  Query Match             99.5%;  Score 982.2;  DB 6;  Length 2193;
  Best Local Similarity   99.7%;  Pred. No. 1.6e-306;
  Matches  984;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||| |||||||||||||||||| ||||||||||||||||||||| |||
Db         64 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTACCTGGTTTTGCTGGCACCTCCTCTC 123

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 183

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 243

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 303

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 363

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 423

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 483

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 543

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 603

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Db        604 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 663

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 723

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Db        724 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 783

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 843

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 903

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 963

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 1023

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||||||||
Db       1024 AGCAACTGGGCATCCGTGTCCTGCAGT 1050


Search completed: June 10, 2006, 18:16:30
Job time : 1127.25 secs
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 10, 2006, 15:46:40 ; Search time 17.1098 Seconds
(without alignments)
7321.729 Million cell updates/sec

Title: US-10-821-670A-29
Perfect score: 987
Sequence: 1 atgcatcctcagcagttggt.....gggcatccgtgtcctgcagt 987

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 253354 seqs, 63461778 residues

Total number of hits satisfying chosen parameters: 506708

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	36.8	3.7	3401	6	US-10-196-749-411	Sequence 411, App
	2	34.8	3.5	3166	7	US-11-293-697-739	Sequence 739, App
c	3	34.4	3.5	1438	6	US-10-953-349-20792	Sequence 20792, A
	4	34.4	3.5	2268	7	US-11-217-529-1612	Sequence 1612, Ap
	5	33.8	3.4	1948	6	US-10-508-063A-4	Sequence 4, Appli
	6	33.2	3.4	2513	7	US-11-293-697-145	Sequence 145, App
	7	32.4	3.3	2152	6	US-10-953-349-38921	Sequence 38921, A
	8	32	3.2	620	6	US-10-953-349-32903	Sequence 32903, A
	9	32	3.2	2024	7	US-11-293-697-1253	Sequence 1253, Ap
	10	31.8	3.2	1404	6	US-10-471-571A-5411	Sequence 5411, Ap
c	11	31.8	3.2	1906	6	US-10-953-349-22720	Sequence 22720, A
c	12	31.4	3.2	1636	6	US-10-953-349-22635	Sequence 22635, A
c	13	31.4	3.2	6051	7	US-11-313-450-9	Sequence 9, Appli
	14	31.2	3.2	1286	7	US-11-145-307A-72	Sequence 72, Appl
	15	31	3.1	2843	7	US-11-293-697-1498	Sequence 1498, Ap
c	16	30.8	3.1	992	6	US-10-953-349-31065	Sequence 31065, A
	17	30.8	3.1	2640	6	US-10-527-411-29	Sequence 29, Appl
	18	30.8	3.1	3930	7	US-11-217-529-76026	Sequence 76026, A
	19	30.6	3.1	2619	7	US-11-302-678-18	Sequence 18, Appl
	20	30.6	3.1	3232	7	US-11-302-678-16	Sequence 16, Appl
c	21	30.4	3.1	296	7	US-11-301-554-517	Sequence 517, App
	22	30.4	3.1	444	7	US-11-217-529-79558	Sequence 79558, A
c	23	30.4	3.1	1467	7	US-11-217-529-79610	Sequence 79610, A
c	24	30.4	3.1	2249	7	US-11-293-697-442	Sequence 442, App
c	25	30.4	3.1	3294	7	US-11-293-697-1397	Sequence 1397, Ap
c	26	30.2	3.1	924	7	US-11-217-529-1898	Sequence 1898, Ap
	27	30.2	3.1	1848	6	US-10-519-335-5	Sequence 5, Appli
	28	30.2	3.1	1878	6	US-10-519-335-3	Sequence 3, Appli
	29	30.2	3.1	1932	6	US-10-519-335-1	Sequence 1, Appli
	30	30	3.0	1376	6	US-10-527-411-71	Sequence 71, Appl
	31	30	3.0	1376	6	US-10-527-411-73	Sequence 73, Appl
	32	30	3.0	1376	6	US-10-527-411-75	Sequence 75, Appl
	33	30	3.0	1376	6	US-10-527-411-77	Sequence 77, Appl
	34	30	3.0	1385	6	US-10-527-411-69	Sequence 69, Appl
	35	30	3.0	2600	6	US-10-527-411-33	Sequence 33, Appl
	36	30	3.0	2600	6	US-10-527-411-35	Sequence 35, Appl
	37	30	3.0	2600	6	US-10-527-411-37	Sequence 37, Appl
	38	30	3.0	2609	6	US-10-527-411-31	Sequence 31, Appl
	39	30	3.0	2625	6	US-10-527-411-150	Sequence 150, App
	40	30	3.0	2625	6	US-10-527-411-164	Sequence 164, App
	41	30	3.0	2625	6	US-10-527-411-166	Sequence 166, App
	42	30	3.0	2625	6	US-10-527-411-168	Sequence 168, App
	43	30	3.0	2637	6	US-10-527-411-156	Sequence 156, App
	44	30	3.0	2643	6	US-10-527-411-61	Sequence 61, Appl
	45	30	3.0	2667	6	US-10-527-411-160	Sequence 160, App

ALIGNMENTS

RESULT 1
US-10-196-749-411
; Sequence 411, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 411
; LENGTH: 3401
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-196-749-411

Query Match 3.7%; Score 36.8; DB 6; Length 3401;
Best Local Similarity 46.5%; Pred. No. 0.1;
Matches 119; Conservative 0; Mismatches 137; Indels 0; Gaps 0;

```
Qy        540 CAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTG 599
              ||  ||  || ||  | |  | |  |||| |   ||||| ||    | || || ||   |
Db        130 CACCGTCTACTACGTGCACAACATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAG 189

Qy        600 CCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAA 659
              || | | | | |    | |   | |  ||    |    ||| | |  |    |||| ||
Db        190 CCTGACGGGCTACCGCACCTACCGCTGTGCCCACCCCCTGGCCACACTCTTCAAGATCCT 249

Qy        660 GTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAA 719
              |      ||||| ||||    || || ||   | | |||||     | || |||
Db        250 GGCGTCCTTCTACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCATGTACACACTGTG 309

Qy        720 GAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCC 779
              |   ||| || |    |  | || || |   |  || |   |  |  |||   |
Db        310 GTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTTGAGTCGATCCGTGAGGAGAGCAG 369

Qy        780 TGACACCTGGAGCACC 795
                |||  |   | | ||
Db        370 CTACAGCGACATCCCC 385
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RESULT 2
US-11-293-697-739
; Sequence 739, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 739
; LENGTH: 3166
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-739

Query Match 3.5%; Score 34.8; DB 7; Length 3166;
Best Local Similarity 49.5%; Pred. No. 0.43;
Matches 90; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

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Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              || ||||| || ||  |  || |||||  |    ||     | |    |   ||| |   |
Db       1418 GGACAGAGAGGTCAGAAATGAATATAACATCACCATCACCGTGACCGACTTGGGGACACC 1477

Qy        597 CTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCT 656
              | | | |    |||| | | | || || |    |||   |  | |   |    ||   |
Db       1478 CAGGCTGAAAACCGAGCACAACATAACCGTGCTGGTCTCCGACGTCAATGACAACGCCCC 1537

Qy        657 CAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACC 716
              ||  | |    |   | ||  || | | ||| || | || | || ||  || | ||  |
Db       1538 CATCTTCACCCAAACCTCCTACACCCTGTTCGTCCGCGAGAACAACAGCCCCGCCCTGCA 1597

Qy        717 CA 718
              ||
Db       1598 CA 1599
```

RESULT 3
US-10-953-349-20792/c
; Sequence 20792, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20792
; LENGTH: 1438
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-20792

Query Match 3.5%; Score 34.4; DB 6; Length 1438;
Best Local Similarity 50.0%; Pred. No. 0.36;
Matches 86; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

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Qy        243 ATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTT 302
              ||  ||| |||   || | ||  |||     | | |||   |       ||| ||  | |
Db       1331 ATAGGCACATGGAAGCAATTACTCCTTCACCATATGAGAACAACACTGGAGTCAAGCATG 1272

Qy        303 CCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAA 362
              ||||  || ||| |    |||  ||   |    ||| || | || || | | ||   ||
Db       1271 GATCCTAATCCACTAGTTCGAAACTGTGTTAAACTCCTCTCAAATTTTCATGCAATCTAA 1212

Qy        363 AGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGA 414
                ||   |||| |||||| | |    | | | ||     ||| |   ||
Db       1211 CTGTAACACTGATAACATCTTTTTTACCCCTTATGTAATACTTTACTGCTGA 1160
```

RESULT 4
US-11-217-529-1612
; Sequence 1612, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1612
; LENGTH: 2268
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1612

Query Match 3.5%; Score 34.4; DB 7; Length 2268;
Best Local Similarity 59.0%; Pred. No. 0.47;
Matches 59; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

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Qy        150 CAATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGG 209
              ||||||  |||||||||  ||||||      |||  | | |    | ||   ||  |   |
Db       1869 CAATACCCCTGAAGAAAATGACACTGAGGGGAAGTATAATACAATCAAGAAAAGCTCGGA 1928

Qy        210 CTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCA 249
                | || | || |||  | ||   |  ||||||||||  ||
Db       1929 TTATGATGAATCTCATATCACGAATATCAAAGAATTACCA 1968
```

RESULT 5
US-10-508-063A-4
; Sequence 4, Application US/10508063A
; Publication No. US20060088832A1
; GENERAL INFORMATION:

```
;  APPLICANT: Deutsches Krebsforschungszentrum
;  APPLICANT:  ANGEL, Peter
;  APPLICANT:  FURSTENBERGER, Gerhard
;  APPLICANT:  BREITENBACH, Ute
;  APPLICANT:  RICHTER, Harmut
;  APPLICANT:  HESS, Jochen
;  APPLICANT:  TUCKERMAN, Jan
;  TITLE OF INVENTION: TAP-70, A NOVEL MARKER FOR EPITHELIAL TUMORS
;  FILE REFERENCE: 31304-701.831
;  CURRENT APPLICATION NUMBER: US/10/508,063A
;  CURRENT FILING DATE:  2004-09-16
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 1948
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-508-063A-4

  Query Match             3.4%;  Score 33.8;  DB 6;  Length 1948;
  Best Local Similarity   52.4%;  Pred. No. 0.67;
  Matches   99;  Conservative    0;  Mismatches   87;  Indels    3;  Gaps    1;

Qy        495 CCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAG 554
              | ||| ||  | | | | ||    ||   |||  |  | |  || || ||     | |
Db       1111 CAAAGTGGCCAATGGGGCAGAGATGAAGATCTTGGGTGTGTGGGACACAGAAATTAGCCT 1170

Qy        555 GGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGA 614
              ||   | |  |||    |  |  |||| || || || ||  ||| ||   || |  ||||
Db       1171 GGGCAAGACAAAGCTGAAGGCCGAGTTTCTGGTGGCCAACGCCAGC---GCAGAAGAGGC 1227

Qy        615 GAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACAC 674
              |   |   ||  || ||| ||  ||||   | |  |  |||  | | |||| ||  |||
Db       1228 TATTATTGGCACAGACGTCTTGCAGGACCACAATGCCGTGCTGGACTTCGAACACCGCAC 1287

Qy        675 CAGCAGCTT 683
              | ||| | |
Db       1288 CTGCACCCT 1296


RESULT 6
US-11-293-697-145
; Sequence 145, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 145
;   LENGTH: 2513
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-145

  Query Match             3.4%;  Score 33.2;  DB 7;  Length 2513;
  Best Local Similarity   52.1%;  Pred. No. 1.2;
  Matches   74;  Conservative    0;  Mismatches   68;  Indels    0;  Gaps    0;

Qy        627 TGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTT 686
              |||| | |   |||| |||      |  |  | |||| | |||| || | |     || |
Db        973 TGAAATGGCCCTGGATGCTGAGTTCCTGGACGTGTACAAGAACTGCAACGGGGTGGTCAT 1032

Qy        687 CATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAA 746
               ||    ||||| | ||| | |    |   |||  || | |  | | |||    ||||
Db       1033 GATGTTCGACATTACCAAGCAGTGGACCTTCAATTACATTCTCCGGGAGCTTCCAAAAGT 1092

Qy        747 TTCTCGGCATGTGGAAGTGAGC 768
                |    || |||  |||| ||
Db       1093 GCCCACCCACGTGCCAGTGTGC 1114


RESULT 7
US-10-953-349-38921
; Sequence 38921, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38921
;   LENGTH: 2152
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-38921

  Query Match             3.3%;  Score 32.4;  DB 6;  Length 2152;
  Best Local Similarity   47.9%;  Pred. No. 2;
  Matches   93;  Conservative    0;  Mismatches  101;  Indels    0;  Gaps    0;

Qy        524 TCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTC 583
              |||| || ||| || ||||        | |  | |  | | |||| | || |  ||| |
Db        475 TCTCGGCCGAGGAGATCAGCTCCATGATCCTGAACAAGATGAAGGAGACGGCCGAGGCTT 534

Qy        584 AGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACG 643
              |    ||||  ||  |  |   || |  |  | | | ||      | ||   |    |
Db        535 ACCTCGGCACCACCATCAAGAACGCTGTCGTCACCGTCCCGGCCTACTTCAACGACTCCC 594

Qy        644 CTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCA 703
                  ||      |||| |||    |  || |  | || ||  | ||| |  ||||||||
Db        595 AGCGCCAGGCCACCAAGGACGCCGGCGTCATCTCCGGCCTCAACGTCATGCGCATCATCA 654

Qy        704 AACCGGACCCACCC 717
              |   |  | |  ||
Db        655 ACGAGCCCACCGCC 668


RESULT 8
US-10-953-349-32903
; Sequence 32903, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32903
;   LENGTH: 620
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-32903

  Query Match             3.2%;  Score 32;  DB 6;  Length 620;
  Best Local Similarity   47.1%;  Pred. No. 1.3;
  Matches   98;  Conservative    0;  Mismatches  110;  Indels    0;  Gaps    0;

Qy        574 GTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTC 633
              |||||||       | |    ||    || |||||| | |  |   |  ||   |   ||
Db         90 GTGGAGTTGGCAAAAGCTCATGAGATCCAGGCTGCTGTGCTGTTGCACCCTTCTTTTGTT 149

Qy        634 GTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGG 693
                || |||| |||  |  || |||||| || ||  |  | |  | |        ||
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```
Db        150 ACCGTTGACGATATCAAAGAGGTCAAGTGCGCAATTTCTATCCTCGGAGCTGAGATTGAC 209

Qy        694 GACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGG 753

Db        210 AAAATGTCCCCACCGGAGCTAATCAAGCAGTTCGAGCAGGTCCTTTCTTTGAACTCAGGG 269

Qy        754 CATGTGGAAGTGAGCTGGGAATACCCTG 781

Db        270 GTTGGCCACTTCGTCAAGATCTTCCCTG 297
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RESULT 9
US-11-293-697-1253
; Sequence 1253, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1253
; LENGTH: 2024
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-1253

Query Match 3.2%; Score 32; DB 7; Length 2024;
Best Local Similarity 50.7%; Pred. No. 2.6;
Matches 77; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

```
Qy        210 CTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTG 269

Db        496 CTCTGTTGAAAGTTTGTTTCACCAGCAAATACTTTCTTCTTGTGCCAAAAGCTATAACTT 555

Qy        270 TCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGG 329

Db        556 TGATCAATATAGGAAGGTCTTTACTCATTCATCATTGCTTAATCAACAAGAGGAAATAGA 615

Qy        330 AATTTGGTCCACTGATATCTTAAGGGAACAGA 361

Db        616 TATTTGGGGAAAACATCACATATATGATAAAA 647
```

RESULT 10
US-10-471-571A-5411
; Sequence 5411, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 5411
; LENGTH: 1404
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-471-571A-5411

Query Match 3.2%; Score 31.8; DB 6; Length 1404;
Best Local Similarity 57.6%; Pred. No. 2.4;
Matches 57; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

```
Qy        328 GGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTA 387

Db         11 GTAATTTTTTAAATGTAGAGTTAATAGGTACTAAAATAATAACAATGGAAGACTTTTATA 70

Qy        388 AAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426

Db         71 AAATGAAGGAAGAAGAATTTTTCTTAAAATCTAAGCTAC 109
```

RESULT 11
US-10-953-349-22720/c
; Sequence 22720, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22720
; LENGTH: 1906
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-22720

Query Match 3.2%; Score 31.8; DB 6; Length 1906;
Best Local Similarity 61.4%; Pred. No. 2.9;
Matches 51; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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Qy        226 ACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAG 285

Db        918 ACTATCCAAGTCACTGACATTGCAGTTCCCATTATTTAACGCAGTCATATCTATAGAGGA 859

Qy        286 GTTCTGAGCCATTCGTTCCTCCT 308

Db        858 ATTTTGAGCCAATGCTTCCTCCT 836
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RESULT 12
US-10-953-349-22635/c
; Sequence 22635, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22635
; LENGTH: 1636
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-22635

Query Match 3.2%; Score 31.4; DB 6; Length 1636;
Best Local Similarity 46.9%; Pred. No. 3.5;
Matches 98; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

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Qy        650 ACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGG 709

Db       1479 ACACAGTCATGGACTTTTCATATCCATCTCACTCTTGCATGCGGATGATACACCTAATGG 1420

Qy        710 ACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCT 769

Db       1419 ACTGTCCCTTCAGCATTAAATCAAAAGCTTTGTTGATCTCTGAGAATGGAACTGTGTGAG 1360

Qy        770 GGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTAC 829
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Db       1359 TGATGAATTTGTCCACTTCTAGCTCCCCACTCATGTACTTCTCGACAACAGATGGAAGAT 1300

Qy        830 AGGTCCAGGGCAAGAACAACAGAGAAAAG 858
              ||| |  ||   | |      | |||||
Db       1299 CGGTGCGTGGTTTGTAGTTGCCATAAAAG 1271


RESULT 13
US-11-313-450-9/c
; Sequence 9, Application US/11313450
; Publication No. US20060110778A1
; GENERAL INFORMATION:
;  APPLICANT: Adorante, Joeseph S.
;  APPLICANT:  Ehring, George R.
;  TITLE OF INVENTION: High-Throughput Screens For Identifying
;  TITLE OF INVENTION:  Selective Persistent Sodium Channels Channel Blockers
;  FILE REFERENCE: 17407 CIP (AP)
;  CURRENT APPLICATION NUMBER: US/11/313,450
;  CURRENT FILING DATE:  2005-12-19
;  PRIOR APPLICATION NUMBER: 09/989797
;  PRIOR FILING DATE: 2001-11-20
;  PRIOR APPLICATION NUMBER: 60/252771
;  PRIOR FILING DATE: 2000-11-22
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 6051
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-313-450-9

  Query Match             3.2%;  Score 31.4;  DB 7;  Length 6051;
  Best Local Similarity   59.6%;  Pred. No. 7.7;
  Matches   53;  Conservative    0;  Mismatches   36;  Indels    0;  Gaps    0;

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              |||| | ||  || ||   || ||||||    ||||   || ||| | |||| || |||
Db       5636 AACTTCTCCTCCATCTGGATCTTCAGGGCGTCCATCTCCCCAGACTCCCCCAGGACCCTT 5577

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCA 755
                |||| ||   | ||  ||   |||
Db       5576 TTGGTGAAGGCAAAGAGAATGTCCATGCA 5548


RESULT 14
US-11-145-307A-72
; Sequence 72, Application US/11145307A
; Publication No. US20060094035A1
; GENERAL INFORMATION:
;  APPLICANT: Arcturus Bioscience, Inc.
;  APPLICANT:  Erlander, Mark G.
;  APPLICANT:  Ma, Xiao-Jun
;  TITLE OF INVENTION: Identification of Tumors
;  FILE REFERENCE: 022041-002020US
;  CURRENT APPLICATION NUMBER: US/11/145,307A
;  CURRENT FILING DATE:  2005-06-03
;  PRIOR APPLICATION NUMBER: US 60/577,084
;  PRIOR FILING DATE: 2004-06-04
;  NUMBER OF SEQ ID NOS: 268
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72
;   LENGTH: 1286
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-145-307A-72

  Query Match             3.2%;  Score 31.2;  DB 7;  Length 1286;
  Best Local Similarity   50.7%;  Pred. No. 3.5;
  Matches   75;  Conservative    0;  Mismatches   73;  Indels    0;  Gaps    0;

Qy        534 GAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAG 593
              | ||||    |||||  |   ||| |   || ||| ||   ||||    | ||    | |
Db        632 GCAGGTGGAGGTGGAGGAGGAGGAGTTCCAGGAGTTCATCCTGGACACACTGGTCCTCTG 691

Qy        594 TGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAA 653
              || ||||   |||  |||   ||   | || ||| | | |   | || ||
Db        692 CCTGCAGGAGGATGCCACCGAGGCCCTGGGCAGCAATGTGGTGCTTGTCCTGAAGCAGAA 751

Qy        654 GCTCAAGTACGAAAACTACACCAGCAGC 681
              ||||     ||  ||| | | || | ||
Db        752 GCTCCTCAGCGCCAACCAGAACATCCGC 779


RESULT 15
US-11-293-697-1498
; Sequence 1498, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1498
;   LENGTH: 2843
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1498

  Query Match             3.1%;  Score 31;  DB 7;  Length 2843;
  Best Local Similarity   48.6%;  Pred. No. 6.6;
  Matches   85;  Conservative    0;  Mismatches   90;  Indels    0;  Gaps    0;

Qy        563 AGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTAC 622
              ||  |||| ||| | ||    || |       |||  ||||||  ||  | ||||| |
Db       1858 AGGTGTACGCAGAGAAGAAGGAGAATTCACCAGCCCCCCCGGCACCCATGCAGAGCATCT 1917

Qy        623 CCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCT 682
              |||  |   ||  || |   | |  | | ||  ||     |  ||  || |  || ||
Db       1918 CCAGCGGCATCAGGGAGACAGTGAGCCCCCAGGACATCGTGCAGGACGCCATCCACAACT 1977

Qy        683 TCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCC 737
              ||| |  |    ||      | |  || | |   ||| | ||  |   |  | |||
Db       1978 TCTCCCCCGCCTACCAGCACTACACGCAGCAGGCCACGCACGAGGCGCCCAGGCC 2032


Search completed: June 10, 2006, 18:18:55
Job time : 18.1098 secs
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2006, 22:33:03 ; Search time 6252.4 Seconds
(without alignments)
10094.706 Million cell updates/sec

Title: US-10-821-670A-29
Perfect score: 987
Sequence: 1 atgcatcctcagcagttggt.....gggcatccgtgtcctgcagt 987

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 6366136 seqs, 31973710525 residues

Word size : 1

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10: gb_vi:*
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15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	987	100.0	987	2	AR595950	AR595950 Sequence
c	2	987	100.0	987	2	AR595951	AR595951 Sequence
	3	985	99.8	985	2	AR595967	AR595967 Sequence
c	4	985	99.8	985	2	AR595968	AR595968 Sequence
	5	930	94.2	2193	2	AR242435	AR242435 Sequence
	6	930	94.2	2193	2	AR280203	AR280203 Sequence
	7	930	94.2	2193	2	AR322418	AR322418 Sequence
	8	921	93.3	921	2	AR242436	AR242436 Sequence
	9	921	93.3	921	2	AR280204	AR280204 Sequence
	10	921	93.3	921	2	AR322419	AR322419 Sequence
	11	905	91.7	1006	14	FCIL12P40	Y07762 Felis catus
	12	905	91.7	1599	2	AR595956	AR595956 Sequence
c	13	905	91.7	1599	2	AR595957	AR595957 Sequence
	14	885	89.7	990	2	AX076200	AX076200 Sequence
	15	885	89.7	990	2	AX076482	AX076482 Sequence
	16	885	89.7	4522	2	AX076209	AX076209 Sequence
	17	885	89.7	4522	2	AX076476	AX076476 Sequence
	18	870	88.1	921	2	AR242437	AR242437 Sequence
	19	870	88.1	921	2	AR280205	AR280205 Sequence
	20	870	88.1	921	2	AR322420	AR322420 Sequence
	21	870	88.1	921	2	AR595948	AR595948 Sequence
c	22	870	88.1	921	2	AR595949	AR595949 Sequence
	23	870	88.1	1533	2	AR595959	AR595959 Sequence
c	24	870	88.1	1533	2	AR595960	AR595960 Sequence
	25	831	84.2	990	14	FCU83184	U83184 Felis catus
	26	382	38.7	431	14	AF054607	AF054607 Felis cat
	27	83	8.4	990	2	AX154603	AX154603 Sequence
	28	66	6.7	921	2	AR595965	AR595965 Sequence
c	29	66	6.7	921	2	AR595966	AR595966 Sequence
	30	66	6.7	924	2	BD171282	BD171282 Novel can
	31	66	6.7	987	2	AR595969	AR595969 Sequence
c	32	66	6.7	987	2	AR595970	AR595970 Sequence
	33	66	6.7	990	2	AR151061	AR151061 Sequence
	34	66	6.7	990	2	AR151071	AR151071 Sequence
	35	66	6.7	990	2	BD014653	BD014653 Process f
	36	66	6.7	990	2	BD014663	BD014663 Process f
	37	66	6.7	990	2	E15017	E15017 Canine mRNA
	38	66	6.7	990	2	AR316460	AR316460 Sequence
	39	66	6.7	990	2	AR316470	AR316470 Sequence
	40	66	6.7	1533	2	AR595973	AR595973 Sequence
c	41	66	6.7	1533	2	AR595974	AR595974 Sequence
	42	66	6.7	1599	2	AR595971	AR595971 Sequence
c	43	66	6.7	1599	2	AR595972	AR595972 Sequence
	44	66	6.7	2154	2	BD171281	BD171281 Novel can
	45	66	6.7	2267	2	AR596011	AR596011 Sequence
c	46	66	6.7	2267	2	AR596012	AR596012 Sequence
	47	65	6.6	984	2	AX154600	AX154600 Sequence
	48	63	6.4	588	14	AF349536	AF349536 Canis fam
	49	63	6.4	1015	14	CFU49100	U49100 Canis famil
	50	61	6.2	621	7	BV242752	BV242752 S234P6134
	51	61	6.2	984	2	AX154598	AX154598 Sequence
	52	60	6.1	984	2	AX154599	AX154599 Sequence
	53	53	5.4	975	2	AX154602	AX154602 Sequence
	54	51	5.2	452	14	AF333121	AF333121 Canis fam
	55	51	5.2	821	6	RNU16674	U16674 Rattus norv
	56	51	5.2	1008	6	AF133197	AF133197 Rattus no
	57	49	5.0	1425	6	AF421395	AF421395 Sigmodon
	58	44	4.5	224	14	DQ152965	DQ152965 Ovis arie
	59	44	4.5	525	14	CEU10160	U10160 Cervus elap
	60	44	4.5	906	2	BD021808	BD021808 Natural k
	61	44	4.5	906	2	BD021809	BD021809 Natural k
	62	44	4.5	969	2	AX154601	AX154601 Sequence
	63	44	4.5	984	14	AF004024	AF004024 Ovis arie
	64	44	4.5	984	14	AF209435	AF209435 Ovis arie
	65	44	4.5	987	2	AR008950	AR008950 Sequence
	66	44	4.5	987	2	BD007070	BD007070 IL-12 gen
	67	44	4.5	987	2	BD007076	BD007076 Gene expr
	68	44	4.5	987	2	BD105974	BD105974 Animal mo
	69	44	4.5	987	2	BD136034	BD136034 Interfero
	70	44	4.5	987	2	CQ803342	CQ803342 Sequence
	71	44	4.5	987	2	CS131491	CS131491 Sequence
	72	44	4.5	987	2	I28591	I28591 Sequence 1
	73	44	4.5	987	2	AR533404	AR533404 Sequence
	74	44	4.5	987	2	AX154633	AX154633 Sequence
	75	44	4.5	993	14	AY603406	AY603406 Capra hir
	76	44	4.5	993	14	CEU57752	U57752 Cervus elap
	77	44	4.5	1005	5	AY234218	AY234218 Papio anu
	78	44	4.5	1005	5	CTU19834	U19834 Cercocebus
	79	44	4.5	1007	5	AF180563	AF180563 Homo sapi
	80	44	4.5	1008	14	AB246273	AB246273 Bubalus c
	81	44	4.5	1008	14	AB246353	AB246353 Bubalus b
	82	44	4.5	1008	14	AB246358	AB246358 Bubalus b
	83	44	4.5	1012	14	AF007576	AF007576 Capra hir
	84	44	4.5	1012	14	AY198121	AY198121 Bubalus b
	85	44	4.5	1012	14	BTU11815	U11815 Bos taurus
	86	44	4.5	1018	2	AR052857	AR052857 Sequence
	87	44	4.5	1018	2	AR288169	AR288169 Sequence
	88	44	4.5	1018	2	AR567156	AR567156 Sequence
	89	44	4.5	1019	2	E35794	E35794 Process for
	90	44	4.5	1029	2	CQ829448	CQ829448 Sequence
	91	44	4.5	1046	5	BC074723	BC074723 Homo sapi

92	44	4.5	1073	5	BC067498	BC067498 Homo sapi
93	44	4.5	1073	5	BC067499	BC067499 Homo sapi
94	44	4.5	1073	5	BC067500	BC067500 Homo sapi
95	44	4.5	1073	5	BC067501	BC067501 Homo sapi
96	44	4.5	1073	5	BC067502	BC067502 Homo sapi
97	44	4.5	1080	5	MMU19841	U19841 Macaca mula
98	44	4.5	1389	2	AR393788	AR393788 Sequence
99	44	4.5	1389	2	AX084106	AX084106 Sequence
100	44	4.5	1397	2	BD165800	BD165800 Antibody
101	44	4.5	1399	2	AR091391	AR091391 Sequence
102	44	4.5	1399	5	HUMCLMF40	M65272 Human cytot
103	44	4.5	1560	2	AR091395	AR091395 Sequence
104	44	4.5	1623	2	AR091394	AR091394 Sequence
105	44	4.5	1870	2	A92079	A92079 Sequence 3
106	44	4.5	1870	2	AR230691	AR230691 Sequence
107	44	4.5	2307	2	CQ715179	CQ715179 Sequence
108	44	4.5	2318	2	AR228993	AR228993 Sequence
109	44	4.5	2318	5	HUMNKSFP40	M65290 Human natur
110	44	4.5	2362	2	AR082684	AR082684 Sequence
111	44	4.5	2362	2	AR122960	AR122960 Sequence
112	44	4.5	2362	2	I28325	I28325 Sequence 1
113	44	4.5	2362	2	AR309636	AR309636 Sequence
114	44	4.5	2362	2	I89770	I89770 Sequence 1
115	44	4.5	5686	2	BD136048	BD136048 Interfero
116	44	4.5	6139	2	AR091393	AR091393 Sequence
117	39	4.0	993	14	AB107654	AB107654 Lama glam
118	39	4.0	15648	5	AF512686	AF512686 Homo sapi
119	39	4.0	18340	5	AY008847	AY008847 Homo sapi
120	39	4.0	108511	5	AC011418	AC011418 Homo sapi
121	38	3.9	446	14	AF091134	AF091134 Canis fam
122	37	3.7	508	6	AF097507	AF097507 Cavia por
123	37	3.7	999	6	AB025724	AB025724 Cavia por
c 124	35	3.5	681	7	BV440664	BV440664 S237P6324
125	35	3.5	972	8	AY191829	AY191829 Synthetic
126	35	3.5	975	2	AX154597	AX154597 Sequence
127	35	3.5	2090	14	SSU08317	U08317 Sus scrofa
128	32	3.2	1058	14	ECIL12P40	Y11129 Equus cabal
129	32	3.2	1626	8	AF401989	AF401989 Synthetic
c 130	30	3.0	30	2	AX027245	AX027245 Sequence
131	30	3.0	73	2	AR439759	AR439759 Sequence
132	30	3.0	73	2	AX268996	AX268996 Sequence
133	30	3.0	200	5	AY591921	AY591921 Macaca fa
134	30	3.0	600	2	E26663	E26663 Improved me
135	30	3.0	932	14	AY686641S1	AY686641 Equus cab
136	30	3.0	1061	2	AR069654	AR069654 Sequence
137	30	3.0	1143	6	AF128214	AF128214 Mus muscu
138	30	3.0	1143	6	AF128215	AF128215 Mus muscu
139	30	3.0	1381	6	BC103608	BC103608 Mus muscu
140	30	3.0	1381	6	BC103609	BC103609 Mus muscu
141	30	3.0	1381	6	BC103610	BC103610 Mus muscu
142	30	3.0	1381	6	BC103614	BC103614 Mus muscu
143	30	3.0	1409	2	AR393787	AR393787 Sequence
144	30	3.0	1409	2	AX084105	AX084105 Sequence
145	30	3.0	1472	2	AR393786	AR393786 Sequence
146	30	3.0	1472	2	AX084104	AX084104 Sequence
147	30	3.0	1569	2	AR393796	AR393796 Sequence
148	30	3.0	1569	2	AX084114	AX084114 Sequence
149	30	3.0	1582	14	AY686641S2	AY686644 Equus cab
150	30	3.0	1669	8	AF411293	AF411293 Synthetic
151	30	3.0	1840	6	MUSIL40A	M86671 Mus musculu
152	30	3.0	2013	2	AR393795	AR393795 Sequence
153	30	3.0	2013	2	AX084113	AX084113 Sequence
154	30	3.0	2438	2	CQ812173	CQ812173 Sequence
155	30	3.0	2709	2	AR393797	AR393797 Sequence
156	30	3.0	2709	2	AX084115	AX084115 Sequence
157	30	3.0	5252	2	CQ803341	CQ803341 Sequence
158	30	3.0	5966	2	BD136050	BD136050 Interfero
159	30	3.0	9049	2	CQ803350	CQ803350 Sequence
160	30	3.0	10633	2	CQ803349	CQ803349 Sequence
161	30	3.0	11746	2	CQ803348	CQ803348 Sequence
162	30	3.0	38246	2	CQ803351	CQ803351 Sequence
163	30	3.0	285389	12	AC096348	AC096348 Rattus no
164	29	2.9	528	6	AF082494	AF082494 Marmota m
165	29	2.9	984	6	AF288519	AF288519 Marmota m
166	29	2.9	984	6	MMIL12P40	X97019 M.monax mRN
167	29	2.9	1000	6	S82420S3	S82422 interleukin
168	29	2.9	76047	6	AL669944	AL669944 Mouse DNA
169	29	2.9	110000	12	AC073744_2	Continuation (3 of
170	29	2.9	110000	12	AC073744_3	Continuation (4 of
171	29	2.9	189236	6	AL607030	AL607030 Mouse DNA
c 172	29	2.9	268294	12	AC020885	AC020885 Mus muscu
173	29	2.9	287927	12	AC079530	AC079530 Mus muscu
174	28	2.8	28	2	AR595991	AR595991 Sequence
175	28	2.8	37	2	AR595993	AR595993 Sequence
176	28	2.8	2276	6	AB085792	AB085792 Mesocrice
c 177	25	2.5	25	2	AR595992	AR595992 Sequence
c 178	24	2.4	26	2	E26678	E26678 Improved me
179	24	2.4	30	2	BD014607	BD014607 Process f
180	24	2.4	30	2	BD174647	BD174647 Process f
181	24	2.4	39	2	AR151073	AR151073 Sequence
182	24	2.4	39	2	BD014665	BD014665 Process f
183	24	2.4	39	2	E15027	E15027 PCR primer
184	24	2.4	39	2	AR316472	AR316472 Sequence
185	24	2.4	540	2	E32843	E32843 Canine inte
186	24	2.4	540	2	AR361993	AR361993 Sequence
187	24	2.4	987	2	BD007077	BD007077 Gene expr
188	24	2.4	987	2	BD007078	BD007078 Gene expr
189	24	2.4	987	2	BD136035	BD136035 Interfero
190	24	2.4	987	2	BD136036	BD136036 Interfero
191	23	2.3	500	6	S82420S4	S82423 interleukin
192	23	2.3	37305	5	HS344F5	AL031712 Human DNA
c 193	23	2.3	110000	12	AC073744_3	Continuation (4 of
194	23	2.3	142974	12	AC152028	AC152028 Dasypus n
195	23	2.3	195680	5	AC120498	AC120498 Homo sapi
196	23	2.3	265786	5	AE006466	AE006466 Homo sapi
197	23	2.3	268294	12	AC020885	AC020885 Mus muscu
c 198	22	2.2	25	2	AR595994	AR595994 Sequence
199	22	2.2	399	2	CS211342	CS211342 Sequence
200	22	2.2	399	2	CS214984	CS214984 Sequence

ALIGNMENTS

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RESULT 1
AR595950
LOCUS       AR595950                 987 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 29 from patent US 6818444.
ACCESSION   AR595950
VERSION     AR595950.1  GI:56646931
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 29 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 987;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  987;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987


RESULT 2
AR595951/c
LOCUS       AR595951                 987 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 31 from patent US 6818444.
ACCESSION   AR595951
VERSION     AR595951.1  GI:56646932
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 31 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 987;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  987;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88
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Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGCAGT 1


RESULT 3
AR595967
LOCUS       AR595967                985 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 55 from patent US 6818444.
ACCESSION   AR595967
VERSION     AR595967.1  GI:56646948
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 985)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 55 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .985
                     /organism="unknown"
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ORIGIN

  Query Match             99.8%;  Score 985;  DB 2;  Length 985;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 4
AR595968/c
LOCUS       AR595968                985 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 57 from patent US 6818444.
ACCESSION   AR595968
VERSION     AR595968.1  GI:56646949
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 985)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 57 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .985
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             99.8%;  Score 985;  DB 2;  Length 985;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
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Db         745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy         301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy         361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy         421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy         481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy         541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Db         445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy         601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy         661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy         721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy         781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
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Db         205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy         841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Db         145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy         901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy         961 AGCAACTGGGCATCCGTGTCCTGCA 985
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Db          25 AGCAACTGGGCATCCGTGTCCTGCA 1
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RESULT 5
AR242435
LOCUS       AR242435               2193 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 5 from patent US 6472509.
ACCESSION   AR242435
VERSION     AR242435.1  GI:27288852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2193)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 5 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
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ORIGIN

  Query Match             94.2%;  Score 930;  DB 2;  Length 2193;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  930;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          58 CTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCT 117
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Db         121 CTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCT 180

Qy         118 GATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACC 177
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Db         181 GATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACC 240

Qy         178 TGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTC 237
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Db         241 TGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTC 300

Qy         238 AAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCAT 297
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Db         301 AAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCAT 360

Qy         298 TCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAA 357
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Db         361 TCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAA 420

Qy         358 CAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGT 417
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Db         421 CAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGT 480

Qy         418 TTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGC 477
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Db         481 TTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGC 540

Qy         478 AGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAG 537
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 AGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAG 600

Qy         538 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 597
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Db         601 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 660

Qy         598 TGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTC 657
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Db         661 TGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTC 720

Qy         658 AAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCC 717
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Db         721 AAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCC 780

Qy         718 AAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATAC 777
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Db         781 AAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATAC 840

Qy         778 CCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAG 837
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Db         841 CCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAG 900

Qy         838 GGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTC 897
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Db         901 GGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTC 960

Qy         898 GTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCC 957
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 GTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCC 1020

Qy         958 TGGAGCAACTGGGCATCCGTGTCCTGCAGT 987
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Db        1021 TGGAGCAACTGGGCATCCGTGTCCTGCAGT 1050
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RESULT 6
AR280203
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LOCUS       AR280203                2193 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 5 from patent US 6518045.
ACCESSION   AR280203
VERSION     AR280203.1  GI:29715593
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2193)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 5 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .2193
                     /organism="unknown"
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ORIGIN

  Query Match            94.2%;  Score 930;  DB 2;  Length 2193;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  930;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         58 CTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCT 117
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Db        121 CTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCT 180

Qy        118 GATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACC 177
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Db        181 GATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACC 240

Qy        178 TGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTC 237
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Db        241 TGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTC 300

Qy        238 AAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCAT 297
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Db        301 AAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCAT 360

Qy        298 TCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAA 357
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Db        361 TCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAA 420

Qy        358 CAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGT 417
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Db        421 CAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGT 480

Qy        418 TTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGC 477
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Db        481 TTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGC 540

Qy        478 AGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAG 537
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Db        541 AGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAG 600

Qy        538 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 597
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Db        601 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 660

Qy        598 TGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTC 657
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Db        661 TGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTC 720

Qy        658 AAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCC 717
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Db        721 AAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCC 780

Qy        718 AAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATAC 777
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATAC 840

Qy        778 CCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAG 837
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAG 900

Qy        838 GGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTC 897
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTC 960

Qy        898 GTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCC 957
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Db        961 GTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCC 1020

Qy        958 TGGAGCAACTGGGCATCCGTGTCCTGCAGT 987
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Db       1021 TGGAGCAACTGGGCATCCGTGTCCTGCAGT 1050


RESULT 7
AR322418
LOCUS       AR322418                2193 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 5 from patent US 6566097.
ACCESSION   AR322418
VERSION     AR322418.1  GI:33708171
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2193)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 5 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .2193
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  Query Match            94.2%;  Score 930;  DB 2;  Length 2193;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  930;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         58 CTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCT 117
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Qy        118 GATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACC 177
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Db        181 GATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACC 240

Qy        178 TGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTC 237
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Db        241 TGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTC 300

Qy        238 AAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCAT 297
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Db        301 AAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCAT 360

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Qy        358 CAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGT 417
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Db        421 CAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGT 480

Qy        418 TTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGC 477
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGC 540

Qy        478 AGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAG 537
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Db        541 AGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAG 600

Qy        538 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 597
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Db        601 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 660

Qy        598 TGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTC 657
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTC 720

Qy        658 AAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCC 717
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCC 780

Qy        718 AAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATAC 777
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATAC 840

Qy        778 CCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAG 837
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAG 900

Qy        838 GGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTC 897
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Qy        898 GTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCC 957
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Db        961 GTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCC 1020

Qy        958 TGGAGCAACTGGGCATCCGTGTCCTGCAGT 987
                ||||||||||||||||||||||||||||||
Db       1021 TGGAGCAACTGGGCATCCGTGTCCTGCAGT 1050


RESULT 8
AR242436
LOCUS       AR242436                 921 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 6 from patent US 6472509.
ACCESSION   AR242436
VERSION     AR242436.1  GI:27288853
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 6 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .921
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ORIGIN

  Query Match             93.3%;  Score 921;  DB 2;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
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Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
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Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
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Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
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Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

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Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
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Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
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Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
                ||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 9
AR280204
LOCUS       AR280204                 921 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 6 from patent US 6518045.
ACCESSION   AR280204
VERSION     AR280204.1  GI:29715594
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 6 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             93.3%;  Score 921;  DB 2;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
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Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
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Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
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Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
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Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
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Db        901 TGGGCATCCGTGTCCTGCAGT 921
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RESULT 10
AR322419
LOCUS       AR322419                 921 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 6 from patent US 6566097.
ACCESSION   AR322419
VERSION     AR322419.1  GI:33708172
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 6 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .921
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ORIGIN

  Query Match             93.3%;  Score 921;  DB 2;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
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Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
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Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
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Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
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Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
                |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 11
FCIL12P40
LOCUS       FCIL12P40               1006 bp    mRNA    linear   MAM 18-APR-2005
DEFINITION  Felis catus mRNA for interleukin-12 p40 chain.
ACCESSION   Y07762
VERSION     Y07762.1  GI:2102664
KEYWORDS    interleukin-12 p40.
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1
  AUTHORS   Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
  TITLE     Molecular cloning of cat interleukin-12
  JOURNAL   Immunogenetics 45 (6), 462-463 (1997)
   PUBMED   9089110
REFERENCE   2  (bases 1 to 1006)
  AUTHORS   Schijns,V.E.C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
            Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
            Utrecht, NETHERLANDS
FEATURES             Location/Qualifiers
     source          1. .1006
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                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
                     /cell_type="lymphocyte"
                     /tissue_type="peripheral blood"
     gene            1. .1006
                     /gene="IL-12.p40"
     CDS             1. .990
                     /gene="IL-12.p40"
                     /note="heterodimer with IL-12 p35 chain"
                     /codon_start=1
                     /product="interleukin-12 p40 chain"
                     /protein_id="CAA69068.1"
                     /db_xref="GI:2102665"
                     /db_xref="GOA:O02744"
                     /db_xref="InterPro:IPR002996"
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                     /db_xref="UniProtKB/Swiss-Prot:O02744"
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                     LKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFGV
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ORIGIN
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  Query Match             91.7%;  Score 905;  DB 14;  Length 1006;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  955;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91
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Db         32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91

Qy         92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151

Qy        152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211

Qy        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271
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Db        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271

Qy        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331

Qy        332 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 391
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Db        332 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 391

Qy        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451
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Db        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451

Qy        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTG 511
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTG 511

Qy        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571

Qy        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631

Qy        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691
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Db        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691

Qy        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751
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Qy        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811
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Db        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811

Qy        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 871
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 871

Qy        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931
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Db        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931

Qy        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987


RESULT 12
AR595956
LOCUS       AR595956               1599 bp    DNA     linear   PAT 15-DEC-2004
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DEFINITION  Sequence 38 from patent US 6818444.
ACCESSION   AR595956
VERSION     AR595956.1  GI:56646937
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 38 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
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ORIGIN

  Query Match             91.7%;  Score 905;  DB 2;  Length 1599;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  955;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91

Qy         92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151

Qy        152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271
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Qy        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331
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Qy        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451
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Qy        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTG 511
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Qy        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631
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Qy        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691
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Db        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691

Qy        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751
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Db        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751

Qy        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811
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Db        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811

Qy        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 871
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Db        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 871

Qy        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931
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Db        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931

Qy        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987
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Db        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987


RESULT 13
AR595957/c
LOCUS       AR595957               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 40 from patent US 6818444.
ACCESSION   AR595957
VERSION     AR595957.1  GI:56646938
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 40 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             91.7%;  Score 905;  DB 2;  Length 1599;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  955;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91
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Db       1568 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 1509

Qy         92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151
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Db       1508 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 1449

Qy        152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211
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Qy        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271
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Db       1388 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 1329

Qy        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331
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Db       1328 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 1269

Qy        332 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 391
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Db       1268 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 1209

Qy        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451
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Db       1208 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 1149

Qy        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTG 511
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Db       1148 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTG 1089

Qy        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571
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Qy        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631
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Db       1028 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 969

Qy        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691
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Db        968 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 909

Qy        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751
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Db        908 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 849

Qy        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811
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Db        848 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 789

Qy        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 871
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Db        788 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 729

Qy        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931
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Db        728 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 669

Qy        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987
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Db        668 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 613
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RESULT 14
AX076200
LOCUS       AX076200                990 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 1 from Patent WO0104155.
ACCESSION   AX076200
VERSION     AX076200.1  GI:12710825
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 1 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="feline IL-12 p40"
ORIGIN

  Query Match            89.7%;  Score 885;  DB 2;  Length 990;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
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Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
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Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
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Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
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Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
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Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
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Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
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Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
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Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
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RESULT 15
AX076482
LOCUS       AX076482                990 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 8 from Patent WO0104280.
ACCESSION   AX076482
VERSION     AX076482.1  GI:12711034
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 8 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
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FEATURES             Location/Qualifiers
     source          1. .990
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                     /db_xref="taxon:32630"
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ORIGIN

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  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
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Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
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Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
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Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
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Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
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RESULT 16
AX076209
LOCUS       AX076209               4522 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 10 from Patent WO0104155.
ACCESSION   AX076209
VERSION     AX076209.1  GI:12710834
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 10 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
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ORIGIN

  Query Match             89.7%;  Score 885;  DB 2;  Length 4522;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
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Db       3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Db       3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
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Db       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Db       3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
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Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Db       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
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Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
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Db       3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
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Db       3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||||
Db       4007 AGCAACTGGGCATCCGTGTCCTGCAGT 4033
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RESULT 17
AX076476
LOCUS       AX076476                4522 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 2 from Patent WO0104280.
ACCESSION   AX076476
VERSION     AX076476.1  GI:12711028
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 2 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .4522
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="IL-12p40"
ORIGIN

  Query Match             89.7%;  Score 885;  DB 2;  Length 4522;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
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Db       3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Db       3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||||
Db       4007 AGCAACTGGGCATCCGTGTCCTGCAGT 4033
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RESULT 18
AR242437
LOCUS       AR242437                921 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 7 from patent US 6472509.
ACCESSION   AR242437
VERSION     AR242437.1  GI:27288854
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 7 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
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           EPX;
FEATURES             Location/Qualifiers
     source          1. .921
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                     /mol_type="mRNA"
ORIGIN

  Query Match             88.1%;  Score 870;  DB 2;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
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Db           1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy         367 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
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Db         301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy         427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy         487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy         547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy         607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy         667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy         727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy         787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy         847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy         907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy         967 TGGGCATCCGTGTCCTGCAGT 987
               |||||||||||||||||||||
Db         901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 19
AR280205
LOCUS       AR280205                 921 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 7 from patent US 6518045.
ACCESSION   AR280205
VERSION     AR280205.1  GI:29715595
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 7 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .921
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ORIGIN

  Query Match             88.1%;  Score 870;  DB 2;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
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Db         241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy         367 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy         427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy         487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy         547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy         607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy         667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
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Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
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Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
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Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 20
AR322420
LOCUS       AR322420                 921 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 7 from patent US 6566097.
ACCESSION   AR322420
VERSION     AR322420.1  GI:33708173
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 7 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match           88.1%;  Score 870;  DB 2;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
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Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
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Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 21
AR595948
LOCUS       AR595948                 921 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 26 from patent US 6818444.
ACCESSION   AR595948
VERSION     AR595948.1  GI:56646929
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 26 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           88.1%;  Score 870;  DB 2;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 22
AR595949/c
LOCUS       AR595949                921 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 28 from patent US 6818444.
ACCESSION   AR595949
VERSION     AR595949.1  GI:56646930
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 28 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             88.1%;  Score 870;  DB 2;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||
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Db         21 TGGGCATCCGTGTCCTGCAGT 1


RESULT 23
AR595959
LOCUS       AR595959               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 43 from patent US 6818444.
ACCESSION   AR595959
VERSION     AR595959.1  GI:56646940
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 43 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           88.1%;  Score 870;  DB 2;  Length 1533;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy         367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy         427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy         487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
               |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db         421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy         547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy         607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy         667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy         727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy         787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy         847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy         907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy         967 TGGGCATCCGTGTCCTGCAGT 987
               ||||||||||||||||||||
Db         901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 24
AR595960/c
LOCUS       AR595960               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 45 from patent US 6818444.
ACCESSION   AR595960
VERSION     AR595960.1  GI:56646941
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 45 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           88.1%;  Score 870;  DB 2;  Length 1533;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy         367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy         427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114
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Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613


RESULT 25
FCU83184
LOCUS       FCU83184                990 bp    mRNA    linear   MAM 16-JUL-1999
DEFINITION  Felis catus interleukin-12 p40 subunit (IL-12) mRNA, complete cds.
ACCESSION   U83184
VERSION     U83184.1  GI:2735050
KEYWORDS    .
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Nucleotide and predicted peptide sequence of feline interleukin-12
            (IL-12)
  JOURNAL   DNA Seq. 8 (1-2), 77-82 (1997)
   PUBMED   9522125
REFERENCE   2  (bases 1 to 990)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal
            Veterinary Medicine, University of Zurich, Winterthurerstrasse 260,
            Zurich, ZH 8057, Switzerland
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="Felis catus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
     CDS             1. .990
                     /note="cytokine"
                     /codon_start=1
                     /product="interleukin-12 p40 subunit"
                     /protein_id="AAB93835.1"
                     /db_xref="GI:2735051"
                     /translation="MHPQQLVIAWFSLVLLAPPLMAIWELEKNVYVVELDWHPDAPGE
                     MVVLTCDTPEEDDITWTSDQSSEVLGSGKTLTIQVKEFADAGQYTCHKGGEVLSHSFL
                     LIHKKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFTVKSSR
                     GSSDPQGVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPAAEESLPIEVVVDAIHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFGV
                     QVQGKNNREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSNWASVSCS"
ORIGIN

  Query Match           84.2%;  Score 831;  DB 14;  Length 990;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  831;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        157 CCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGT 216
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 CCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGT 216

Qy        217 AAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAA 276
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        217 AAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAA 276

Qy        277 GGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGG 336
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        277 GGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGG 336

Qy        337 TCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAG 396
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        337 TCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAG 396

Qy        397 GCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTG 456
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        397 GCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTG 456

Qy        457 AAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCA 516
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        457 AAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCA 516

Qy        517 GCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTG 576
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        517 GCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTG 576

Qy        577 GAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTG 636
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        577 GAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTG 636

Qy        637 GTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGAC 696
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        637 GTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGAC 696

Qy        697 ATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCAT 756
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        697 ATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCAT 756

Qy        757 GTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTA 816
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        757 GTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTA 816

Qy        817 ACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTG 876
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        817 ACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTG 876

Qy        877 GACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGA 936
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        877 GACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGA 936

Qy        937 GACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        937 GACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987


RESULT 26
AF054607
LOCUS       AF054607                431 bp    mRNA    linear   MAM 26-JUL-2000
```

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DEFINITION  Felis catus interleukin 12 p40 subunit mRNA, partial cds.
ACCESSION   AF054607
VERSION     AF054607.1  GI:3126822
KEYWORDS    .
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1  (bases 1 to 431)
  AUTHORS   Harley,R., Helps,C.R., Harbour,D.A., Gruffydd-Jones,T.J. and
            Day,M.J.
  TITLE     Cytokine mRNA expression in lesions in cats with chronic
            gingivostomatitis
  JOURNAL   Clin. Diagn. Lab. Immunol. 6 (4), 471-478 (1999)
   PUBMED   10391845
REFERENCE   2  (bases 1 to 431)
  AUTHORS   Harley,R., Helps,C.R., Gruffydd-Jones,T.J., Day,M.J. and
            Harbour,D.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-1998) Clinical Veterinary Science, University of
            Bristol, Langford House, Langford, Bristol BS40 7DU, U.K.
FEATURES             Location/Qualifiers
     source          1. .431
                     /organism="Felis catus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
                     /cell_line="FL4"
                     /cell_type="T cell"
                     /note="persistant FIV infection"
     CDS             <1. .>431
                     /codon_start=1
                     /product="interleukin 12 p40 subunit"
                     /protein_id="AAC15980.1"
                     /db_xref="GI:3126823"
                     /translation="CHKGXEVLSHSXVLIXEKEDGIWSTDILREQKESKNKIFLKCEA
                     KNYSGRFTCWWLTAISTDLKFTVKSSRGSSDPQGVTCGAATLSAEKVRVDNRDYKKYT
                     VECQEGSACPAAEESLPIEVVVDAIHKLKYENYTSSFFIRD"
ORIGIN

  Query Match            38.7%;  Score 382;  DB 14;  Length 431;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-200;
  Matches  382;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        317 AAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATA 376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         50 AAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATA 109

Qy        377 AGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGA 436
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        110 AGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGA 169

Qy        437 CGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCC 496
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 CGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCC 229

Qy        497 AAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGG 556
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 AAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGG 289

Qy        557 ATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGA 616
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 ATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGA 349

Qy        617 GCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCA 676
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 GCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCA 409

Qy        677 GCAGCTTCTTCATCAGGGACAT 698
              |||||||||||||||||||||
Db        410 GCAGCTTCTTCATCAGGGACAT 431
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RESULT 27
AX154603
LOCUS       AX154603                990 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 7 from Patent WO0140257.
ACCESSION   AX154603
VERSION     AX154603.1  GI:14536186
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 7 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match            8.4%;  Score 83;  DB 2;  Length 990;
  Best Local Similarity  100.0%;  Pred. No. 5.6e-34;
  Matches   83;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        865 AGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGC 924
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 AGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGC 924

Qy        925 GTGCAAGCCAGAGACCGCTACTA 947
              |||||||||||||||||||||||
Db        925 GTGCAAGCCAGAGACCGCTACTA 947


RESULT 28
AR595965
LOCUS       AR595965                921 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 52 from patent US 6818444.
ACCESSION   AR595965
VERSION     AR595965.1  GI:56646946
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 52 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match            6.7%;  Score 66;  DB 2;  Length 921;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy        597 CTGCCC 602
              ||||||
Db        531 CTGCCC 536


RESULT 29
AR595966/c
LOCUS       AR595966                921 bp    DNA     linear   PAT 15-DEC-2004
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DEFINITION  Sequence 54 from patent US 6818444.
ACCESSION   AR595966
VERSION     AR595966.1  GI:56646947
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 54 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy        597 CTGCCC 602
              ||||||
Db        391 CTGCCC 386


RESULT 30
BD171282
LOCUS       BD171282                924 bp    DNA     linear   PAT 18-FEB-2003
DEFINITION  Novel canine cytokine protein.
ACCESSION   BD171282
VERSION     BD171282.1  GI:28412572
KEYWORDS    JP 2002241398-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 924)
  AUTHORS   Imamura,T., Maeda,H., Tokiyoshi,Y. and Eda,Y.
  TITLE     Novel canine cytokine protein
  JOURNAL   Patent: JP 2002241398-A 2 28-AUG-2002;
            CHEMO SERO THERAPEUT RES INST
COMMENT     OS   Canine splenocyte
            PN   JP 2002241398-A/2
            PD   28-AUG-2002
            PF   03-JUN-1997 JP 1997161936
            PI   TAKAYUKI IMAMURA,HIROAKI MAEDA,YUKIO TOKIYOSHI,YASUYUKI EDA PC
              C07K14/52,A61K38/00,A61K39/395,C07K16/24,C12N5/10,C12N15/09, PC
            C12P21/02//
            PC   C12P21/08,(C12P21/02,C12R1:91),A61K37/02,C12N5/00,C12N15/00 CC
              Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .924
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 924;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 533

Qy        597 CTGCCC 602
              ||||||
Db        534 CTGCCC 539


RESULT 31
AR595969
LOCUS       AR595969                987 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 58 from patent US 6818444.
ACCESSION   AR595969
VERSION     AR595969.1  GI:56646950
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 58 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 32
AR595970/c
LOCUS       AR595970                987 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 60 from patent US 6818444.
ACCESSION   AR595970
VERSION     AR595970.1  GI:56646951
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 60 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy        597 CTGCCC 602
              ||||||
Db        391 CTGCCC 386


RESULT 33
```

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AR151061
LOCUS       AR151061                990 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 1 from patent US 6231850.
ACCESSION   AR151061
VERSION     AR151061.1  GI:15117111
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12
  JOURNAL   Patent: US 6231850-A 1 15-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 34
AR151071
LOCUS       AR151071                990 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 11 from patent US 6231850.
ACCESSION   AR151071
VERSION     AR151071.1  GI:15117121
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12
  JOURNAL   Patent: US 6231850-A 11 15-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 35
BD014653
LOCUS       BD014653                990 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy.
ACCESSION   BD014653
VERSION     BD014653.1  GI:22555436
KEYWORDS    JP 2001161378-A/1.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F.
  TITLE     Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy
  JOURNAL   Patent: JP 2001161378-A 1 19-JUN-2001;
            TORAY INDUSTRIES INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 2001161378-A/1
            PD   19-JUN-2001
            PF   26-SEP-2000 JP 2000292946
            PI   FUMIYOSHI OKANO
            PC   C12N15/09,A61K38/00,A61P17/00,A61P17/00,A61P31/04,A61P31/04,
            PC   A61P35/00,
            PC   A61P37/00,C07K1/18,C07K1/22,C07K14/54,C12P21/02//(C12P21/02,
            PC   C12R1:91),
            PC   (C12P21/02,C12R1:93),C12N15/00,A61K37/02
            CC   Process for producing highly pure protein, interleukin 12,  CC
                 protein
            CC   inhibiting interleukin-12 activity, remedies for mammalian  CC
                 immunopathy and
            CC   method of treating immunopathy
            FH   Key             Location/Qualifiers
            FT   CDS             (1). .(987)
            FT   mat_peptide     (67). .(987).
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="Canis sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9616"
ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 36
BD014663
LOCUS       BD014663                990 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy.
ACCESSION   BD014663
VERSION     BD014663.1  GI:22555446
KEYWORDS    JP 2001161378-A/11.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F.
  TITLE     Process for producing highly pure protein, interleukin 12, protein
            inhibiting interleukin-12 activity, remedies for mammalian
            immunopathy and method of treating immunopathy
  JOURNAL   Patent: JP 2001161378-A 11 19-JUN-2001;
            TORAY INDUSTRIES INC
COMMENT     OS   Canis sp. (dog)
```

```
            PN   JP 2001161378-A/11
            PD   19-JUN-2001
            PF   26-SEP-2000 JP 2000292946
            PI   FUMIYOSHI OKANO
            PC   C12N15/09,A61K38/00,A61P17/00,A61P17/00,A61P31/04,A61P31/04,
            PC   A61P35/00,
            PC   A61P37/00,C07K1/18,C07K1/22,C07K14/54,C12P21/02//(C12P21/02,
            PC   C12R1:91),
            PC   (C12P21/02,C12R1:93),C12N15/00,A61K37/02
            CC   Process for producing highly pure protein, interleukin 12,  CC
                 protein
            CC   inhibiting interleukin-12 activity, remedies for mammalian  CC
                 immunopathy and
            CC   method of treating immunopathy
            FH   Key             Location/Qualifiers
            FT   CDS             (1). .(987)
            FT   mat_peptide     (67). .(987).
FEATURES            Location/Qualifiers
     source         1. .990
                    /organism="Canis sp."
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9616"
ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 37
E15017
LOCUS       E15017                  990 bp    DNA     linear   PAT 28-JUL-1999
DEFINITION  Canine mRNA for interleukin 12 40kDa subunit,complete cds.
ACCESSION   E15017
VERSION     E15017.1  GI:5709700
KEYWORDS    JP 1998036397-A/1.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F.
  TITLE     CANINE INTERLEUKIN 12 AND ITS PRODUCTION
  JOURNAL   Patent: JP 1998036397-A 1 10-FEB-1998;
            TORAY IND INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 1998036397-A/1
            PD   10-FEB-1998
            PF   08-NOV-1996 JP 1996296789
            PR   08-NOV-1995 JP 95P   289729, 23-MAY-1996 JP 96P   128104 PI
            OKANO FUMIYOSHI
            PC   C07K14/54,C07H21/04,C12N5/10,C12N15/09,C12P21/02,(C12N5/10, PC
              C12R1:91),
            PC   (C12P21/02,C12R1:91);
            CC   strandedness: Double;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .990
            FT                   /organism='Canis sp.'
            FT                   /tissue_type='liver'
            FT   CDS             1. .990
            FT                   /product='interleukin 12 40kDa subunit'.
FEATURES            Location/Qualifiers
     source         1. .990
                    /organism="Canis sp."
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9616"
ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 38
AR316460
LOCUS       AR316460                990 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 1 from patent US 6562334.
ACCESSION   AR316460
VERSION     AR316460.1  GI:33695288
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12 administration as an immune disease treatment
  JOURNAL   Patent: US 6562334-A 1 13-MAY-2003;
            Toray Industries, Inc.;;
            JPX;
FEATURES            Location/Qualifiers
     source         1. .990
                    /organism="unknown"
                    /mol_type="mRNA"
ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 39
AR316470
LOCUS       AR316470                990 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 11 from patent US 6562334.
ACCESSION   AR316470
VERSION     AR316470.1  GI:33695298
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12 administration as an immune disease treatment
  JOURNAL   Patent: US 6562334-A 11 13-MAY-2003;
            Toray Industries, Inc.;;
            JPX;
FEATURES            Location/Qualifiers
     source         1. .990
                    /organism="unknown"
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                     /mol_type="mRNA"
ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 40
AR595973
LOCUS       AR595973               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 66 from patent US 6818444.
ACCESSION   AR595973
VERSION     AR595973.1  GI:56646954
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 66 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy        597 CTGCCC 602
              ||||||
Db        531 CTGCCC 536


RESULT 41
AR595974/c
LOCUS       AR595974               1533 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 68 from patent US 6818444.
ACCESSION   AR595974
VERSION     AR595974.1  GI:56646955
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1533)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 68 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1533
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy        597 CTGCCC 602
              ||||||
Db       1003 CTGCCC 998


RESULT 42
AR595971
LOCUS       AR595971               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 61 from patent US 6818444.
ACCESSION   AR595971
VERSION     AR595971.1  GI:56646952
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 61 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 43
AR595972/c
LOCUS       AR595972               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 63 from patent US 6818444.
ACCESSION   AR595972
VERSION     AR595972.1  GI:56646953
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 63 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .1599
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004
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```
Qy        597 CTGCCC 602
              ||||||
Db       1003 CTGCCC 998


RESULT 44
BD171281
LOCUS       BD171281               2154 bp    DNA     linear   PAT 18-FEB-2003
DEFINITION  Novel canine cytokine protein.
ACCESSION   BD171281
VERSION     BD171281.1  GI:28412571
KEYWORDS    JP 2002241398-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 2154)
  AUTHORS   Imamura,T., Maeda,H., Tokiyoshi,Y. and Eda,Y.
  TITLE     Novel canine cytokine protein
  JOURNAL   Patent: JP 2002241398-A 1 28-AUG-2002;
            CHEMO SERO THERAPEUT RES INST
COMMENT     OS   Canine splenocyte
            PN   JP 2002241398-A/1
            PD   28-AUG-2002
            PF   03-JUN-1997 JP 1997161936
            PI   TAKAYUKI IMAMURA,HIROAKI MAEDA,YUKIO TOKIYOSHI,YASUYUKI EDA PC
              C07K14/52,A61K38/00,A61K39/395,C07K16/24,C12N5/10,C12N15/09, PC
            C12P21/02//
            PC   C12P21/08,(C12P21/02,C12R1:91),A61K37/02,C12N5/00,C12N15/00 CC
              Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .2154
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 2154;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 650

Qy        597 CTGCCC 602
              ||||||
Db        651 CTGCCC 656


RESULT 45
AR596011
LOCUS       AR596011               2267 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 107 from patent US 6818444.
ACCESSION   AR596011
VERSION     AR596011.1  GI:56646992
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2267)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 107 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES              Location/Qualifiers
     source           1. .2267
                      /organism="unknown"
                      /mol_type="genomic DNA"
ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 749

Qy        597 CTGCCC 602
              ||||||
Db        750 CTGCCC 755


RESULT 46
AR596012/c
LOCUS       AR596012               2267 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 109 from patent US 6818444.
ACCESSION   AR596012
VERSION     AR596012.1  GI:56646993
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2267)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 109 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES              Location/Qualifiers
     source           1. .2267
                      /organism="unknown"
                      /mol_type="genomic DNA"
ORIGIN

  Query Match             6.7%;  Score 66;  DB 2;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1578 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1519

Qy        597 CTGCCC 602
              ||||||
Db       1518 CTGCCC 1513


RESULT 47
AX154600
LOCUS       AX154600                984 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 4 from Patent WO0140257.
ACCESSION   AX154600
VERSION     AX154600.1  GI:14536183
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 4 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES              Location/Qualifiers
     source           1. .984
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="Synthetic Sequence"
ORIGIN

  Query Match             6.6%;  Score 65;  DB 2;  Length 984;
  Best Local Similarity   100.0%;  Pred. No. 5.7e-24;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

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Qy        451 GATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGT 510
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGT 510

Qy        511 GGAGC 515
              |||||
Db        511 GGAGC 515


RESULT 48
AF349536
LOCUS       AF349536                588 bp    mRNA    linear   MAM 17-MAY-2001
DEFINITION  Canis familiaris interleukin-12 subunit p40 mRNA, partial cds.
ACCESSION   AF349536
VERSION     AF349536.1  GI:14133584
KEYWORDS    .
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 588)
  AUTHORS   Fonfara,S., Groene,A., Koenig,M. and Baumgaertner,W.
  TITLE     Sequence of canine interleukin-12-p40 mRNA in DH82-cells
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 588)
  AUTHORS   Fonfara,S., Groene,A., Koenig,M. and Baumgaertner,W.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-FEB-2001) Institute of Pathology,
            Justus-Liebig-University, Frankfurter Str. 96, Giessen 35392,
            Germany
FEATURES             Location/Qualifiers
     source          1. .588
                     /organism="Canis familiaris"
                     /mol_type="mRNA"
                     /db_xref="taxon:9615"
                     /cell_line="DH82"
     CDS             <1. .>588
                     /codon_start=3
                     /product="interleukin-12 subunit p40"
                     /protein_id="AAK54070.1"
                     /db_xref="GI:14133585"
                     /translation="QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVV
                     LTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIH
                     KKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFS
                     DPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGS"
ORIGIN

  Query Match             6.4%;  Score 63;  DB 14;  Length 588;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-23;
  Matches   63;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         88 GTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACC 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 GTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACC 140

Qy        148 TGC 150
              |||
Db        141 TGC 143


RESULT 49
CFU49100
LOCUS       CFU49100                1015 bp    mRNA    linear   MAM 13-MAR-1996
DEFINITION  Canis familiaris interleukin-12 p40 subunit mRNA, complete cds.
ACCESSION   U49100
VERSION     U49100.1  GI:1223907
KEYWORDS    .
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 1015)
  AUTHORS   Belke-Louis,G.F. and Buettner,M.
  TITLE     Cloning and sequence analysis of the p35 and p40 subunits of canine
            interleukin-12
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1015)
  AUTHORS   Belke-Louis,G.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-FEB-1996) Georg F. Belke-Louis, Institute of Med.
            Microbiology, Veterinaerstr. 13, Muenchen, D-80539, Germany
FEATURES             Location/Qualifiers
     source          1. .1015
                     /organism="Canis familiaris"
                     /mol_type="mRNA"
                     /db_xref="taxon:9615"
     CDS             1. .990
                     /codon_start=1
                     /product="interleukin-12 p40 subunit"
                     /protein_id="AAA92059.1"
                     /db_xref="GI:1223908"
                     /translation="MHPQQLVISWFSLVLLASSLMTIWELEKDVYVVELDWHPDAPGE
                     MVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLL
                     LIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSR
                     GFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHK
                     LKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCV
                     QAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSDWASVSCS"
ORIGIN

  Query Match             6.4%;  Score 63;  DB 14;  Length 1015;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-23;
  Matches   63;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         88 GTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACC 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 GTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACC 147

Qy        148 TGC 150
              |||
Db        148 TGC 150


RESULT 50
BV242752
LOCUS       BV242752                621 bp    DNA     linear   STS 19-JAN-2005
DEFINITION  S234P6134RD4.T0 EnglishShepherd Canis familiaris STS genomic,
            sequence tagged site.
ACCESSION   BV242752
VERSION     BV242752.1  GI:57305294
KEYWORDS    STS.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 621)
  AUTHORS   Lindblad-Toh,K.
  TITLE     The genome sequence of Canis familiaris
  JOURNAL   Unpublished (2004)
COMMENT
            Contact: Kerstin Lindblad-Toh
            Whitehead Institute for Biomedical Research, Center for Genome
            Research
            320 Charles Street, Cambridge, MA 02141, USA
            Tel: 6172521477
            Fax: 6172580903
            Email: kersli@genome.wi.mit.edu
            Primer A: No sequence submitted
            Primer B: No sequence submitted
            STS size: 621
            Protocol:
            WGS-discovery (WGS):
            Paired-end low-coverage whole genome shotgun reads were generated
```

```
            from 9 breeds
            (German Shepherd, Rottweiler, Bedlington Terrier, Beagle, Labrador
            Retriever, English
            Shepherd, Italian Greyhound, Alaskan Malamute and the Portuguese
            Water Dog -100,000 each)
            and five other canids (Chinese, Alaskan, Indian and Spanish Gray
            Wolf as well as the
            Californian Coyote).
            The WGS reads were placed uniquely on the CanFam1.0 boxer assembly
            and SNP detection was
            carried out by SSAHA-SNP. 863872 reads were annotated as STSs and
            485941 SNPs were
            annotated with alleles from the boxer and the breed or canid from
            which the particular
            read came. The validation rate for these SNPs was estimated at
            approximately 98%.
            WGA-discovery (WGA) of Boxer/Poodle SNPs:
            A second set of SNPs was generated using a similar methodology
            except that the contigs
            from the 1.5x poodle assembly (Kirkness 2003) were used instead of
            WGS reads. Since this
            sequence lacked base quality scores, arbitrary quality scores of
            phred 40 were assigned
            before the poddle seqeunce was placed uniquely on the CanFam1.0
            boxer assembly and SNP
            detection was carried out by SSAHA-SNP. 1637780 SNPs were annotated
            with alleles from the
            boxer and the poodle. The validation rate for these SNPs was
            estimated at approximately TBD%.
            Internal-WGA-discovery (I-WGA):
            A third set of SNPs were discovered by comparing reads in the WGA
            assembly. SNPs were
            defined as mismatch positions that had a base quality of >= 30 on
            both reads in a region
            that aligned without gaps, and with at most one additional mismatch
            in the ten flanking
            bases. For each allele, at least one additional read had to confirm
            it. 731476 SNPs were
            annotated with alleles between the two boxer alleles. The
            validation rate for these SNPs
            was estimated at approximately TBD%.
FEATURES             Location/Qualifiers
     source          1. .621
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /strain="EnglishShepherd"
                     /db_xref="taxon:9615"
                     /map="+ 4 22-568 54361767-54362313"
                     /clone_lib="EnglishShepherd"
     STS             <1. .>621
ORIGIN

  Query Match             6.2%;  Score 61;  DB 7;  Length 621;
  Best Local Similarity   100.0%;  Pred. No. 1e-21;
  Matches   61;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        873 CGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGC 932
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 CGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGC 328

Qy        933 C 933
              |
Db        329 C 329


RESULT 51
AX154598
LOCUS       AX154598                984 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 2 from Patent WO0140257.
ACCESSION   AX154598
VERSION     AX154598.1  GI:14536181
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 2 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .984
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match             6.2%;  Score 61;  DB 2;  Length 984;
  Best Local Similarity   100.0%;  Pred. No. 9.5e-22;
  Matches   61;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        673 ACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTG 732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        673 ACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTG 732

Qy        733 A 733
              |
Db        733 A 733


RESULT 52
AX154599
LOCUS       AX154599                984 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 3 from Patent WO0140257.
ACCESSION   AX154599
VERSION     AX154599.1  GI:14536182
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 3 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .984
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match             6.1%;  Score 60;  DB 2;  Length 984;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-21;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAAC 723
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAAC 723


RESULT 53
AX154602
LOCUS       AX154602                975 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 6 from Patent WO0140257.
ACCESSION   AX154602
VERSION     AX154602.1  GI:14536185
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
```

```
  JOURNAL   Patent: WO 0140257-A 6 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .975
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match             5.4%;  Score 53;  DB 2;  Length 975;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-17;
  Matches   53;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        895 GTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTA 947
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 GTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTA 926


RESULT 54
AF333121
LOCUS       AF333121                452 bp    mRNA    linear   MAM 06-FEB-2001
DEFINITION  Canis familiaris interleukin 12 subunit p40 mRNA, partial cds.
ACCESSION   AF333121
VERSION     AF333121.1  GI:12667429
KEYWORDS    .
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 452)
  AUTHORS   Markus,S. and Baumgaertner,W.
  TITLE     Expression of canine interleukin-12 subunit p40 mRNA in a
            continuous macrophage cell line
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 452)
  AUTHORS   Markus,S. and Baumgaertner,W.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-JAN-2001) Department of Veterinary Pathology,
            Justus-Liebig-University of Giessen, Frankfurter Strasse 96,
            Giessen 35392, Germany
FEATURES             Location/Qualifiers
     source          1. .452
                     /organism="Canis familiaris"
                     /mol_type="mRNA"
                     /db_xref="taxon:9615"
                     /cell_line="DH 82"
                     /cell_type="macrophage"
                     /note="amplified using primer pair p77s/p34as"
     CDS             <1. .>452
                     /codon_start=2
                     /product="interleukin 12 subunit p40"
                     /protein_id="AAK01441.1"
                     /db_xref="GI:12667430"
                     /translation="TCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHK
                     GGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAIST
                     DLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGS"
ORIGIN

  Query Match             5.2%;  Score 51;  DB 14;  Length 452;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-16;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGA 587
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGA 444


RESULT 55
RNU16674
LOCUS       RNU16674                821 bp    mRNA    linear   ROD 07-NOV-1994
DEFINITION  Rattus norvegicus interleukin-12p40 mRNA, partial cds.
ACCESSION   U16674
VERSION     U16674.1  GI:565093
KEYWORDS    .
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 821)
  AUTHORS   Goodman,R.E. and Toews,G.B.
  TITLE     A partial cDNA of the coding region of rat IL-12p40, cloned by
            RT/PCR from Staphlococcal endotoxin stimulated splenocytes
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 821)
  AUTHORS   Goodman,R.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-OCT-1994) Richard E. Goodman, Internal
            Medicine/Pulmonary, University of Michigan, 1150 W. Medical Center
            Dr., 3311 Med. Sci. I, Ann Arbor, MI 48109-0652, USA
FEATURES             Location/Qualifiers
     source          1. .821
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Fischer"
                     /db_xref="taxon:10116"
                     /tissue_type="cultured splenocytes (SEA plus SEB
                     stimulation)"
     CDS             17. .>821
                     /note="encodes the N-terminal 268 amino acids of the
                     expected 335 amino acids encoded by the mouse gene"
                     /codon_start=1
                     /product="interleukin-12p40"
                     /protein_id="AAA52229.1"
                     /db_xref="GI:565094"
                     /translation="MCHQKLTFSWFAMVLLVSPLMAMWELEKDVYVVEVDWRPDAPGE
                     TVTLTCDSPEEDDITWTSDQRRGVIGSGKTLTITVREFLDAGQYTCHRGGETLSHSHL
                     LLHKKENGIWSTEILKNFKNKTFLKREAPNYSGRFTCSWLVHRNTDLKFNIKSSSSSP
                     ESRAVTCGAASLSAEKVTLNQRDYEKYSVACQEDVTCPTAEETLPIELVVEAQQQNKY
                     ENYSTSFFIRDIIKPDPPKNLQVKPLKNSQVEVSWEYPDSWSTPHSYFSL"
ORIGIN

  Query Match             5.2%;  Score 51;  DB 6;  Length 821;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-16;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCA 728
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 CAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCA 735


RESULT 56
AF133197
LOCUS       AF133197                1008 bp    mRNA    linear   ROD 08-APR-1999
DEFINITION  Rattus norvegicus interleukin-12 p40 precursor, mRNA, complete cds.
ACCESSION   AF133197
VERSION     AF133197.1  GI:4574731
KEYWORDS    .
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 1008)
  AUTHORS   Khalife,J., Pierrot,C., Cocude,C., Cetre,C., Godin,C. and Capron,A.
  TITLE     Molecular cloning and sequencing of the rat interleukin-12 p40 gene
  JOURNAL   Eur. Cytokine Netw. 9 (1), 69-73 (1998)
  PUBMED    9613680
REFERENCE   2  (bases 1 to 1008)
  AUTHORS   Khalife,J., Pierrot,C., Cocude,C., Cetre,C., Godin,C. and Capron,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAR-1999) InSERM U167, 1, rue du professeur Calmette,
            Lille 59019, France
FEATURES             Location/Qualifiers
```

```
     source          1. .1008
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Fischer"
                     /db_xref="taxon:10116"
     CDS             1. .1008
                     /note="IL-12P40"
                     /codon_start=1
                     /product="interleukin-12 p40 precursor"
                     /protein_id="AAD24190.1"
                     /db_xref="GI:4574732"
                     /translation="MCHQKLTFSWFAMVLLVSPLMAMWELEKDVYVVEVDWRPDAPGE
                     TVTLTCDSPEEDDITWTSDQRRGVIGSGKTLTITVREFLDAGQYTCHRGGETLSHSHL
                     LLHKKENGIWSTEILKNFKNKTFLKCEAPNYSGRFTCSWLVHRNTDLKFNIKSSSSSP
                     ESRAVTCGRASLSAEKVTLNQRDYEKYSVACQEDVTCPTAEETLPIELVVEAQQQNKY
                     ENYSTSFFIRDIIKPDPPKNLQVKPLKNSQVEVSWEYPDSWSTPHSYFSLKFFVRIQR
                     KKEKTKETEEECNQKGAFLVEKTSAEVQCKGANICVQAQDRYYNSSCSKWTCVPCRGR
                     S"
ORIGIN

  Query Match             5.2%;  Score 51;  DB 6;  Length 1008;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-16;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCA 728
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 CAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCA 719


RESULT 57
AF421395
LOCUS       AF421395               1425 bp    mRNA    linear   ROD 07-JUL-2004
DEFINITION  Sigmodon hispidus interleukin 12 p40 subunit precursor, mRNA,
            complete cds.
ACCESSION   AF421395
VERSION     AF421395.1  GI:16304138
KEYWORDS    .
SOURCE      Sigmodon hispidus (hispid cotton rat)
  ORGANISM  Sigmodon hispidus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Cricetidae; Sigmodontinae; Sigmodon.
REFERENCE   1  (bases 1 to 1425)
  AUTHORS   Blanco,J.C., Pletneva,L., Boukhvalova,M., Richardson,J.Y.,
            Harris,K.A. and Prince,G.A.
  TITLE     The cotton rat: an underutilized animal model for human infectious
            diseases can now be exploited using specific reagents to cytokines,
            chemokines, and interferons
  JOURNAL   J. Interferon Cytokine Res. 24 (1), 21-28 (2004)
   PUBMED   14980081
REFERENCE   2  (bases 1 to 1425)
  AUTHORS   Pletneva,L.M., Bacot,S., Blanco,J.C., Langley,R.J. and Prince,G.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-SEP-2001) Molecular Biology, Virion Systems Inc.,
            9610 Medical Center Drive, Suite 100, Rockville, MD 20850, USA
FEATURES             Location/Qualifiers
     source          1. .1425
                     /organism="Sigmodon hispidus"
                     /mol_type="mRNA"
                     /db_xref="taxon:42415"
     CDS             25. .1008
                     /codon_start=1
                     /product="interleukin 12 p40 subunit precursor"
                     /protein_id="AAL16936.1"
                     /db_xref="GI:16304139"
                     /translation="MCHQKLTISWFAMVLLVSPLMAIWELEKDVYVVEVDWSPGAPGE
                     RVVLTCDTSEEDDIIWTSDQSSEVVGSGKTLIVQVKEFSDAGQYTCHKGGETLSHSRL
                     LLHKKEDGIWSTDILKDQKDPKNKTFLKCEAANYSGRFTCWWLTAVSTDLKFSLKSSS
                     SSSDSRSVTCGAASLSTEKVTVDQRDYNKYSVACQEDITCPTAEETLPIELVMEAQHK
                     YKYENYSTGFFIRDIIKPDPPKNLQLKPLKSSQVEVSWEYPDSWSTPHSYFSLKFFVQ
                     VYRKKEKKGESLLVDKPSAKIRCSKGGEVRVRAQDHYYNSSWSEWASVSCN"
ORIGIN

  Query Match             5.0%;  Score 49;  DB 6;  Length 1425;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-15;
  Matches   49;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        680 GCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCA 728
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        704 GCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCA 752


RESULT 58
DQ152965
LOCUS       DQ152965               224 bp    mRNA    linear   MAM 07-NOV-2005
DEFINITION  Ovis aries interleukin-12 p40 subunit precursor (IL-12) mRNA,
            partial cds.
ACCESSION   DQ152965
VERSION     DQ152965.1  GI:77744673
KEYWORDS    .
SOURCE      Ovis aries (sheep)
  ORGANISM  Ovis aries
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Caprinae; Ovis.
REFERENCE   1  (bases 1 to 224)
  AUTHORS   Ingham,A.B., Menzies,M.L. and Kijas,J.W.
  TITLE     Sequence diversity and rates of molecular evolution between sheep
            and cattle genes
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 224)
  AUTHORS   Ingham,A.B., Menzies,M.L. and Kijas,J.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-2005) Livestock Industries, CSIRO, QBP 306
            Carmody Rd, St Lucia, Queensland 4067, Australia
FEATURES             Location/Qualifiers
     source          1. .224
                     /organism="Ovis aries"
                     /mol_type="mRNA"
                     /db_xref="taxon:9940"
     gene            <1. .>224
                     /gene="IL-12"
     CDS             <1. .>224
                     /gene="IL-12"
                     /codon_start=2
                     /product="interleukin-12 p40 subunit precursor"
                     /protein_id="ABB02298.1"
                     /db_xref="GI:77744674"
                     /translation="IEVVMEAVHKLKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQ
                     VEVSWEYPDTWSTPHSYFSLTFCVQVQGKN"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 14;  Length 224;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db         41 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 84


RESULT 59
CEU10160
LOCUS       CEU10160               525 bp    mRNA    linear   MAM 09-JUL-1994
DEFINITION  Cervus elaphus interleukin 12 mRNA, partial cds.
ACCESSION   U10160
VERSION     U10160.1  GI:508867
KEYWORDS    .
SOURCE      Cervus elaphus (red deer)
  ORGANISM  Cervus elaphus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Cervidae; Cervinae; Cervus.
REFERENCE   1  (bases 1 to 525)
  AUTHORS   Lockhart,E.A.
  TITLE     Cloning and sequencing of cervine IL-12
```

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  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 525)
  AUTHORS   Lockhart,E.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-MAY-1994) Euan A. Lockhart, Microbiology, Deer
            Research Laboratory, University of Otago, Union St., Dunedin, New
            Zealand
FEATURES             Location/Qualifiers
     source          1. .525
                     /organism="Cervus elaphus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9860"
     CDS             <1. .>525
                     /standard_name="IL-12"
                     /codon_start=2
                     /product="interleukin 12"
                     /protein_id="AAA19658.1"
                     /db_xref="GI:508868"
                     /translation="AGQYTCHKGGEVLSRSLLLLHKKEDGIWSTDILKDQKEPKAKSF
                     LKCEAKDYSGHFTCWWLTAISTDLKFSVKSSRGSSDPRGVTCGAMSLSTEKVIVDHRE
                     YKKYTVECQEGSACPAAEESLPIEVVVEAVHKLKYENYTSSFFIRDIIKPDPPKNLQL
                     RPLKNSRQVEVSWE"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 14;  Length 525;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        413 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 456


RESULT 60
BD021808
LOCUS       BD021808                906 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Natural killer stimulatory factor.
ACCESSION   BD021808
VERSION     BD021808.1  GI:22563031
KEYWORDS    JP 2001245678-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 906)
  AUTHORS   Trinchieri,G., Perussia,B., Kobayashi,M., Clark,S.C., Wong,G.G. and
            Hewick,R.M.
  TITLE     Natural killer stimulatory factor
  JOURNAL   Patent: JP 2001245678-A 1 11-SEP-2001;
            GENETICS INSTITUTE INC,THE WISTAR INSTITUTE
COMMENT     OS   Unidentified
            PN   JP 2001245678-A/1
            PD   11-SEP-2001
            PF   10-JAN-2001 JP 2001002839
            PR   10-NOV-1988 US       269945,07-FEB-1989 US       307817 PI
            GIORGIO TRINCHIERI,BICE PERUSSIA,MICHIKO KOBAYASHI,STEVEN C  PI
            CLARK,
            PI   GORDON G WONG,RODNEY M HEWICK
            PC   C12N15/09,A61K38/00,A61K39/395,A61P35/00,A61P35/02,A61P37/04,
            PC   A61P43/00,
            PC   C07K16/24,G01N33/53//C07K14/52,C12N15/00,A61K37/02 CC
            Natural killer stimulatory factor
            FH   Key             Location/Qualifiers
            FT   source          1. .906
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .906
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 2;  Length 906;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        693 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 736


RESULT 61
BD021809
LOCUS       BD021809                906 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Natural killer stimulatory factor.
ACCESSION   BD021809
VERSION     BD021809.1  GI:22563032
KEYWORDS    JP 2001245678-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 906)
  AUTHORS   Trinchieri,G., Perussia,B., Kobayashi,M., Clark,S.C., Wong,G.G. and
            Hewick,R.M.
  TITLE     Natural killer stimulatory factor
  JOURNAL   Patent: JP 2001245678-A 2 11-SEP-2001;
            GENETICS INSTITUTE INC,THE WISTAR INSTITUTE
COMMENT     OS   Unidentified
            PN   JP 2001245678-A/2
            PD   11-SEP-2001
            PF   10-JAN-2001 JP 2001002839
            PR   10-NOV-1988 US       269945,07-FEB-1989 US       307817 PI
            GIORGIO TRINCHIERI,BICE PERUSSIA,MICHIKO KOBAYASHI,STEVEN C  PI
            CLARK,
            PI   GORDON G WONG,RODNEY M HEWICK
            PC   C12N15/09,A61K38/00,A61K39/395,A61P35/00,A61P35/02,A61P37/04,
            PC   A61P43/00,
            PC   C07K16/24,G01N33/53//C07K14/52,C12N15/00,A61K37/02 CC
            Natural killer stimulatory factor
            FH   Key             Location/Qualifiers
            FT   source          1. .906
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 2;  Length 906;
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  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        693 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 736


RESULT 62
AX154601
LOCUS       AX154601                969 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 5 from Patent WO0140257.
ACCESSION   AX154601
VERSION     AX154601.1  GI:14536184
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 5 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .969
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
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                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 2;  Length 969;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        649 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 692


RESULT 63
AF004024
LOCUS       AF004024                 984 bp    mRNA    linear   MAM 14-NOV-2000
DEFINITION  Ovis aries interleukin-12 p40 subunit precursor, mRNA, complete
            cds.
ACCESSION   AF004024
VERSION     AF004024.2  GI:5870870
KEYWORDS    .
SOURCE      Ovis aries (sheep)
  ORGANISM  Ovis aries
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Caprinae; Ovis.
REFERENCE   1  (bases 1 to 984)
  AUTHORS   Swinburne,S.J., Russ,G.R. and Krishnan,R.
  TITLE     Ovine interleukin 12 has biological activity on ovine and human
            activated peripheral blood mononuclear cells
  JOURNAL   Cytokine 12 (10), 1546-1552 (2000)
   PUBMED   11023671
REFERENCE   2  (bases 1 to 984)
  AUTHORS   Swinburne,S.J., Russ,G.R. and Krishnan,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-MAY-1997) Transplantation Immunology Laboratory,
            Queen Elizabeth Hospital, 28 Woodville Road, Adelaide, South
            Australia 5011, Australia
REFERENCE   3  (bases 1 to 984)
  AUTHORS   Swinburne,S.J., Russ,G.R. and Krishnan,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-SEP-1999) Transplantation Immunology Laboratory, The
            Queen Elizabeth Hospital, 28 Woodville Rd., Adelaide, South
            Australia, Australia
  REMARK    Sequence update by submitter
COMMENT     On Sep 13, 1999 this sequence version replaced gi:2199555.
FEATURES             Location/Qualifiers
     source          1. .984
                     /organism="Ovis aries"
                     /mol_type="mRNA"
                     /db_xref="taxon:9940"
                     /cell_type="peripheral blood mononuclear"
     CDS             1. .984
                     /function="cytokine"
                     /note="IL-12"
                     /codon_start=1
                     /product="interleukin-12 p40 subunit precursor"
                     /protein_id="AAB61368.2"
                     /db_xref="GI:5870871"
                     /translation="MHPQQLVVSWFSLVLLASPIVAIWELEKNVYVVELDWYPNAPGE
                     TVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSRSLL
                     LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCSWLTAISTNLKFSVKSSR
                     GSSDPRGVTCGAASLSAEKVSMDHREYNKYTVECQEGSACPAAEESLPIEVVMEAVHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                     QVQGKNKREKKLFTDQTSAKVTCHKDANIRVQARDRYYSSFWSEWASVSCS"
     sig_peptide     1. .66
     mat_peptide     67. .981
                     /product="interleukin-12 p40 subunit"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 14;  Length 984;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707


RESULT 64
AF209435
LOCUS       AF209435                 984 bp    mRNA    linear   MAM 03-FEB-2000
DEFINITION  Ovis aries interleukin 12 p40 subunit precursor (IL-12 p40) mRNA,
            complete cds.
ACCESSION   AF209435
VERSION     AF209435.1  GI:6636341
KEYWORDS    .
SOURCE      Ovis aries (sheep)
  ORGANISM  Ovis aries
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Caprinae; Ovis.
REFERENCE   1  (bases 1 to 984)
  AUTHORS   De Rose,R., Scheerlinck,J.-P.Y., Casey,G., Wood,P.R., Tennent,J.M.
            and Chaplin,P.J.
  TITLE     Ovine Interleukin 12: Analysis of biological function and species
            comparison
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 984)
  AUTHORS   De Rose,R., Scheerlinck,J.-P.Y., Casey,G., Wood,P.R., Tennent,J.M.
            and Chaplin,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-NOV-1999) Animal Health, CSIRO, Park Drive and
            Flemington Road, Parkville, Victoria 3052, Australia
FEATURES             Location/Qualifiers
     source          1. .984
                     /organism="Ovis aries"
                     /mol_type="mRNA"
                     /strain="Merino"
                     /db_xref="taxon:9940"
                     /cell_type="mononuclear"
                     /tissue_type="peripheral blood"
     gene            1. .984
                     /gene="IL-12 p40"
     CDS             1. .984
                     /gene="IL-12 p40"
                     /note="cytokine; contains 10 cysteine residues"
                     /codon_start=1
                     /product="interleukin 12 p40 subunit precursor"
                     /protein_id="AAF20151.1"
                     /db_xref="GI:6636342"
                     /translation="MHPQQLVVSWFSLVLLASPIVAIWELEKNVYVVELDWYPNAPGE
                     TVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSRSLL
                     LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCSWLTAISTNLKFSVKSSR
                     GSSDPRGVTCGAASLSAEKVSMDHREYNKYTVECQEGSACPAAEESLPIEVVMEAVHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                     QVQGKNKREKKLFADQTSAKVTCHKDANIRVQARDRYYSSFWSEWASVSCS"
     sig_peptide     1. .66
                     /gene="IL-12 p40"
     mat_peptide     67. .981
                     /gene="IL-12 p40"
                     /product="interleukin 12 p40 subunit"
     misc_feature    667. .669
                     /gene="IL-12 p40"
                     /note="putative N-linked site; glycosylation site"
     misc_feature    793. .795
                     /gene="IL-12 p40"
                     /note="putative O-linked site; glycosylation site"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 14;  Length 984;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707


RESULT 65
AR008950
LOCUS       AR008950                 987 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 1 from patent US 5756085.
ACCESSION   AR008950
VERSION     AR008950.1  GI:3967755
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Sykes,M. and Wolf,S.F.
  TITLE     Use of interleukin-12 to prevent graft versus host disease
  JOURNAL   Patent: US 5756085-A 1 26-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 66
BD007070
LOCUS       BD007070                 987 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  IL-12 gene expression and delivery systems and uses.
ACCESSION   BD007070
VERSION     BD007070.1  GI:18635441
KEYWORDS    JP 2001503257-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Nodosutoromu,J., Freemark,B. and Dishupande,D.
  TITLE     IL-12 gene expression and delivery systems and uses
  JOURNAL   Patent: JP 2001503257-A 1 13-MAR-2001;
            BARENTISU INC,SYNTEX INC
COMMENT     OS   Unidentified
            PN   JP 2001503257-A/1
            PD   13-MAR-2001
            PF   10-OCT-1997 JP 1998519514
            PR   18-OCT-1996 US    60/028676
            PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
            C12N15/09,A61K31/711,A61K38/00,A61K47/18,A61K47/28,A61K48/00, PC
            A61P11/06,
            PC   C12N15/00,A61K37/02
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .987
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .987
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                     /db_xref="taxon:32644"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 67
BD007076
LOCUS       BD007076                 987 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Gene expression and delivery systems and uses.
ACCESSION   BD007076
VERSION     BD007076.1  GI:18635447
KEYWORDS    JP 2001503258-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Nodosutoromu,J., Freemark,B. and Dishupande,D.
  TITLE     Gene expression and delivery systems and uses
  JOURNAL   Patent: JP 2001503258-A 1 13-MAR-2001;
            BARENTISU INC
COMMENT     OS   Unidentified
            PN   JP 2001503258-A/1
            PD   13-MAR-2001
            PF   10-OCT-1997 JP 1998519520
            PR   18-OCT-1996 US    60/028687
            PI   JEFF NODOSUTOROMU,BLUCE FREEMARK,DIPA DISHUPANDE PC
            C12N15/09,A61K48/00,A61P11/06,A61P35/00,A61P43/00//C07K14/54, PC
            C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .987
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 68
BD105974
LOCUS       BD105974                 987 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Animal model for evaluation of vaccines.
ACCESSION   BD105974
VERSION     BD105974.1  GI:23200792
KEYWORDS    JP 2002501375-A/24.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Chang,L.J.
  TITLE     Animal model for evaluation of vaccines
  JOURNAL   Patent: JP 2002501375-A 24 15-JAN-2002;
            LUNG JI CHANG
COMMENT     PN   JP 2002501375-A/24
            PD   15-JAN-2002
            PF   09-APR-1998 JP 1998543062
            PR   09-APR-1997 US    08/838702,01-MAY-1997 US    08/848760 PR
            09-DEC-1997 US    60/069163
            PI   LUNG JI CHANG
            PC   A01K67/027,C12N7/01,C12N1/10,C07K14/16,A61K39/008,C12N1/36, PC
              C12N7/04,
            PC   A61K39/21
            CC   Strandedness: Double;
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            CC   Topology: Linear;
            CC   /desc = 'DNA'
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .987
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 69
BD136034
LOCUS       BD136034                 987 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Interferon alpha plasmid and delivery system and method of
            preparing and using the same.
ACCESSION   BD136034
VERSION     BD136034.1  GI:23230979
KEYWORDS    JP 2002506647-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.
  TITLE     Interferon alpha plasmid and delivery system and method of
            preparing and using the same
  JOURNAL   Patent: JP 2002506647-A 1 05-MAR-2002;
            VALENTIS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002506647-A/1
            PD   05-MAR-2002
            PF   12-MAR-1999 JP 2000536861
            PR   19-MAR-1998 US    60/078654
            PI   JEFF NORDSTROM,FEDERICA PERICLE,ALAIN ROLLAND,ROBERT RALSTON
            PC   C12N15/09,A61K38/21,A61K48/00,A61P35/00,C07K14/54,C07K14/56,
            PC   C12N1/15,
            PC   C12N1/19,C12N1/21,C12N5/10//A61K9/127,C12N15/00,A61K37/66, PC
             C12N5/00
            CC   Interferon alpha plasmid and delivery system and method of  CC
                   preparing and
            CC   using the same
            FH   Key             Location/Qualifiers
            FT   source          1. .987
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .987
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                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 70
CQ803342
LOCUS       CQ803342                 987 bp    DNA     linear   PAT 10-MAY-2004
DEFINITION  Sequence 2 from Patent WO2004035799.
ACCESSION   CQ803342
VERSION     CQ803342.1  GI:47110208
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Waehler,R. and Schnieders,F.
  TITLE     Viral vectors and the use of the same for gene therapy
  JOURNAL   Patent: WO 2004035799-A 2 29-APR-2004;
            Universitaetsklinikum Hamburg-Eppendorf (DE)
FEATURES              Location/Qualifiers
     source           1. .987
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 71
CS131491
LOCUS       CS131491                 987 bp    DNA     linear   PAT 02-AUG-2005
DEFINITION  Sequence 10 from Patent WO2005066348.
ACCESSION   CS131491
VERSION     CS131491.1  GI:71794159
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Gillies,S.
  TITLE     Compounds for targeting
  JOURNAL   Patent: WO 2005066348-A 10 21-JUL-2005;
            Antisoma PLC (GB); EMD Lexigen Research Center Corp. (US)
FEATURES              Location/Qualifiers
     source           1. .987
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="HuIL12 p40 subunit"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 72
I28591
LOCUS       I28591                   987 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 1 from patent US 5573764.
ACCESSION   I28591
VERSION     I28591.1  GI:1819367
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
```

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  AUTHORS   Sykes,M. and Wolf,S.F.
  TITLE     Use of interleukin-12 to prevent graft versus host disease
  JOURNAL   Patent: US 5573764-A 1 12-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 73
AR533404
LOCUS       AR533404                 987 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 24 from patent US 6730512.
ACCESSION   AR533404
VERSION     AR533404.1  GI:53923070
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Chang,L.-J.
  TITLE     Combination immunogene therapy
  JOURNAL   Patent: US 6730512-A 24 04-MAY-2004;
            Amdl, Inc.; Tustin, CA
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 74
AX154633
LOCUS       AX154633                 987 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 37 from Patent WO0140257.
ACCESSION   AX154633
VERSION     AX154633.1  GI:14536197
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 37 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 75
AY603406
LOCUS       AY603406                 993 bp    mRNA    linear   MAM 18-JUL-2004
DEFINITION  Capra hircus interleukin 12 p40 subunit precursor, mRNA, complete
            cds.
ACCESSION   AY603406
VERSION     AY603406.1  GI:50261479
KEYWORDS    .
SOURCE      Capra hircus (goat)
  ORGANISM  Capra hircus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Caprinae; Capra.
REFERENCE   1  (bases 1 to 993)
  AUTHORS   Rasool,T.J., Hosamani,M., Shebannavar,S., Sreekumar,E. and
            Singh,R.K.
  TITLE     cloning and sequencing of goat cytokines
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 993)
  AUTHORS   Rasool,T.J., Hosamani,M., Shebannavar,S., Sreekumar,E. and
            Singh,R.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-APR-2004) Division of Virology, Indian Veterinary
            Research Institute, Mukteswar, Nainital, Uttaranchal 263138, India
FEATURES             Location/Qualifiers
     source          1. .993
                     /organism="Capra hircus"
                     /mol_type="mRNA"
                     /isolation_source="peripheral blood mononuclear cells
                     stimulated with Concanavalin A"
                     /db_xref="taxon:9925"
                     /note="breed: Pashmina"
     CDS             1. .984
                     /note="cytokine"
                     /codon_start=1
                     /product="interleukin 12 p40 subunit precursor"
                     /protein_id="AAT72316.1"
                     /db_xref="GI:50261480"
                     /translation="MHPQQLVVSWFSLVLLASPIVAIWELEKNVYVVELDWYPNAPGE
                     TVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSRSLL
                     LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCSWLTAISTNLKFSVKSSR
                     GSSDPRGVTCGAASLSAEKVSMDHREYNKYTVECQEGSACPAAEESLPIEVVMEAVHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                     QVQGKNKREKKLFTDQTSAKVTCHKDANIRVQARDRYYSSFWSEWASVSCS"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 14;  Length 993;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707


RESULT 76
CEU57752
LOCUS       CEU57752                 993 bp    mRNA    linear   MAM 28-OCT-1999
DEFINITION  Cervus elaphus interleukin-12 p40 subunit mRNA, complete cds.
ACCESSION   U57752
VERSION     U57752.1  GI:1373387
KEYWORDS    .
SOURCE      Cervus elaphus (red deer)
  ORGANISM  Cervus elaphus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Cervidae; Cervinae; Cervus.
REFERENCE   1  (bases 1 to 993)
  AUTHORS   Lockhart,E., Slobbe,L. and Buchan,G.
  TITLE     The characterisation of a cervine immunoregulatory cytokine,
            interleukin 12
  JOURNAL   DNA Seq. 10 (2), 139-148 (1999)
   PUBMED   10376218
REFERENCE   2  (bases 1 to 993)
  AUTHORS   Lockhart,E.A. and Buchan,G.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-MAY-1996) Euan A. Lockhart, Microbiology, University
            of Otago, Cumberland St, Dunedin, New Zealand
FEATURES             Location/Qualifiers
     source          1. .993
                     /organism="Cervus elaphus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9860"
                     /cell_type="peripheral blood mononuclear cells"
     CDS             1. .984
                     /codon_start=1
                     /product="interleukin-12 p40 subunit"
                     /protein_id="AAB02258.1"
                     /db_xref="GI:1373388"
                     /translation="MHPQQLVVSWFSLVLLTSPIVAIWELEKNVYVVELDWYPDAPGE
                     TVVLRCDTPEEDGITWTSDQSSEVLGSGKTLTVQVKEFGDAGQYTCHKGGEVLSRSLL
                     LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCWWLTAISTDLKFSVKSSR
                     GSSDPRGVTCGAASLSTEKVIVDHREYKKYTVECQEGSACPAAEESLPIEVVVEAVHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                     QVQGKNKREKKLFMDQTSAKVTCHKDASIRVQARDRYYNSFWSEWASVSCS"
     primer_bind     1. .33
     primer_bind     complement(961. .993)
ORIGIN

  Query Match             4.5%;  Score 44;  DB 14;  Length 993;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707


RESULT 77
AY234218
LOCUS       AY234218                1005 bp    mRNA    linear   PRI 07-APR-2003
DEFINITION  Papio anubis interleukin-12 alpha p40 subunit precursor (IL12a)
            mRNA, complete cds.
ACCESSION   AY234218
VERSION     AY234218.1  GI:29569754
KEYWORDS    .
SOURCE      Papio anubis (olive baboon)
  ORGANISM  Papio anubis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Papio.
REFERENCE   1  (bases 1 to 1005)
  AUTHORS   Villinger,F.
  TITLE     Nonhuman primate cytokines
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1005)
  AUTHORS   Villinger,F.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-FEB-2003) Pathology & Laboratory Medicine, Emory
            University School of Medicine, Woodruff Memorial Building Rm 2339,
            1639 Pierce Drive, Atlanta, GA 30322, USA
FEATURES             Location/Qualifiers
     source          1. .1005
                     /organism="Papio anubis"
                     /mol_type="mRNA"
                     /db_xref="taxon:9555"
     gene            1. .1005
                     /gene="IL12a"
     CDS             9. .995
                     /gene="IL12a"
                     /codon_start=1
                     /product="interleukin-12 alpha p40 subunit precursor"
                     /protein_id="AAO85331.1"
                     /db_xref="GI:29569755"
                     /translation="MCHQQLVISWFSLVFLASPLMAIWELKKDVYVVELDWYPDAPGE
                     MVVLTCDTPEEDGITWTLDQSGEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSHSLL
                     LLHKKEDGIWSTDVLKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                     GSSNPQGVTCGAVTLSAERVRGDNKEYEYSVECQEDSACPAAEERLPIEVMVDAIHKL
                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQAEVSWEYPDTWSTPHSYFSLTFCIQ
                     VQGKSKREKKDRIFTDKTSATVICRKNASFSVQAQDRYYSSSWSEWASVPCS"
     sig_peptide     9. .74
                     /gene="IL12a"
     mat_peptide     75. .992
                     /gene="IL12a"
                     /product="interleukin-12 alpha p40 subunit"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 5;  Length 1005;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        669 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 712


RESULT 78
CTU19834
LOCUS       CTU19834                1005 bp    mRNA    linear   PRI 03-FEB-1996
DEFINITION  Cercocebus torquatus interleukin-12 alpha p40 subunit (IL-12a)
            mRNA, complete cds.
ACCESSION   U19834
VERSION     U19834.1  GI:644785
KEYWORDS    .
SOURCE      Cercocebus torquatus (red-crowned mangabey)
  ORGANISM  Cercocebus torquatus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Cercocebus.
REFERENCE   1  (bases 1 to 1005)
  AUTHORS   Villinger,F., Brar,S.S., Mayne,A., Chikkala,N. and Ansari,A.A.
  TITLE     Comparative sequence analysis of cytokine genes from human and
            nonhuman primates
  JOURNAL   J. Immunol. 155 (8), 3946-3954 (1995)
   PUBMED   7561102
REFERENCE   2  (bases 1 to 1005)
  AUTHORS   Villinger,F.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JAN-1995) Francois J. Villinger, Emory University,
            Pathology, 1327 Clifton Rd, Atlanta, GA 30322, USA
FEATURES             Location/Qualifiers
     source          1. .1005
                     /organism="Cercocebus torquatus"
                     /mol_type="mRNA"
                     /sub_species="atys"
                     /db_xref="taxon:9530"
                     /clone="FPn IL-12a"
                     /cell_type="peripheral blood mononuclear cells"
                     /tissue_type="blood"
     gene            1. .1005
                     /gene="IL-12a"
     CDS             9. .995
                     /gene="IL-12a"
                     /function="NK cell stimulatory factor"
                     /codon_start=1
                     /product="interleukin-12 alpha p40 subunit"
                     /protein_id="AAA86701.1"
                     /db_xref="GI:644786"
                     /translation="MCHQQLVISWFSLVFLASPLMAIWELKKDVYVVELDWYPDAPGE
                     MVVLTCDTPEEDGITWTLDQSGEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSHSLL
                     LPHKKEDGIWSTDILKDQKEPKNETFLRCEAKNYSGRITCWWLSTISTDLTFSIISSR
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                    GSSNPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEERLPIEVMVDAIHKL
                    KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCIQ
                    VQGKSKREKKDRIFTDKTSATVICRKNASFSVQAQDRYYSSSWNEWTSVPCS"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 5;  Length 1005;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        669 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 712


RESULT 79
AF180563
LOCUS       AF180563                1007 bp    mRNA    linear   PRI 26-SEP-1999
DEFINITION  Homo sapiens interleukin 12, P40 mRNA, complete cds.
ACCESSION   AF180563
VERSION     AF180563.1  GI:5923854
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1007)
  AUTHORS   Hongyuan,J. and Meiyun,Z.
  TITLE     Cloning and sequence analysis of IL-12 cDNA from Chinese
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1007)
  AUTHORS   Hongyuan,J. and Meiyun,Z.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-AUG-1999) Hepatitis, Institute of Virology, CAPM, 100
            Yingxinjie, Xuanwuqu, Beijing 100052, China
FEATURES             Location/Qualifiers
     source          1. .1007
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_type="peripheral mononuclear"
     CDS             7. .993
                     /note="NKSF/CLMF; IL12p40; 40kD"
                     /codon_start=1
                     /product="interleukin 12, P40"
                     /protein_id="AAD56386.1"
                     /db_xref="GI:5923855"
                     /translation="MCHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGE
                     MVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLL
                     LLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                     GSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKL
                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
                     VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 5;  Length 1007;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        667 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 710


RESULT 80
AB246273
LOCUS       AB246273                1008 bp    mRNA    linear   MAM 13-JAN-2006
DEFINITION  Bubalus carabanensis IL-12p40 mRNA for interleukin-12p40, complete
            cds.
ACCESSION   AB246273
VERSION     AB246273.1  GI:84871695
KEYWORDS    .
SOURCE      Bubalus carabanensis
  ORGANISM  Bubalus carabanensis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bubalus.
REFERENCE   1
  AUTHORS   Mingala,C.N., Raadan,O., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Comparative assessment of Th1 and Th2 cytokines of swamp type
            buffalo and other bubaline breeds by molecular cloning, sequencing
            and phylogenetics
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1008)
  AUTHORS   Mingala,C.N., Odbileg,R., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JAN-2006) Claro N Mingala, Graduate School of
            Veterinary Medicine, Hokkaido University, Department of Disease
            Control, Laboratory of Infectious Diseases; Kita-ku Kita 18 Nishi
            9, Sapporo, Hokkaido 060-0818, Japan (E-mail:cnmingala@hotmail.com,
            Tel:81-11-706-5216, Fax:81-11-706-5217)
FEATURES             Location/Qualifiers
     source          1. .1008
                     /organism="Bubalus carabanensis"
                     /mol_type="mRNA"
                     /db_xref="taxon:346063"
                     /sex="female"
                     /cell_type="PBMC"
     gene            1. .1008
                     /gene="IL-12p40"
     CDS             1. .984
                     /gene="IL-12p40"
                     /codon_start=1
                     /product="interleukin-12p40"
                     /protein_id="BAE75850.1"
                     /db_xref="GI:84871696"
                     /translation="MHPQQLVVSWFSLVLLASPIVAIWELEKNVYIVELDWYPDAPGE
                     TVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSRSLL
                     LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCWWLTAISTDLKFSVKSSR
                     GSSDPRGVTCGAASLSAEKVSVDHREYNKYTVECQEGSTCPAAEESLLIEVVVEAVHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                     QVQGKNKREKKLFMDQTSAKVTCHKDANVRVQARDRYYSSFWSEWASVSCS"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 14;  Length 1008;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707


RESULT 81
AB246353
LOCUS       AB246353                1008 bp    mRNA    linear   MAM 13-JAN-2006
DEFINITION  Bubalus bubalis IL-12p40 mRNA for interleukin-12p40, complete cds.
ACCESSION   AB246353
VERSION     AB246353.1  GI:84871717
KEYWORDS    .
SOURCE      Bubalus bubalis (water buffalo)
  ORGANISM  Bubalus bubalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bubalus.
REFERENCE   1
  AUTHORS   Mingala,C.N., Raadan,O., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Comparative assessment of Th1 and Th2 cytokines of swamp type
            buffalo and other bubaline breeds by molecular cloning, sequencing
            and phylogenetics
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1008)
  AUTHORS   Mingala,C.N., Odbileg,R., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2006) Claro N Mingala, Graduate School of
            Veterinary Medicine, Hokkaido University, Department of Disease
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            Control, Laboratory of Infectious Diseases; Kita-ku Kita 18 Nishi
            9, Sapporo, Hokkaido 060-0818, Japan (E-mail:cnmingala@hotmail.com,
            Tel:81-11-706-5216, Fax:81-11-706-5217)
FEATURES              Location/Qualifiers
     source           1. .1008
                      /organism="Bubalus bubalis"
                      /mol_type="mRNA"
                      /db_xref="taxon:89462"
                      /sex="female"
                      /cell_type="PBMC"
                      /note="Bulgarian Murrah buffalo - crossbreed between
                      Mediterranean and Indian buffalo both are Riverine type
                      water buffalo"
     gene             1. .1008
                      /gene="IL-12p40"
     CDS              1. .984
                      /gene="IL-12p40"
                      /codon_start=1
                      /product="interleukin-12p40"
                      /protein_id="BAE75858.1"
                      /db_xref="GI:84871718"
                      /translation="MHPQQLVVSWFSLVLLASPIVAIWELEKNVYVVELDWYPDAPGE
                      TVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSRSLL
                      LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCWWLTAISTDLKFSVKSSR
                      GSSDPRGVTCEAASLSAEKVSVDHREYNKYTVECQEGSTCPAAEESLLIEVVVEAVHK
                      LKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                      QVQGKNKREKKLFMDQTSAKVTCHKDANVRVQARDRYYSSFWSEWASVSCS"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 14;  Length 1008;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707


RESULT 82
AB246358
LOCUS       AB246358               1008 bp    mRNA    linear   MAM 14-JAN-2006
DEFINITION  Bubalus bubalis x Bubalus carabanensis IL-12p40 mRNA for
            interleukin-12p40, complete cds.
ACCESSION   AB246358
VERSION     AB246358.1  GI:84875356
KEYWORDS    .
SOURCE      Bubalus bubalis x Bubalus carabanensis
  ORGANISM  Bubalus bubalis x Bubalus carabanensis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bubalus.
REFERENCE   1
  AUTHORS   Mingala,C.N., Raadan,O., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Comparative assessment of Th1 and Th2 cytokines of swamp type
            buffalo and other bubaline breeds by molecular cloning, sequencing
            and phylogenetics
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1008)
  AUTHORS   Mingala,C.N., Odbileg,R., Konnai,S., Ohashi,K. and Onuma,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2006) Claro N Mingala, Graduate School of
            Veterinary Medicine, Hokkaido University, Department of Disease
            Control, Laboratory of Infectious Diseases; Kita-ku Kita 18 Nishi
            9, Sapporo, Hokkaido 060-0818, Japan (E-mail:cnmingala@hotmail.com,
            Tel:81-11-706-5216, Fax:81-11-706-5217)
FEATURES              Location/Qualifiers
     source           1. .1008
                      /organism="Bubalus bubalis x Bubalus carabanensis"
                      /mol_type="mRNA"
                      /db_xref="taxon:365610"
                      /sex="female"
                      /cell_type="PBMC"
                      /note="Philippine carabao crossbreed (CB) - crossbreed
                      between Philippine carabao (Swamp type water buffalo) and
                      Indian Murrah buffalo (Riverine type water buffalo)"
     gene             1. .1008
                      /gene="IL-12p40"
     CDS              1. .984
                      /gene="IL-12p40"
                      /codon_start=1
                      /product="interleukin-12p40"
                      /protein_id="BAE75892.1"
                      /db_xref="GI:84875357"
                      /translation="MHPQQLVVSWFSLVLLASPIVAIWELEKNVYVVELDWYPDAPGE
                      TVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSRSLL
                      LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSEHFTGWWLTAISTNLKFSVKSSR
                      GSSDPRGVTCGAASLSAEKVSVDHREYNKYTVECQEGSTCPAAEESLLIEVVVEAVHK
                      LKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                      QVQGKNKREKKLFMDQTSAKVTCHKDANVRVQARDRYYSSFWSEWASVSCS"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 14;  Length 1008;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707


RESULT 83
AF007576
LOCUS       AF007576               1012 bp    mRNA    linear   MAM 14-JUL-1997
DEFINITION  Capra hircus interleukin 12 p40 subunit (IL-12) mRNA, complete cds.
ACCESSION   AF007576
VERSION     AF007576.1  GI:2253433
KEYWORDS    .
SOURCE      Capra hircus (goat)
  ORGANISM  Capra hircus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Caprinae; Capra.
REFERENCE   1  (bases 1 to 1012)
  AUTHORS   Beyer,J.C., Cheevers,W.P. and Kumpula-McWhirter,N.M.
  TITLE     CLoning of caprine IL-12 40 kDa subunit
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1012)
  AUTHORS   Beyer,J.C., Cheevers,W.P. and Kumpula-McWhirter,N.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JUN-1997) Veterinary Microbiology and Pathology,
            Washington State University, P.O. Box 647040, Pullman, WA
            99164-7040, USA
FEATURES              Location/Qualifiers
     source           1. .1012
                      /organism="Capra hircus"
                      /mol_type="mRNA"
                      /db_xref="taxon:9925"
                      /cell_type="LPS-stimulated microglial cell"
     gene             1. .1012
                      /gene="IL-12"
     CDS              1. .984
                      /gene="IL-12"
                      /codon_start=1
                      /product="interleukin 12 p40 subunit"
                      /protein_id="AAB62945.1"
                      /db_xref="GI:2253434"
                      /translation="MHPQQLVVSWFSLVLLASPIVAIWELEKNVYVVELDWYPNAPGE
                      TVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSRSLL
                      LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCSWLTAISTNLKFSVKSSR
                      GSSDPRGVTCGAASLSAEKVSMDHREYNKYTVECQEGSACPAAEESLPIEVVMEAVHK
                      LKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                      QVQGKNKREKKLFTDQTSAKVTCHKDANIRVQARDRYYSSFWSEWASVSCS"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 14;  Length 1012;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
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  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707


RESULT 84
AY198121
LOCUS       AY198121               1012 bp    mRNA    linear   MAM 09-JUN-2005
DEFINITION  Bubalus bubalis interleukin 12 p40 subunit precursor, mRNA,
            complete cds.
ACCESSION   AY198121
VERSION     AY198121.1  GI:28192687
KEYWORDS    .
SOURCE      Bubalus bubalis (water buffalo)
  ORGANISM  Bubalus bubalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bubalus.
REFERENCE   1  (bases 1 to 1012)
  AUTHORS   Premraj,A., Sreekumar,E., Nautiyal,B. and Rasool,T.J.
  TITLE     Interleukin-12 subunits p35 and p40 of Indian water buffalo
            (Bubalus bubalis) maintain high sequence homology with those of
            other ruminants
  JOURNAL   Eur. J. Immunogenet. 32 (3), 179-186 (2005)
REFERENCE   2  (bases 1 to 1012)
  AUTHORS   Premraj,A., Sreekumar,E. and Rasool,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-DEC-2002) Animal Biotechnology, Rajiv Gandhi Center
            for Biotechnology, Jagathy, Thycaud PO, Trivandrum, Kerala 695014,
            India
FEATURES             Location/Qualifiers
     source          1. .1012
                     /organism="Bubalus bubalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:89462"
     CDS             1. .984
                     /note="cytokine; 40 kDa subunit"
                     /codon_start=1
                     /product="interleukin 12 p40 subunit precursor"
                     /protein_id="AAO25629.1"
                     /db_xref="GI:28192688"
                     /translation="MHPQQLVVSWFSLVLLASPIVAIWELEKNVYIVELDWYPDAPGE
                     TVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSRSLL
                     LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCWWLTAISTDLKFSVKSSR
                     GSADPRGVTCGAASLSAEKVSVDHREYNKYTVECQEGSTCPAAEESLLIEVVVEAVHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                     QVQGKNKREKKLFMDQTSAKVTCHKDANVRVQARDRYYSSFWSEWASVSCS"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 14;  Length 1012;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707


RESULT 85
BTU11815
LOCUS       BTU11815               1012 bp    mRNA    linear   MAM 27-JAN-1996
DEFINITION  Bos taurus interleukin 12 40 kDa subunit mRNA, complete cds.
ACCESSION   U11815
VERSION     U11815.1  GI:555795
KEYWORDS    .
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 1012)
  AUTHORS   Zarlenga,D.S., Canals,A., Aschenbrenner,R.A. and Gasbarre,L.C.
  TITLE     Enzymatic amplification and molecular cloning of cDNA encoding the
            small and large subunits of bovine interleukin 12
  JOURNAL   Biochim. Biophys. Acta 1270 (2-3), 215-217 (1995)
   PUBMED   7727547
REFERENCE   2  (bases 1 to 1012)
  AUTHORS   Zarlenga,D.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JUL-1994) Dante S. Zarlenga, U.S. Department of
            Agriculture, ARS, LPSI, PIL, Beltsville, MD 20705, USA
FEATURES             Location/Qualifiers
     source          1. .1012
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /strain="Holstein"
                     /db_xref="taxon:9913"
                     /clone="BIL12 40"
                     /sex="male"
                     /cell_type="lymphocytes and macrophages"
                     /tissue_type="lymphoid"
     CDS             1. .984
                     /codon_start=1
                     /product="interleukin 12 40 kDa subunit"
                     /protein_id="AAA85792.1"
                     /db_xref="GI:555796"
                     /translation="MHPQQLVVSWFSLVLLASPIVAMWELEKNVYVVELDWYPDAPGE
                     TVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSRSLL
                     LLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCWWLTAISTDLKFSVKSSR
                     GSSDPRGVTCGAALLSAEKVSLEHREYNKYTVECQEGSACPAAEESLLIEVVVEAVHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCV
                     QVQGKNKREKKLFMDQTSAKVTCHKDANVRVQARDRYYSSFWSEWASVSCS"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 14;  Length 1012;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
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Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707


RESULT 86
AR052857
LOCUS       AR052857               1018 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 194 from patent US 5833975.
ACCESSION   AR052857
VERSION     AR052857.1  GI:5977719
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1018)
  AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
  TITLE     Canarypox virus expressing cytokine and/or tumor-associated antigen
            DNA sequence
  JOURNAL   Patent: US 5833975-A 194 10-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .1018
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 2;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 87
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AR288169
LOCUS       AR288169                1018 bp    mRNA    linear   PAT 12-JUN-2003
DEFINITION  Sequence 194 from patent US 6537594.
ACCESSION   AR288169
VERSION     AR288169.1  GI:31675448
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1018)
  AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
  TITLE     Vaccina virus comprising cytokine and/or tumor associated antigen
            genes
  JOURNAL   Patent: US 6537594-A 194 25-MAR-2003;
            Virogenetics Corporation; Troy, NY
FEATURES             Location/Qualifiers
     source          1. .1018
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 2;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 88
AR567156
LOCUS       AR567156                1018 bp    mRNA    linear   PAT 08-OCT-2004
DEFINITION  Sequence 194 from patent US 6780407.
ACCESSION   AR567156
VERSION     AR567156.1  GI:53984798
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1018)
  AUTHORS   Paoletti,E., Tartaglia,J. and Cox,W.I.
  TITLE     Pox virus comprising DNA sequences encoding CEA and B7 antigen
  JOURNAL   Patent: US 6780407-A 194 24-AUG-2004;
            Aventis Pasteur; Swiftwater, PA
FEATURES             Location/Qualifiers
     source          1. .1018
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 2;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 89
E35794
LOCUS       E35794                  1019 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Process for producing interleukin 12.
ACCESSION   E35794
VERSION     E35794.1  GI:18624618
KEYWORDS    JP 2000157274-A/6.
SOURCE      Bos sp.
  ORGANISM  Bos sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 1019)
  AUTHORS   Nakamura,M., Takehara,K. and Ohara,E.
  TITLE     Process for producing interleukin 12
  JOURNAL   Patent: JP 2000157274-A 6 13-JUN-2000;
            DAI ICHI SEIYAKU CO LTD
COMMENT     OS   Bos sp. (bovine)
            PN   JP 2000157274-A/6
            PD   13-JUN-2000
            PF   20-NOV-1998 JP 1998331052
            PR
            PI   MASAYUKI NAKAMURA,KAZUAKI TAKEHARA,EIJI OHARA PC
            C12N15/09,C07K14/54,C12N5/10,C12P21/02//(C12N15/09,C12R1:91), PC
            (C12N5/10,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00, PC
            (C12N15/00,C12R1:91),(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .1019
            FT                   /organism='Bos sp. (bovine)'.
FEATURES             Location/Qualifiers
     source          1. .1019
                     /organism="Bos sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:29061"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 2;  Length 1019;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db        675 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 718


RESULT 90
CQ829448
LOCUS       CQ829448                1029 bp    DNA     linear   PAT 05-JUL-2004
DEFINITION  Sequence 7 from Patent WO2004052929.
ACCESSION   CQ829448
VERSION     CQ829448.1  GI:49732784
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Vandenbroeck,K. and Alloza,I.
  TITLE     Recombinant cell line
  JOURNAL   Patent: WO 2004052929-A 7 24-JUN-2004;
            The Queen's University of Belfast (GB)
FEATURES             Location/Qualifiers
     source          1. .1029
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="cDNA for beta chain of IL-12"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 2;  Length 1029;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        676 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 719


RESULT 91
BC074723
LOCUS       BC074723                1046 bp    mRNA    linear   PRI 28-JUL-2005
DEFINITION  Homo sapiens interleukin 12B (natural killer cell stimulatory
            factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA
            (cDNA clone MGC:103792 IMAGE:30915173), complete cds.
ACCESSION   BC074723
VERSION     BC074723.2  GI:50960609
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```
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1046)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1046)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JUN-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     On Aug 4, 2004 this sequence version replaced gi:49901500.
            Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Genome Sequence Centre, British Columbia Cancer
            Center
            cDNA Library Preparation: British Columbia Cancer Research Center
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
            Martin Hirst, Thomas Zeng, Ryan Morin, Michelle Moksa, Johnson
            Pang, Diana Mah, Jing Wang, Kieth Fichter, Eric Chuah, Allen
            Delaney, Rob Kirkpatrick, Agnes Baross, Sarah Barber, Mabel
            Brown-John, Steve S. Chand, William Chow, Ryan Babakaiff, Dave
            Wong, Corey Matsuo, Jaclyn Beland, Susan Gibson, Luis delRio, Ruth
            Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
            Kim MacDonald,  Mike R. Mayo, Josh Moran, Diana Palmquist, JR
            Santos, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang,
            Jacquie Schein, Asim Siddiqui,Steven Jones, Rob Holt, Marco Marra.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRBU Plate: 1 Row: A Column: 6.
FEATURES             Location/Qualifiers
     source          1. .1046
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:103792 IMAGE:30915173"
                     /tissue_type="Brain, PCR rescued clones"
                     /clone_lib="NIH_MGC_272"
                     /lab_host="DH10B"
                     /note="Vector: pCR4 Topo TA with reversed insert"
     gene            1. .1046
                     /gene="IL12B"
                     /note="synonyms: CLMF2, IL-12B, NKSF, CLMF"
                     /db_xref="GeneID:3593"
                     /db_xref="MIM:161561"
     CDS             32. .1018
                     /gene="IL12B"
                     /codon_start=1
                     /product="interleukin 12B, precursor"
                     /protein_id="AAH74723.1"
                     /db_xref="GI:50960610"
                     /db_xref="GeneID:3593"
                     /db_xref="MIM:161561"
                     /translation="MCHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGE
                     MVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLL
                     LLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
                     GSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKL
                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
                     VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 5;  Length 1046;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-12;
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Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 92
BC067498
LOCUS       BC067498               1073 bp    mRNA    linear   PRI 28-JUL-2005
DEFINITION  Homo sapiens interleukin 12B (natural killer cell stimulatory
            factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA
            (cDNA clone MGC:79355 IMAGE:6971868), complete cds.
ACCESSION   BC067498
VERSION     BC067498.1  GI:45768642
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1073)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1073)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
```

```
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 172 Row: d Column: 13
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 24497437.
FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_195"
                     /lab_host="DH10B"
                     /note="Vector: pDNR-Dual"
     gene            1. .1073
                     /gene="IL12B"
                     /note="synonyms: CLMF2, IL-12B, NKSF, CLMF"
                     /db_xref="GeneID:3593"
                     /db_xref="MIM:161561"
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                     LLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSR
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                     KYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQ
                     VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 5;  Length 1073;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db        665 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 708


RESULT 93
BC067499
LOCUS       BC067499                1073 bp    mRNA    linear   PRI 28-JUL-2005
DEFINITION  Homo sapiens interleukin 12B (natural killer cell stimulatory
            factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA
            (cDNA clone MGC:79356 IMAGE:6971869), complete cds.
ACCESSION   BC067499
VERSION     BC067499.1  GI:45768645
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1073)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
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            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
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            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1073)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 172 Row: d Column: 12
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 24497437.
FEATURES             Location/Qualifiers
     source          1. .1073
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:79356 IMAGE:6971869"
                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH_MGC_195"
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                     /note="Vector: pDNR-Dual"
     gene            1. .1073
                     /gene="IL12B"
                     /note="synonyms: CLMF2, IL-12B, NKSF, CLMF"
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                     /gene="IL12B"
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VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"
ORIGIN

Query Match 4.5%; Score 44; DB 5; Length 1073;
Best Local Similarity 100.0%; Pred. No. 2.6e-12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
||||||||||||||||||||||||||||||||||||||||||||
Db 665 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 708

RESULT 94
BC067500
LOCUS BC067500 1073 bp mRNA linear PRI 28-JUL-2005
DEFINITION Homo sapiens interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA (cDNA clone MGC:79358 IMAGE:6971872), complete cds.
ACCESSION BC067500
VERSION BC067500.1 GI:45768649
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1073)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
CONSRTM Mammalian Gene Collection Program Team
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REFERENCE 2 (bases 1 to 1073)
AUTHORS .
CONSRTM NIH MGC Project
TITLE Direct Submission
JOURNAL Submitted (19-MAR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 172 Row: d Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 24497437.
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:79358 IMAGE:6971872"
/tissue_type="PCR rescued clones"
/clone_lib="NIH_MGC_195"
/lab_host="DH10B"
/note="Vector: pDNR-Dual"
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/gene="IL12B"
/note="synonyms: CLMF2, IL-12B, NKSF, CLMF"
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/db_xref="MIM:161561"
CDS 5. .991
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VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"
ORIGIN

Query Match 4.5%; Score 44; DB 5; Length 1073;
Best Local Similarity 100.0%; Pred. No. 2.6e-12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db 665 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 708

RESULT 95
BC067501
LOCUS BC067501 1073 bp mRNA linear PRI 28-JUL-2005
DEFINITION Homo sapiens interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA (cDNA clone MGC:79359 IMAGE:6971873), complete cds.
ACCESSION BC067501
VERSION BC067501.1 GI:45767736
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1073)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,

```
          Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1073)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 172 Row: d Column: 22
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 24497437.
FEATURES             Location/Qualifiers
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                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH_MGC_195"
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                     /note="Vector: pDNR-Dual"
     gene            1. .1073
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                     /note="synonyms: CLMF2, IL-12B, NKSF, CLMF"
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                     /db_xref="MIM:161561"
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                     VQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS"
ORIGIN

  Query Match             4.5%;  Score 44;  DB 5;  Length 1073;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        665 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 708


RESULT 96
BC067502
LOCUS       BC067502                1073 bp    mRNA    linear   PRI 28-JUL-2005
DEFINITION  Homo sapiens interleukin 12B (natural killer cell stimulatory
            factor 2, cytotoxic lymphocyte maturation factor 2, p40), mRNA
            (cDNA clone MGC:79360 IMAGE:6971874), complete cds.
ACCESSION   BC067502
VERSION     BC067502.1  GI:45768652
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1073)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
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            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1073)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 172 Row: d Column: 23
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RESULT 97
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DEFINITION  Macaca mulatta interleukin-12 alpha (IL-12a) mRNA, complete cds.
ACCESSION   U19841
VERSION     U19841.1  GI:644799
KEYWORDS    .
SOURCE      Macaca mulatta (rhesus monkey)
  ORGANISM  Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 1080)
  AUTHORS   Villinger,F., Brar,S.S., Mayne,A., Chikkala,N. and Ansari,A.A.
  TITLE     Comparative sequence analysis of cytokine genes from human and
            nonhuman primates
  JOURNAL   J. Immunol. 155 (8), 3946-3954 (1995)
   PUBMED   7561102
REFERENCE   2  (bases 1 to 1080)
  AUTHORS   Villinger,F.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JAN-1995) Francois J. Villinger, Emory University,
            Pathology, 1327 Clifton Rd, Atlanta, GA 30322, USA
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DEFINITION  Sequence 4 from patent US 6617135.
ACCESSION   AR393788
VERSION     AR393788.1  GI:40120790
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1389)
  AUTHORS   Gillies,S.D. and Lo,K.-M.
  TITLE     Multiple cytokine protein complexes
  JOURNAL   Patent: US 6617135-A 4 09-SEP-2003;
            EMD Lexigen Research Center Corp.; Billerica, MA
FEATURES             Location/Qualifiers
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DEFINITION  Sequence 4 from Patent WO0110912.
ACCESSION   AX084106
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VERSION     AX084106.1  GI:13185656
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Gillies,S.D. and Lo,K.M.
  TITLE     Multiple cytokine-antibody complexes
  JOURNAL   Patent: WO 0110912-A 4 15-FEB-2001;
            Lexigen Pharmaceuticals Corp. (US)
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DEFINITION  Antibody against cytotoxic lymphocyte maturing factors.
ACCESSION   BD165800
VERSION     BD165800.1  GI:27871612
KEYWORDS    JP 2002167400-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 1397)
  AUTHORS   Chizzonite,R.A., Gately,M.K., Gubler,U.A., Hulmes,J.D., Pan,Y.C.E.,
            Podlanski,F.J. and Stern,A.S.
  TITLE     Antibody against cytotoxic lymphocyte maturing factors
  JOURNAL   Patent: JP 2002167400-A 1 11-JUN-2002;
            PROTEIN DESIGN LABS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002167400-A/1
            PD   11-JUN-2002
            PF   14-AUG-2001 JP 2001246031
            PR   22-DEC-1989 US       455708,09-MAY-1990 US       520935 PR
            27-AUG-1990 US       572284
            PI   RICHARD ANTHONY CHIZZONITE,MAURICE KENT GATELY,ULRICH ANDREAS
            PI   GUBLER,
            PI   JEFFREY DAVID HULMES,YU CHING EUGENE PAN,FRANK JOHN PODLANSKI,
            PI   ALVIN SETH STERN
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c	4	987	100.0	987	14	ADV34684	Adv34684 Feline si
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	6	985	99.8	985	6	ABK98961	Abk98961 Feline in
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	92	44	4.5	1397	2	AAT97969 Aat97969 40 kDa su
	93	44	4.5	1397	2	AAV00401 Aav00401 40 kDa su
	94	44	4.5	1397	2	AAV37767 Aav37767 Cytotoxic
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	103	44	4.5	2336	14	AEE03207 Aee03207 Human int
	104	44	4.5	2347	12	ACF57534 Acf57534 Human IL1
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	106	44	4.5	2347	14	ADZ26728 Adz26728 Human IL1
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	114	44	4.5	5686	2	AAZ40415 Aaz40415 Plasmid p
	115	44	4.5	5686	12	ADF77239 Adf77239 Human IL-
	116	44	4.5	6139	3	AAZ40023 Aaz40023 Interleuk
	117	44	4.5	8578	6	AAD31546 Aad31546 pIRES-hB7
	118	44	4.5	8578	6	AAD31545 Aad31545 pIRES-hB7
	119	44	4.5	8608	6	AAD31548 Aad31548 pIRES-hB7
	120	44	4.5	8623	6	AAD31547 Aad31547 pIRES-hB7
	121	44	4.5	8629	6	AAD31552 Aad31552 pIRES-IL1
	122	44	4.5	8638	6	AAD31549 Aad31549 pIRES-hB7
	123	44	4.5	8644	6	AAD31551 Aad31551 pIRES-IL1
	124	44	4.5	8659	6	AAD31550 Aad31550 pIRES-IL1
	125	44	4.5	11453	10	ADG25152 Adg25152 Vector pS
	126	44	4.5	11569	10	ADG25150 Adg25150 Vector pA
	127	39	4.0	1007	10	ACD26421 Acd26421 cDNA enco
	128	39	4.0	2390	12	ADM29103 Adm29103 Human int
	129	39	4.0	18110	6	ABK15357 Abk15357 Human int
	130	39	4.0	18340	5	AAD19368 Aad19368 Mammalian
c	131	35	3.5	270	12	ACH83638 Ach83638 Human gen
c	132	35	3.5	556	12	ACH69938 Ach69938 Human gen
	133	35	3.5	975	5	AAD15203 Aad15203 Modified
c	134	30	3.0	30	3	AAA48905 Aaa48905 Probe 12.
	135	30	3.0	73	4	AAS15322 Aas15322 Mouse IL-
	136	30	3.0	600	2	AAX78397 Aax78397 IL-12p40
	137	30	3.0	600	2	AAX25947 Aax25947 Interleuk
	138	30	3.0	1008	13	ADS00008 Ads00008 Murine in
	139	30	3.0	1008	14	ADW97243 Adw97243 Murine p4
	140	30	3.0	1056	2	AAV28472 Aav28472 Murine in
	141	30	3.0	1061	2	AAT35200 Aat35200 Mouse int
	142	30	3.0	1409	4	AAF76879 Aaf76879 Murine p4
	143	30	3.0	1472	4	AAF76878 Aaf76878 Murine p4
	144	30	3.0	1569	4	AAF76888 Aaf76888 Single-ch
	145	30	3.0	1610	12	ADQ14470 Adq14470 DNA encod
	146	30	3.0	1840	8	ACA61265 Aca61265 DNA encod
	147	30	3.0	2013	4	AAF76887 Aaf76887 Murine p3
	148	30	3.0	2334	14	AEE03206 Aee03206 Murine in
	149	30	3.0	2438	12	ADO43004 Ado43004 DNA encod
	150	30	3.0	2709	4	AAF76889 Aaf76889 Coding se
	151	30	3.0	5252	12	ADO07652 Ado07652 Tricistro
	152	30	3.0	5966	2	AAZ40417 Aaz40417 Plasmid p
	153	30	3.0	5966	12	ADF77241 Adf77241 Mouse IL-
	154	30	3.0	5985	12	ADQ82718 Adq82718 Anticance
	155	30	3.0	6295	2	AAV02043 Aav02043 Plasmid p
	156	30	3.0	7287	2	AAV02042 Aav02042 Plasmid p
	157	30	3.0	9049	12	ADO07661 Ado07661 Viral vec
	158	30	3.0	10633	12	ADO07660 Ado07660 Viral vec
	159	30	3.0	11458	10	ADG25151 Adg25151 Vector pA
	160	30	3.0	11746	12	ADO07659 Ado07659 Viral vec
	161	30	3.0	28191	14	AEE03204 Aee03204 Adenovira
	162	30	3.0	28892	14	AEE03202 Aee03202 Adenovira
	163	30	3.0	38246	12	ADO07662 Ado07662 Viral vec
	164	28	2.8	28	6	ABK98985 Abk98985 Feline PC
	165	28	2.8	28	14	ADV34735 Adv34735 Feline IL
	166	28	2.8	37	6	ABK98987 Abk98987 Feline PC
	167	28	2.8	37	14	ADV34737 Adv34737 Feline IL
c	168	25	2.5	25	6	ABK98986 Abk98986 Feline PC
c	169	25	2.5	25	14	ADV34736 Adv34736 Feline IL
c	170	25	2.5	25	14	AEC56176 Aec56176 Antisense
c	171	24	2.4	26	2	AAX78412 Aax78412 Rat GADPH
c	172	24	2.4	26	2	AAX25927 Aax25927 IL12 p40
	173	24	2.4	30	4	AAI65149 Aai65149 Canine IL
	174	24	2.4	30	8	ACD27994 Acd27994 Interleuk
	175	24	2.4	39	2	AAV13826 Aav13826 Primer fo
	176	24	2.4	39	2	AAX03164 Aax03164 PCR prime
	177	24	2.4	39	2	AAX35627 Aax35627 PCR prime
	178	24	2.4	39	4	AAI64390 Aai64390 PCR prime
	179	24	2.4	540	2	AAX27732 Aax27732 Recombina
	180	24	2.4	540	3	AAA13801 Aaa13801 Canine in
	181	24	2.4	987	2	AAZ40406 Aaz40406 Human int
	182	24	2.4	987	2	AAZ40405 Aaz40405 Human int
	183	24	2.4	987	12	ADF77278 Adf77278 Human IL-
	184	24	2.4	987	12	ADF77277 Adf77277 Human IL-
	185	23	2.3	200	2	AAV03357 Aav03357 Homo sapi
c	186	22	2.2	25	6	ABK98988 Abk98988 Feline PC
c	187	22	2.2	25	14	ADV34738 Adv34738 Feline IL
	188	22	2.2	399	14	AEE14792 Aee14792 Hamster S
	189	22	2.2	399	14	AEE11150 Aee11150 Hamster c
c	190	22	2.2	87350	2	AAX83003 Aax83003 Human WRN
c	191	22	2.2	87543	7	ADJ84092 Adj84092 Human WRN
	192	21	2.1	21	3	AAA48904 Aaa48904 Reverse p
c	193	21	2.1	21	3	AAA48903 Aaa48903 Forward p
	194	21	2.1	21	12	ADG14584 Adg14584 IL-12p40
	195	21	2.1	23	2	AAX78422 Aax78422 Rat GADPH
	196	21	2.1	23	2	AAX25940 Aax25940 IL12 p40
	197	21	2.1	44	2	AAV56632 Aav56632 Feline FL
	198	20	2.0	20	5	AAD19313 Aad19313 Mammalian
c	199	20	2.0	20	10	ABX33973 Abx33973 Human int
c	200	20	2.0	20	10	ABX33972 Abx33972 Human int

ALIGNMENTS

```
RESULT 1
ABK98944
ID   ABK98944 standard; cDNA; 987 BP.
XX
AC   ABK98944;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p40-987 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69303.
XX
```

```
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 51-53; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 987 BP; 283 A; 250 C; 246 G; 208 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 987;  DB 6;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  987;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987


RESULT 2
ABK98945/c
ID   ABK98945 standard; cDNA; 987 BP.
XX
AC   ABK98945;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p40-987 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 3; Page 54; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
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SQ   Sequence 987 BP; 208 A; 246 C; 250 G; 283 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 987;  DB 6;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  987;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGCAGT 1
```

```
RESULT 3
ADV34682
ID   ADV34682 standard; cDNA; 987 BP.
XX
AC   ADV34682;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12p40 full-length cDNA, nFeIL-12p40 987.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .987
FT                   /*tag=  a
FT                   /product= "PFeIL-12p40 329 protein "
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34683.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 23; SEQ ID NO 29; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12p40 subunit protein
CC   encoding full-length cDNA.
XX
SQ   Sequence 987 BP; 283 A; 250 C; 246 G; 208 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 987;  DB 14;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  987;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
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Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
```

RESULT 4
ADV34684/c
ID ADV34684 standard; DNA; 987 BP.
XX
AC ADV34684;
XX
DT 24-FEB-2005 (first entry)
XX
DE Feline single chain IL-12p40 complementary DNA, nFeIL-12p40 987.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Felis catus.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 3; SEQ ID NO 31; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain IL-12p40 subunit full-length
CC complementary DNA.
XX
SQ Sequence 987 BP; 208 A; 246 C; 250 G; 283 T; 0 U; 0 Other;

```
  Query Match            100.0%;  Score 987;  DB 14;  Length 987;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  987;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448
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Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGCAGT 1
```

RESULT 5
ABK98962/c
ID ABK98962 standard; cDNA; 985 BP.
XX
AC ABK98962;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p40-N985 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Example 3; Page 75-76; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 985 BP; 207 A; 245 C; 250 G; 283 T; 0 U; 0 Other;

```
  Query Match             99.8%;  Score 985;  DB 6;  Length 985;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146
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Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGCA 1
```

RESULT 6
ABK98961
ID ABK98961 standard; cDNA; 985 BP.
XX
AC ABK98961;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p40-N985 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69311.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Example 3; Page 73-74; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 985 BP; 283 A; 250 C; 245 G; 207 T; 0 U; 0 Other;

Query Match 99.8%; Score 985; DB 6; Length 985;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 985; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985
```

RESULT 7
ADV34707
ID ADV34707 standard; cDNA; 985 BP.
XX
AC ADV34707;
XX

```
DT   24-FEB-2005  (first entry)
XX
DE   Feline N-terminal IL-12p40 protein encoding cDNA, nFeIL-12p40-N985.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .984
FT                   /*tag=  a
FT                   /product= "PCaIL-12P40-N328 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34708.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 55; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline N-terminal single chain IL-12p40 protein
CC   encoding cDNA.
XX
SQ   Sequence 985 BP; 283 A; 250 C; 245 G; 207 T; 0 U; 0 Other;

  Query Match             99.8%;  Score 985;  DB 14;  Length 985;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 8
ADV34709/c
ID   ADV34709 standard; DNA; 985 BP.
XX
AC   ADV34709;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline N-terminal IL-12p40 protein complementary DNA, nFeIL-12p40-N985.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
```

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XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 57; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline N-terminal single chain IL-12p40
CC   complementary DNA.
XX
SQ   Sequence 985 BP; 207 A; 245 C; 250 G; 283 T; 0 U; 0 Other;

  Query Match             99.8%;  Score 985;  DB 14;  Length 985;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGCA 1


RESULT 9
AAV56625
ID   AAV56625 standard; cDNA; 2193 BP.
XX
AC   AAV56625;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp40 cDNA.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             64. .1053
FT                   /*tag=  a
FT   sig_peptide     64. .129
FT                   /*tag=  b
FT   mat_peptide     130. .1050
FT                   /*tag=  c
FT                   /product= "FLAFp40"
FT                   /note= "feline cytokine"
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP001824.
XX
PR   04-JUN-1996;   96JP-00165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76173.
XX
PT   Novel féline cytokine protein - useful for treating feline auto:immune
PT   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS   Claim 19; Page 52-54; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine protein, FLAFp40. This
CC   protein can be used in the production of a FLAFp35/FLAFp40 heterodimer
CC   which can potentiate the cytotoxic activity of feline cytotoxic T
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CC   lymphocyte cells. Such proteins are used for treatment of feline
CC   autoimmune diseases e.g. as caused by feline herpes virus or feline
CC   calcivirus
XX
SQ   Sequence 2193 BP; 680 A; 451 C; 493 G; 569 T; 0 U; 0 Other;

  Query Match             94.2%;  Score 930;  DB 2;  Length 2193;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  930;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         58 CTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCT 117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCT 180

Qy        118 GATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACC 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACC 240

Qy        178 TGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTC 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTC 300

Qy        238 AAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCAT 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCAT 360

Qy        298 TCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAA 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAA 420

Qy        358 CAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGT 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGT 480

Qy        418 TTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGC 477
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGC 540

Qy        478 AGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAG 537
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAG 600

Qy        538 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 597
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 660

Qy        598 TGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTC 657
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTC 720

Qy        658 AAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCC 717
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCC 780

Qy        718 AAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATAC 777
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATAC 840

Qy        778 CCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAG 837
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAG 900

Qy        838 GGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTC 897
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTC 960

Qy        898 GTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCC 957
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCC 1020

Qy        958 TGGAGCAACTGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||||||||||
Db       1021 TGGAGCAACTGGGCATCCGTGTCCTGCAGT 1050
```

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RESULT 10
AAV56626
ID   AAV56626 standard; cDNA; 921 BP.
XX
AC   AAV56626;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp40 cDNA mature transcript #1.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP001824.
XX
PR   04-JUN-1996;   96JP-00165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76174.
XX
PT   Novel feline cytokine protein - useful for treating feline auto:immune
PT   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS   Claim 20; Page 55; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine mature protein, FLAFp40.
CC   This protein can be used in the production of a FLAFp35/FLAFp40
CC   heterodimer which can potentiate the cytotoxic activity of feline
CC   cytotoxic T lymphocyte cells. Such proteins are used for treatment of
CC   feline autoimmune diseases e.g. as caused by feline herpes virus or
CC   feline calcivirus
XX
SQ   Sequence 921 BP; 276 A; 227 C; 231 G; 187 T; 0 U; 0 Other;

  Query Match             93.3%;  Score 921;  DB 2;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360
```

```
Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921
```

RESULT 11
ABK98950
ID ABK98950 standard; cDNA; 1599 BP.
XX
AC ABK98950;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12-1599 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69306.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 58-60; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

```
  Query Match             91.7%;  Score 905;  DB 6;  Length 1599;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  955;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91

Qy         92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151

Qy        152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211

Qy        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271

Qy        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331

Qy        332 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 391

Qy        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451

Qy        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTG 511
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTG 511

Qy        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571

Qy        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631

Qy        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691

Qy        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751

Qy        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811

Qy        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 871
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 871

Qy        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931

Qy        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987
```

RESULT 12
ABK98951/c
ID ABK98951 standard; cDNA; 1599 BP.
XX
AC ABK98951;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12-1599 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 61-62; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

Query Match 91.7%; Score 905; DB 6; Length 1599;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 955; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy         32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1568 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 1509

Qy         92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1508 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 1449

Qy        152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1448 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 1389

Qy        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1388 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 1329

Qy        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1328 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 1269

Qy        332 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1268 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 1209

Qy        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1208 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 1149

Qy        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTG 511
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db       1148 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTG 1089

Qy        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1088 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 1029

Qy        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1028 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 969

Qy        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        968 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 909

Qy        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        908 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 849

Qy        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 789

Qy        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 871
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        788 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 729

Qy        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 669

Qy        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 613
```

RESULT 13
ADV34691
ID ADV34691 standard; cDNA; 1599 BP.
XX
AC ADV34691;

```
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1599
FT                   /*tag=  a
FT                   /product= "PFeIL-12p533 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34692.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 38; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

  Query Match             91.7%;  Score 905;  DB 14;  Length 1599;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  955;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91

Qy         92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151

Qy        152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211

Qy        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271

Qy        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331

Qy        332 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 391

Qy        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451

Qy        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTG 511
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTG 511

Qy        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571

Qy        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631

Qy        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691

Qy        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751

Qy        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811

Qy        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 871
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 871

Qy        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931

Qy        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987


RESULT 14
ADV34693/c
ID   ADV34693 standard; DNA; 1599 BP.
XX
AC   ADV34693;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 complementary DNA, nFeIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
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```
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 40; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 complementary DNA.
XX
SQ   Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

  Query Match            91.7%;  Score 905;  DB 14;  Length 1599;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches  955;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1568 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 1509

Qy         92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1508 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 1449

Qy        152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1448 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 1389

Qy        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1388 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 1329

Qy        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1328 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 1269

Qy        332 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1268 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 1209

Qy        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1208 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 1149

Qy        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTG 511
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       1148 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTG 1089

Qy        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1088 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 1029

Qy        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1028 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 969

Qy        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        968 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 909

Qy        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        908 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 849

Qy        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 789

Qy        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 871
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        788 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 729

Qy        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 669

Qy        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 613


RESULT 15
AAF26082
ID   AAF26082 standard; DNA; 990 BP.
XX
AC   AAF26082;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p40 encoding DNA SEQ ID 8.
XX
KW   Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW   interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS   Felis sp.
XX
PN   WO200104280-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002262.
XX
PR   08-JUL-1999;   99CH-00001258.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
XX
PI   Leutenegger C,  Schroff M,  Wittig B,  Lutz H;
XX
DR   WPI; 2001-147190/15.
XX
PT   Vaccine for treating or preventing lentivirus infection in cats, contains
PT   nucleic acid sequence encoding viral protein under control of eukaryotic
PT   promoter.
XX
PS   Claim 14; Page 36; 37pp; German.
XX
CC   This invention describes a novel vaccine (A) for prevention or treatment
CC   of lentivirus infection in felines which comprises an immunizing nucleic
CC   acid sequence (I) that contains, or comprises, at least part of a gene
CC   encoding a protein (II) of the virus, under control of a eukaryotic
CC   promoter functional in the relevant animal. (II) is especially the
CC   envelope (env) protein. The invention also describes (1) vaccine (A)
CC   containing an immunizing protein, or fragment, from a lentivirus plus at
CC   least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC   lentivirus protein, or fragment, especially derived from feline immune
CC   deficiency virus (FIV), by expressing the corresponding nucleic acid
CC   sequence in a host cell. The products of the invention have antiviral
CC   activity. The vaccine (A) and related protein-based vaccines, are
CC   particularly used to treat or prevent lentivirus infections in domestic
CC   cats, especially feline immune deficiency virus (FIV). Vaccination with
CC   (A) allows differentiation between vaccinated and infected animals, from
CC   the antibody status. The vaccines may be formulated with an adjuvant
CC   (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC   immune response, particularly a Th1 response
XX
SQ   Sequence 990 BP; 283 A; 249 C; 248 G; 210 T; 0 U; 0 Other;
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  Query Match           89.7%;  Score 885;  DB 4;  Length 990;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
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RESULT 16
AAF26085
ID   AAF26085 standard; DNA; 990 BP.
XX
AC   AAF26085;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p40 encoding DNA.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS   Felis sp.
XX
PN   WO200104155-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002263.
XX
PR   08-JUL-1999;   99CH-00001259.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Lutz H,  Leutenegger C,  Pedersen N,  Schroff M,  Wittig B;
XX
DR   WPI; 2001-147178/15.
XX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs.
XX
PS   Claim 3; Page 30; 35pp; German.
XX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
CC   following: (i) as immunostimulant, for preventative or therapeutic use;
CC   and (ii) treating tumors and autoimmune diseases, or diseases associated
CC   with a Th1 defect, especially pre-existing infections by feline immune
CC   deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ   Sequence 990 BP; 283 A; 249 C; 248 G; 210 T; 0 U; 0 Other;
```

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  Query Match           89.7%;  Score 885;  DB 4;  Length 990;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987


RESULT 17
AAF26076
ID   AAF26076 standard; DNA; 4522 BP.
XX
AC   AAF26076;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p40 encoding DNA SEQ ID 2.
XX
KW   Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW   interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS   Felis sp.
XX
PN   WO200104280-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE002262.
XX
PR   08-JUL-1999;   99CH-00001258.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
XX
PI   Leutenegger C,  Schroff M,  Wittig B,  Lutz H;
XX
DR   WPI; 2001-147190/15.
XX
PT   Vaccine for treating or preventing lentivirus infection in cats, contains
PT   nucleic acid sequence encoding viral protein under control of eukaryotic
PT   promoter.
XX
PS   Disclosure; Page 29-31; 37pp; German.
XX
CC   This invention describes a novel vaccine (A) for prevention or treatment
CC   of lentivirus infection in felines which comprises an immunizing nucleic
CC   acid sequence (I) that contains, or comprises, at least part of a gene
CC   encoding a protein (II) of the virus, under control of a eukaryotic
CC   promoter functional in the relevant animal. (II) is especially the
CC   envelope (env) protein. The invention also describes (1) vaccine (A)
CC   containing an immunizing protein, or fragment, from a lentivirus plus at
CC   least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC   lentivirus protein, or fragment, especially derived from feline immune
CC   deficiency virus (FIV), by expressing the corresponding nucleic acid
CC   sequence in a host cell. The products of the invention have antiviral
CC   activity. The vaccine (A) and related protein-based vaccines, are
CC   particularly used to treat or prevent lentivirus infections in domestic
CC   cats, especially feline immune deficiency virus (FIV). Vaccination with
CC   (A) allows differentiation between vaccinated and infected animals, from
CC   the antibody status. The vaccines may be formulated with an adjuvant
CC   (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC   immune response, particularly a Th1 response
XX
SQ   Sequence 4522 BP; 1180 A; 1126 C; 1106 G; 1110 T; 0 U; 0 Other;

  Query Match            89.7%;  Score 885;  DB 4;  Length 4522;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406
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Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db       3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||
Db       4007 AGCAACTGGGCATCCGTGTCCTGCAGT 4033
```

RESULT 18
AAF26094
ID AAF26094 standard; DNA; 4522 BP.
XX
AC AAF26094;
XX
DT 24-APR-2001 (first entry)
XX
DE Plasmid pMol-fil12p40 DNA SEQ ID 10.
XX
KW Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS Synthetic.
XX
PN WO200104155-A2.
XX
PD 18-JAN-2001.
XX
PF 08-JUL-2000; 2000WO-DE002263.
XX
PR 08-JUL-1999; 99CH-00001259.
XX
PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA (UYZU-) UNIV ZUERICH.
PA (REGC) UNIV CALIFORNIA.
XX
PI Lutz H, Leutenegger C, Pedersen N, Schroff M, Wittig B;
XX
DR WPI; 2001-147178/15.
XX
PT Recombinant feline interleukin-12, useful as immunostimulant and for
PT treating e.g. viral infections in cats, and related nucleic acid
PT constructs.
XX
PS Example 1c; Page 33-35; 35pp; German.
XX
CC This invention describes a novel feline interleukin-12 (fIL-12)
CC polypeptide (I) that is expressed, by recombinant gene expression in
CC eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC of subunits p35 and p40. These proteins are formed so that, in equimolar
CC concentrations and in presence of an immunizing antigen, they can be
CC administered to carnivores, particularly domestic cats. The invention
CC also describes a nucleic acid construct (II) encoding fIL-12 containing
CC sequences at least 95% identical with the p40- and p35-encoding sequences
CC (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC as immunostimulants for immunization against infectious diseases and/or
CC for treating infections or tumors in felines, especially domestic cats.
CC The products of the invention have immunostimulatory, antiviral and
CC antitumor activity. Nucleic acid constructs that encode (II) are useful
CC as adjuvants for prophylactic immunization against viral diseases and for
CC treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC is useful for carnivores, and particularly domestic cats in the
CC following: (i) as immunostimulant, for preventative or therapeutic use;
CC and (ii) treating tumors and autoimmune diseases, or diseases associated
CC with a Th1 defect, especially pre-existing infections by feline immune
CC deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ Sequence 4522 BP; 1180 A; 1126 C; 1106 G; 1110 T; 0 U; 0 Other;

```
  Query Match             89.7%;  Score 885;  DB 4;  Length 4522;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db       3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||
Db       4007 AGCAACTGGGCATCCGTGTCCTGCAGT 4033
```

RESULT 19
AAV56627
ID AAV56627 standard; cDNA; 921 BP.
XX
AC AAV56627;
XX
DT 23-NOV-1998 (first entry)
XX
DE Feline FLAFp40 cDNA mature transcript #2.
XX
KW Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW T lymphocyte cell; autoimmune disease; ds.
XX
OS Felis catus.
XX
PN WO9746583-A1.
XX
PD 11-DEC-1997.
XX
PF 29-MAY-1997; 97WO-JP001824.
XX
PR 04-JUN-1996; 96JP-00165249.
XX
PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI Imamura T, Maeda H, Fujiyasu T, Imagawa Y, Tokiyoshi S;
XX
DR WPI; 1998-042118/04.
DR P-PSDB; AAW76174.
XX
PT Novel feline cytokine protein - useful for treating feline auto:immune
PT diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS Claim 21; Page 56-57; 94pp; Japanese.
XX
CC This sequence encodes a novel feline cytokine mature protein, FLAFp40.
CC This protein can be used in the production of a FLAFp35/FLAFp40
CC heterodimer which can potentiate the cytotoxic activity of feline
CC cytotoxic T lymphocyte cells. Such proteins are used for treatment of
CC feline autoimmune diseases e.g. as caused by feline herpes virus or
CC feline calcivirus
XX
SQ Sequence 921 BP; 276 A; 228 C; 230 G; 187 T; 0 U; 0 Other;

```
  Query Match             88.1%;  Score 870;  DB 2;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921
```

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RESULT 20
ABK98942
ID   ABK98942 standard; cDNA; 921 BP.
XX
AC   ABK98942;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p40-921 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69302.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 49-50; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 921 BP; 277 A; 227 C; 230 G; 187 T; 0 U; 0 Other;

  Query Match             88.1%;  Score 870;  DB 6;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy         367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy         427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy         487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
               |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db         421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy         547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy         607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy         667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy         727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy         787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy         847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy         907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy         967 TGGGCATCCGTGTCCTGCAGT 987
               |||||||||||||||||||||
Db         901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 21
ABK98943/c
ID   ABK98943 standard; cDNA; 921 BP.
XX
AC   ABK98943;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p40-921 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
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XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Disclosure; Page 51; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 921 BP; 187 A; 230 C; 227 G; 277 T; 0 U; 0 Other;

  Query Match            88.1%;  Score 870;  DB 6;  Length 921;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCAGT 1


RESULT 22
ADV34681/c
ID   ADV34681 standard; DNA; 921 BP.
XX
AC   ADV34681;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain mature IL-12p40 complementary DNA, nFeIL-12p40 921.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 28; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain mature IL-12p40 subunit
CC   complementary DNA.
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XX
SQ   Sequence 921 BP; 187 A; 230 C; 227 G; 277 T; 0 U; 0 Other;

  Query Match           88.1%;  Score 870;  DB 14;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCAGT 1

RESULT 23
ADV34679
ID   ADV34679 standard; cDNA; 921 BP.
XX
AC   ADV34679;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain mature IL-12p40 protein cDNA, nFeIL-12p40 921.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .921
FT                   /*tag= a
FT                   /product= "PFeIL-12p40 307 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34680.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 23; SEQ ID NO 26; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain mature IL-12p40 subunit
CC   protein encoding cDNA.
XX
SQ   Sequence 921 BP; 277 A; 227 C; 230 G; 187 T; 0 U; 0 Other;

  Query Match           88.1%;  Score 870;  DB 14;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 24
ABK98954/c
ID   ABK98954 standard; cDNA; 1533 BP.
XX
AC   ABK98954;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1533 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 66-67; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

  Query Match             88.1%;  Score 870;  DB 6;  Length 1533;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613


RESULT 25
ABK98953
ID   ABK98953 standard; cDNA; 1533 BP.
XX
AC   ABK98953;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1533 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69307.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 63-64; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

  Query Match             88.1%;  Score 870;  DB 6;  Length 1533;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
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                    ||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 26
ADV34697/c
ID   ADV34697 standard; DNA; 1533 BP.
XX
AC   ADV34697;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 complementary DNA, nFeIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 45; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12 complementary DNA.
XX
SQ   Sequence 1533 BP; 337 A; 365 C; 378 G; 453 T; 0 U; 0 Other;

  Query Match             88.1%;  Score 870;  DB 14;  Length 1533;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy         367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy         427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy         487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
               ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy         547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy         607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy         667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy         727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy         787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy         847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy         907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy         967 TGGGCATCCGTGTCCTGCAGT 987
               ||||||||||||||||||||
Db         633 TGGGCATCCGTGTCCTGCAGT 613


RESULT 27
ADV34695
ID   ADV34695 standard; cDNA; 1533 BP.
XX
AC   ADV34695;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12 protein encoding cDNA, nFeIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1533
FT                   /*tag=  a
FT                   /product= "PFeIL-12 511 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
```

PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
DR P-PSDB; ADV34696.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Claim 24; SEQ ID NO 43; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the feline single chain IL-12 protein encoding cDNA.
XX
SQ Sequence 1533 BP; 453 A; 378 C; 365 G; 337 T; 0 U; 0 Other;

Query Match 88.1%; Score 870; DB 14; Length 1533;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 920; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921
```

RESULT 28
AAD15209
ID AAD15209 standard; DNA; 990 BP.
XX
AC AAD15209;
XX
DT 01-NOV-2001 (first entry)
XX
DE Modified human cytokine p40 encoding DNA from clone R16-51.
XX
KW Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW p40; mutant; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX

FH	Key	Location/Qualifiers
FT	CDS	1. .990
FT		/*tag= a
FT		/product= "Modified p40 protein precursor"
FT	sig_peptide	1. .66
FT		/*tag= b
FT	mat_peptide	67. .987
FT		/*tag= c
FT		/product= "Mature modified p40 protein"

XX
PN WO200140257-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000WO-US032664.
XX
PR 02-DEC-1999; 99US-0169035P.
PR 28-NOV-2000; 2000US-00725324.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Leong SR, Punnonen J;
XX
DR WPI; 2001-502381/55.
DR P-PSDB; AAE08602.
XX
PT Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT retinopathy and cancer.
XX
PS Claim 1; Page 137-138; 223pp; English.

```
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p40 protein encoding
CC   DNA
XX
SQ   Sequence 990 BP; 270 A; 250 C; 254 G; 216 T; 0 U; 0 Other;

  Query Match             8.4%;  Score 83;  DB 5;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-31;
  Matches   83;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        865 AGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGC 924
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 AGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGC 924

Qy        925 GTGCAAGCCAGAGACCGCTACTA 947
              |||||||||||||||||||||||
Db        925 GTGCAAGCCAGAGACCGCTACTA 947


RESULT 29
ABK98959
ID   ABK98959 standard; cDNA; 921 BP.
XX
AC   ABK98959;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p40-921 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69310.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 71; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 921 BP; 272 A; 221 C; 234 G; 194 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 6;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy        597 CTGCCC 602
              ||||||
Db        531 CTGCCC 536


RESULT 30
ABK98960/c
ID   ABK98960 standard; cDNA; 921 BP.
XX
AC   ABK98960;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p40-921 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Disclosure; Page 73; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 921 BP; 194 A; 234 C; 221 G; 272 T; 0 U; 0 Other;
```

```
  Query Match             6.7%;  Score 66;  DB 6;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy        597 CTGCCC 602
              ||||||
Db        391 CTGCCC 386


RESULT 31
ADV34706/c
ID   ADV34706 standard; DNA; 921 BP.
XX
AC   ADV34706;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain mature IL-12p40 complementary DNA, nCaIL-12p40 921.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Disclosure; SEQ ID NO 54; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p40 subunit reverse
CC   complementary DNA.
XX
SQ   Sequence 921 BP; 194 A; 234 C; 221 G; 272 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 14;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy        597 CTGCCC 602
              ||||||
Db        391 CTGCCC 386


RESULT 32
ADV34704
ID   ADV34704 standard; cDNA; 921 BP.
XX
AC   ADV34704;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain mature IL-12p40 protein cDNA, nCaIL-12p40 921.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .921
FT                   /*tag=  a
FT                   /product= "PCaIL-12P40 307 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34705.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 52; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p40 subunit protein
CC   encoding cDNA.
XX
SQ   Sequence 921 BP; 272 A; 221 C; 234 G; 194 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 14;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy        597 CTGCCC 602
              ||||||
Db        531 CTGCCC 536


RESULT 33
AAX18177
```

```
ID   AAX18177 standard; cDNA; 924 BP.
XX
AC   AAX18177;
XX
DT   07-MAY-1999  (first entry)
XX
DE   Canine mature CLAF p40 subunit coding sequence.
XX
KW   CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW   viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW   canine infectious hepatitis; ds.
XX
OS   Canis sp.
XX
PN   WO9855511-A1.
XX
PD   10-DEC-1998.
XX
PF   26-MAY-1998;   98WO-JP002295.
XX
PR   03-JUN-1997;   97JP-00161936.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Tokiyoshi S,  Eda Y;
XX
DR   WPI; 1999-070260/06.
DR   P-PSDB; AAW74323.
XX
PT   Canine cytokine protein which activates canine cytotoxic T lymphocytes -
PT   is useful for treatment of viral and autoimmune diseases in dogs.
XX
PS   Claim 8; Page 32; 51pp; Japanese.
XX
CC   This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC   the invention. CLAF activates lymphocytes, especially canine cytotoxic T
CC   cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC   recognising it may be used in the treatment of viral diseases in dogs
CC   (such as canine distemper, canine parvovirus and canine infectious
CC   hepatitis). The antibodies may also be used in isolation of CLAF from
CC   culture of the transformant host cells by affinity chromatography. The
CC   p40 homodimer can be used for the treatment of autoimmune diseases in
CC   dogs
XX
SQ   Sequence 924 BP; 273 A; 222 C; 234 G; 195 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 2;  Length 924;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 533

Qy        597 CTGCCC 602
              ||||||
Db        534 CTGCCC 539


RESULT 34
ABK98963
ID   ABK98963 standard; cDNA; 987 BP.
XX
AC   ABK98963;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p40-987 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69312.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 76-77; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 987 BP; 279 A; 244 C; 248 G; 216 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 6;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 35
ABK98964/c
ID   ABK98964 standard; cDNA; 987 BP.
XX
AC   ABK98964;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12p40-987 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
```

PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Example 4; Page 78; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 987 BP; 216 A; 248 C; 244 G; 279 T; 0 U; 0 Other;

Query Match 6.7%; Score 66; DB 6; Length 987;
Best Local Similarity 100.0%; Pred. No. 2.4e-22;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy 597 CTGCCC 602
||||||
Db 391 CTGCCC 386

RESULT 36
ADV34712/c
ID ADV34712 standard; DNA; 987 BP.
XX
AC ADV34712;
XX
DT 24-FEB-2005 (first entry)
XX
DE Canine single chain IL-12p40 complementary DNA, nCaIL-12p40 987.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; ds.
XX
OS Canis familiaris.
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
XX
PT New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT p40 subunit protein and a nucleic acid linker, useful in preparing a
PT vaccine against infectious diseases in feline animals.
XX
PS Example 4; SEQ ID NO 60; 103pp; English.
XX
CC The present invention relates to the feline interleukin (IL)-12p35 or p40
CC subunit protein and their encoding nucleic acid molecules and a nucleic
CC acid linker. The invention also provides the feline caspase (casp)-1,
CC feline IL-18 single chain and canine IL-12 single chain proteins and
CC their nucleic acid molecules. The nucleic acid molecule is useful in
CC preparing a vaccine against infectious diseases in feline animals. The
CC present sequence is the canine single chain IL-12p40 subunit full-length
CC complementary DNA.
XX
SQ Sequence 987 BP; 216 A; 248 C; 244 G; 279 T; 0 U; 0 Other;

Query Match 6.7%; Score 66; DB 14; Length 987;
Best Local Similarity 100.0%; Pred. No. 2.4e-22;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy 597 CTGCCC 602
||||||
Db 391 CTGCCC 386

RESULT 37
ADV34710
ID ADV34710 standard; cDNA; 987 BP.
XX
AC ADV34710;
XX
DT 24-FEB-2005 (first entry)
XX
DE Canine single chain IL-12p40 full-length cDNA, nCaIL-12p40 987.
XX
KW DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW infectious disease; antimicrobial; gene; ss.
XX
OS Canis familiaris.
XX
FH Key Location/Qualifiers
FT CDS 1. .987
FT /*tag= a
FT /product= "PCaIL-12P40-329 protein"
FT /partial
FT /note= "No stop codon"
XX
PN US2004248261-A1.
XX
PD 09-DEC-2004.
XX
PF 09-APR-2004; 2004US-00821670.
XX
PR 04-AUG-2000; 2000US-0223016P.
PR 27-JUL-2001; 2001US-00917265.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2005-020565/02.
DR P-PSDB; ADV34711.
XX

```
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 58; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p40 subunit protein
CC   encoding full-length cDNA.
XX
SQ   Sequence 987 BP; 279 A; 244 C; 248 G; 216 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 14;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 38
AAV13816
ID   AAV13816 standard; cDNA to mRNA; 990 BP.
XX
AC   AAV13816;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P40 subunit cDNA.
XX
KW   Canine; interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour;
KW   antiviral; vaccine adjuvant; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
FT                   /product= "interleukin-12_P40_subunit"
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-00296789.
XX
PR   08-NOV-1995;   95JP-00289729.
PR   23-MAY-1996;   96JP-00128104.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   P-PSDB; AAW41790.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected.
XX
PS   Claim 8; Page 8; 12pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin-12 (IL-12) P40 subunit.
CC   A canine IL-12 comprising a P40 and P35 subunit is capable of inducing an
CC   antiviral activating factor and the expression of class II MHC molecules
CC   in canine tumour cells, stimulating proliferation of canine blastogenic
CC   lymphocytes and activating canine leukocytes to inhibit canine tumour
CC   cells. The canine IL-12 can be used in veterinary medicines, e.g.
CC   antitumour, antivirus and vaccine adjuvant activities are expected
XX
SQ   Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 39
AAV13817
ID   AAV13817 standard; cDNA to mRNA; 990 BP.
XX
AC   AAV13817;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P40 subunit cDNA.
XX
KW   Canine; interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour;
KW   antiviral; vaccine adjuvant; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
FT                   /product= "interleukin-12_P40_subunit"
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-00296789.
XX
PR   08-NOV-1995;   95JP-00289729.
PR   23-MAY-1996;   96JP-00128104.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   P-PSDB; AAW41791.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected.
XX
PS   Claim 10; Page 10-11; 12pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin-12 (IL-12) P40 subunit.
CC   A canine IL-12 comprising a P40 and P35 subunit is capable of inducing an
CC   antiviral activating factor and the expression of class II MHC molecules
CC   in canine tumour cells, stimulating proliferation of canine blastogenic
CC   lymphocytes and activating canine leukocytes to inhibit canine tumour
CC   cells. The canine IL-12 can be used in veterinary medicines, e.g.
CC   antitumour, antivirus and vaccine adjuvant activities are expected
XX
SQ   Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 40
AAX03162
ID   AAX03162 standard; cDNA to mRNA; 990 BP.
XX
AC   AAX03162;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Nucleic acid encoding canine interleukin 12.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
FT                   /product= "interleukin_12"
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP002031.
XX
PR   16-MAY-1997;   97JP-00127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   P-PSDB; AAW84373.
XX
PT   New therapeutic and prophylactic agents - comprise genetically-engineered
PT   canine interleukin 12, used to treat, e.g. canine and feline
PT   immunological diseases.
XX
PS   Claim 1; Page 30-32; 45pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin 12 (IL-12) protein. The
CC   IL-12 protein can be used in therapeutic or prophylactic agents. The
CC   agents can be used to prevent and treat canine and feline immunological
CC   diseases including dog and cat tumours, skin diseases, viral infections
CC   and allergic diseases, especially tumours, breast tumour, oesinophilic
CC   granuloma, epidermoid tumour, skin tumour, lipoma, othematoma,
CC   pneumonoedema, skin soft pedicled soft tumour and anal tumour; skin
CC   diseases, otitis externa, dermatitis, eczema, fungal diseases of the
CC   skin, pyoderma, allergic dermatitis, nettle rash, traumatic dermatitis
CC   and hair loss; infections; dog Parvovirus infection and distemper virus,
CC   cat plaque virus infection and feline leukaemia, and allergic diseases,
CC   e.g. pollinosis
XX
SQ   Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 41
AAX03152
ID   AAX03152 standard; cDNA to mRNA; 990 BP.
XX
AC   AAX03152;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Nucleic acid encoding canine interleukin 12.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
FT                   /product= "interleukin_12"
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP002031.
XX
PR   16-MAY-1997;   97JP-00127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   P-PSDB; AAW84371.
XX
PT   New therapeutic and prophylactic agents - comprise genetically-engineered
PT   canine interleukin 12, used to treat, e.g. canine and feline
PT   immunological diseases.
XX
PS   Claim 1; Page 23-25; 45pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin 12 (IL-12) protein. The
CC   IL-12 protein can be used in therapeutic or prophylactic agents. The
CC   agents can be used to prevent and treat canine and feline immunological
CC   diseases including dog and cat tumours, skin diseases, viral infections
CC   and allergic diseases, especially tumours, breast tumour, oesinophilic
CC   granuloma, epidermoid tumour, skin tumour, lipoma, othematoma,
CC   pneumonoedema, skin soft pedicled soft tumour and anal tumour; skin
CC   diseases, otitis externa, dermatitis, eczema, fungal diseases of the
CC   skin, pyoderma, allergic dermatitis, nettle rash, traumatic dermatitis
CC   and hair loss; infections; dog Parvovirus infection and distemper virus,
CC   cat plaque virus infection and feline leukaemia, and allergic diseases,
CC   e.g. pollinosis
XX
SQ   Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 U; 0 Other;
```

```
  Query Match             6.7%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 42
AAX35625
ID   AAX35625 standard; cDNA to mRNA; 990 BP.
XX
AC   AAX35625;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-00133345.
XX
PR   16-MAY-1997;   97JP-00127690.
PR   07-AUG-1997;   97JP-00213755.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   P-PSDB; AAY02342.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) - for
PT   prevention and treatment of dog and cat immune diseases.
XX
PS   Claim 1; Page 14-15; 16pp; Japanese.
XX
CC   The present sequence encodes canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment of dog
CC   and cat immune diseases. The treatment used an agent comprising dog IL-12
CC   (CaIL12) proteins to form a heterodimer. The agent is useful for
CC   preventing and treating dog and cat immune diseases, including tumours,
CC   skin diseases, infectious diseases and allergic diseases
XX
SQ   Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 43
AAX35615
ID   AAX35615 standard; cDNA to mRNA; 990 BP.
XX
AC   AAX35615;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-00133345.
XX
PR   16-MAY-1997;   97JP-00127690.
PR   07-AUG-1997;   97JP-00213755.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   P-PSDB; AAY02339.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) - for
PT   prevention and treatment of dog and cat immune diseases.
XX
PS   Claim 1; Page 12; 16pp; Japanese.
XX
CC   The present sequence encodes canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment of dog
CC   and cat immune diseases. The treatment used an agent comprising dog IL-12
CC   (CaIL12) proteins to form a heterodimer. The agent is useful for
CC   preventing and treating dog and cat immune diseases, including tumours,
CC   skin diseases, infectious diseases and allergic diseases
XX
SQ   Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 2;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 44
AAI64378
ID   AAI64378 standard; DNA; 990 BP.
XX
AC   AAI64378;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine coding sequence #1.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
```

```
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
FT                   /product= "Canine protein #1"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .987
FT                   /*tag=  c
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-00292946.
XX
PR   01-OCT-1999;   99JP-00281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   P-PSDB; AAG66480.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian.
XX
PS   Claim 6; Page 14; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention
XX
SQ   Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 4;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 45
AAI64388
ID   AAI64388 standard; DNA; 990 BP.
XX
AC   AAI64388;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine coding sequence #3.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  a
FT                   /product= "Canine protein #1"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .987
FT                   /*tag=  c
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-00292946.
XX
PR   01-OCT-1999;   99JP-00281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   P-PSDB; AAG66482.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian.
XX
PS   Claim 6; Page 16-17; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention
XX
SQ   Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 4;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 46
ADZ25698
ID   ADZ25698 standard; cDNA; 990 BP.
XX
AC   ADZ25698;
XX
DT   16-JUN-2005  (first entry)
XX
DE   Canine interleukin 12 P40 encoding cDNA SEQ ID NO:3.
XX
KW   interleukin-12; antiviral; gene; ss.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .990
FT                   /*tag=  b
FT                   /product= "interleukin-12 P40"
FT   sig_peptide     1. .66
FT                   /*tag=  a
FT   mat_peptide     67. .987
FT                   /*tag=  c
FT                   /product= "interleukin-12 P40"
XX
PN   JP2003284585-A.
XX
PD   07-OCT-2003.
XX
PF   28-MAR-2002; 2002JP-00090161.
XX
```

PR 28-MAR-2002; 2002JP-00090161.
XX
PA (TORA) TORAY IND INC.
XX
DR WPI; 2003-885430/82.
DR P-PSDB; ADZ25702.
XX
PT Large scale production of interleukin-12 for pharmaceutical applications,
PT comprises infecting an insect cell with a recombinant virus containing
PT gene encoding IL-12, and producing IL-12 by carrying out spinner culture
PT of insect cell.
XX
PS Example; SEQ ID NO 3; 8pp; Japanese.
XX
CC The invention related to the large scale production of interleukin-12 (IL
CC -12), which involves infecting an insect cell with a recombinant virus
CC containing a gene encoding IL-12, and producing IL-12 by carrying out
CC spinner culture of insect cell. The method is useful for producing IL-12,
CC preferably canine IL-12. IL-12 has pharmaceutical applications. The
CC present sequence encodes canine IL-12 P40, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 U; 0 Other;

Query Match 6.7%; Score 66; DB 11; Length 990;
Best Local Similarity 100.0%; Pred. No. 2.4e-22;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy 597 CTGCCC 602
||||||
Db 597 CTGCCC 602

RESULT 47
ABK98967
ID ABK98967 standard; cDNA; 1533 BP.
XX
AC ABK98967;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12-1533 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69314.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 83-85; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 1533 BP; 446 A; 368 C; 369 G; 350 T; 0 U; 0 Other;

Query Match 6.7%; Score 66; DB 6; Length 1533;
Best Local Similarity 100.0%; Pred. No. 2.4e-22;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy 597 CTGCCC 602
||||||
Db 531 CTGCCC 536

RESULT 48
ABK98968/c
ID ABK98968 standard; cDNA; 1533 BP.
XX
AC ABK98968;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12-1533 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Claim 6; Page 86-87; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a

```
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 6;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy        597 CTGCCC 602
              ||||||
Db       1003 CTGCCC 998


RESULT 49
ADV34718/c
ID   ADV34718 standard; DNA; 1533 BP.
XX
AC   ADV34718;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12 complementary DNA, nCaIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 68; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 complementary DNA.
XX
SQ   Sequence 1533 BP; 350 A; 369 C; 368 G; 446 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 14;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy        597 CTGCCC 602
              ||||||
Db       1003 CTGCCC 998


RESULT 50
ADV34716
ID   ADV34716 standard; cDNA; 1533 BP.
XX
AC   ADV34716;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12 protein cDNA, nCaIL-12 1533.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1533
FT                   /*tag=  a
FT                   /product= "PCaIL-12 511 protein"
FT                   /partial
FT                   /note= "No start and stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34717.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 66; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1533 BP; 446 A; 368 C; 369 G; 350 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 14;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530
```

```
Qy        597 CTGCCC 602
              ||||||
Db        531 CTGCCC 536


RESULT 51
ABK98965
ID   ABK98965 standard; cDNA; 1599 BP.
XX
AC   ABK98965;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1599 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69313.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 79-80; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 452 A; 392 C; 383 G; 372 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 6;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 52
ABK98966/c
ID   ABK98966 standard; cDNA; 1599 BP.
XX
AC   ABK98966;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Canine interleukin-12 nCaIL-12-1599 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Canis familiaris.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 82-83; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 372 A; 383 C; 392 G; 452 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 6;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy        597 CTGCCC 602
              ||||||
Db       1003 CTGCCC 998


RESULT 53
ADV34715/c
ID   ADV34715 standard; DNA; 1599 BP.
XX
AC   ADV34715;
XX
DT   24-FEB-2005  (first entry)
```

```
XX
DE   Canine single chain IL-12 complementary DNA, nCaIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 63; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 complementary DNA.
XX
SQ   Sequence 1599 BP; 372 A; 383 C; 392 G; 452 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 14;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy        597 CTGCCC 602
              ||||||
Db       1003 CTGCCC 998


RESULT 54
ADV34713
ID   ADV34713 standard; cDNA; 1599 BP.
XX
AC   ADV34713;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12 protein cDNA, nCaIL-12 1599.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1599
FT                   /*tag=  a
FT                   /product= "PCaIL-12 533 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34714.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 61; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12 protein encoding cDNA.
XX
SQ   Sequence 1599 BP; 452 A; 392 C; 383 G; 372 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 14;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 55
AAX18176
ID   AAX18176 standard; cDNA; 2154 BP.
XX
AC   AAX18176;
XX
DT   07-MAY-1999  (first entry)
XX
DE   Canine full length CLAF p40 subunit coding sequence.
XX
KW   CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW   viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW   canine infectious hepatitis; ds.
XX
OS   Canis sp.
XX
PN   WO9855511-A1.
XX
PD   10-DEC-1998.
XX
PF   26-MAY-1998;   98WO-JP002295.
XX
PR   03-JUN-1997;   97JP-00161936.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
```

XX
PI Imamura T, Maeda H, Tokiyoshi S, Eda Y;
XX
DR WPI; 1999-070260/06.
DR P-PSDB; AAW74322.
XX
PT Canine cytokine protein which activates canine cytotoxic T lymphocytes -
PT is useful for treatment of viral and autoimmune diseases in dogs.
XX
PS Claim 8; Page 30-31; 51pp; Japanese.
XX
CC This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC the invention. CLAF activates lymphocytes, especially canine cytotoxic T
CC cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC recognising it may be used in the treatment of viral diseases in dogs
CC (such as canine distemper, canine parvovirus and canine infectious
CC hepatitis). The antibodies may also be used in isolation of CLAF from
CC culture of the transformant host cells by affinity chromatography. The
CC p40 homodimer can be used for the treatment of autoimmune diseases in
CC dogs
XX
SQ Sequence 2154 BP; 663 A; 448 C; 477 G; 566 T; 0 U; 0 Other;

Query Match 6.7%; Score 66; DB 2; Length 2154;
Best Local Similarity 100.0%; Pred. No. 2.4e-22;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 591 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 650

Qy 597 CTGCCC 602
||||||
Db 651 CTGCCC 656

RESULT 56
ABK99006/c
ID ABK99006 standard; cDNA; 2267 BP.
XX
AC ABK99006;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12p40-2267 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Example 4; Page 99-100; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a canine interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 2267 BP; 591 A; 504 C; 468 G; 704 T; 0 U; 0 Other;

Query Match 6.7%; Score 66; DB 6; Length 2267;
Best Local Similarity 100.0%; Pred. No. 2.4e-22;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1578 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1519

Qy 597 CTGCCC 602
||||||
Db 1518 CTGCCC 1513

RESULT 57
ABK99005
ID ABK99005 standard; cDNA; 2267 BP.
XX
AC ABK99005;
XX
DT 21-OCT-2002 (first entry)
XX
DE Canine interleukin-12 nCaIL-12p40-2267 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Canis familiaris.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
DR P-PSDB; ABG69317.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Example 4; Page 97-98; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,

```
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a canine interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 2267 BP; 704 A; 468 C; 504 G; 591 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 6;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 749

Qy        597 CTGCCC 602
              ||||||
Db        750 CTGCCC 755


RESULT 58
ADV34757
ID   ADV34757 standard; cDNA; 2267 BP.
XX
AC   ADV34757;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p40 protein cDNA, nCaIL-12p40 2267.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             154. .1143
FT                   /*tag=  a
FT                   /product= "PCaIL-12p40 329 protein"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34758.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 107; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p40 subunit protein
CC   encoding cDNA.
XX
SQ   Sequence 2267 BP; 704 A; 468 C; 504 G; 591 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 14;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 749

Qy        597 CTGCCC 602
              ||||||
Db        750 CTGCCC 755


RESULT 59
ADV34759/c
ID   ADV34759 standard; DNA; 2267 BP.
XX
AC   ADV34759;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Canine single chain IL-12p40 complementary DNA, nCaIL-12p35 2267.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Canis familiaris.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 4; SEQ ID NO 109; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the canine single chain IL-12p40 subunit
CC   complementary DNA.
XX
SQ   Sequence 2267 BP; 591 A; 504 C; 468 G; 704 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 66;  DB 14;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1578 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1519
```

```
Qy        597 CTGCCC 602
              ||||||
Db       1518 CTGCCC 1513


RESULT 60
AAD15206
ID   AAD15206 standard; DNA; 984 BP.
XX
AC   AAD15206;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p40 encoding DNA from clone B1-81.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p40; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .984
FT                   /*tag=  a
FT                   /product= "Modified p40 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .981
FT                   /*tag=  c
FT                   /product= "Mature modified p40 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08599.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 1; Page 137; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p40 protein encoding
CC   DNA
XX
SQ   Sequence 984 BP; 272 A; 254 C; 247 G; 211 T; 0 U; 0 Other;

  Query Match             6.6%;  Score 65;  DB 5;  Length 984;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-22;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        451 GATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGT 510
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGT 510

Qy        511 GGAGC 515
              |||||
Db        511 GGAGC 515


RESULT 61
ADT04849
ID   ADT04849 standard; DNA; 1015 BP.
XX
AC   ADT04849;
XX
DT   13-JAN-2005  (first entry)
XX
DE   Canine interleukin-12 (IL-12) p40 DNA.
XX
KW   gene expression; insect; ds; interleukin-12; IL-12.
XX
OS   Canis familiaris.
XX
PN   JP2004290182-A.
XX
PD   21-OCT-2004.
XX
PF   06-FEB-2004; 2004JP-00030183.
XX
PR   10-MAR-2003; 2003JP-00062907.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2004-740760/73.
XX
PT   Novel gene vector for expression in insect useful for expression of
PT   foreign gene such as dog interleukin 12 gene, comprises two promoters.
XX
PS   Claim 4; SEQ ID NO 5; 13pp; Japanese.
XX
CC   The invention relates to a novel gene vector for expression in an insect
CC   comprising at least two promoters, particularly the polyhedrin promoter
CC   and p10 promoter. The vector contains at least two types of foreign
CC   protein expression gene and the gene product of the vector is produced
CC   using a gene recombinant baculovirus, particularly a recombinant silkworm
CC   nuclear polyhedrosis virus. The baculovirus is proliferated in a
CC   silkworm. The vector of the invention may be useful for expression of a
CC   foreign gene, such as canine interleukin 12. Within the vector, two types
CC   of foreign protein expression genes are integrated simultaneously for
CC   their simultaneous expression. The current sequence is that of the canine
CC   interleukin-12 (IL-12) p40 DNA of the invention.
XX
SQ   Sequence 1015 BP; 285 A; 251 C; 254 G; 225 T; 0 U; 0 Other;

  Query Match             6.4%;  Score 63;  DB 13;  Length 1015;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-21;
  Matches   63;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         88 GTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACC 147
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 GTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACC 147

Qy        148 TGC 150
              |||
Db        148 TGC 150


RESULT 62
AAD15204
ID   AAD15204 standard; DNA; 984 BP.
XX
AC   AAD15204;
XX
DT   01-NOV-2001  (first entry)
XX
```

```
DE   Modified human cytokine p40 encoding DNA from clone B8-96.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p40; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .984
FT                   /*tag=  a
FT                   /product= "Modified p40 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .981
FT                   /*tag=  c
FT                   /product= "Mature modified p40 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08597.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 1; Page 136; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p40 protein encoding
CC   DNA
XX
SQ   Sequence 984 BP; 270 A; 249 C; 259 G; 206 T; 0 U; 0 Other;

  Query Match             6.2%;  Score 61;  DB 5;  Length 984;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-20;
  Matches   61;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        673 ACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTG 732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        673 ACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTG 732

Qy        733 A 733
              |
Db        733 A 733


RESULT 63
AAD15205
ID   AAD15205 standard; DNA; 984 BP.
XX
AC   AAD15205;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p40 encoding DNA from clone B2-52.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p40; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .984
FT                   /*tag=  a
FT                   /product= "Modified p40 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .981
FT                   /*tag=  c
FT                   /product= "Mature modified p40 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08598.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 1; Page 136-137; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p40 protein encoding
CC   DNA
XX
SQ   Sequence 984 BP; 267 A; 246 C; 254 G; 217 T; 0 U; 0 Other;

  Query Match             6.1%;  Score 60;  DB 5;  Length 984;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-19;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAAC 723
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAAC 723


RESULT 64
AAD15208
ID   AAD15208 standard; DNA; 975 BP.
XX
AC   AAD15208;
XX
DT   01-NOV-2001  (first entry)
XX
```

```
DE   Modified human cytokine p40 encoding DNA from clone A16-94.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p40; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .975
FT                   /*tag=  a
FT                   /product= "Modified p40 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .972
FT                   /*tag=  c
FT                   /product= "Mature modified p40 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08601.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 1; Page 137; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p40 protein encoding
CC   DNA
XX
SQ   Sequence 975 BP; 261 A; 250 C; 255 G; 209 T; 0 U; 0 Other;

  Query Match             5.4%;  Score 53;  DB 5;  Length 975;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-16;
  Matches   53;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        895 GTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTA 947
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 GTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTA 926


RESULT 65
AAQ04701
ID   AAQ04701 standard; DNA; 906 BP.
XX
AC   AAQ04701;
XX
DT   25-MAR-2003  (revised)
DT   11-OCT-1990  (first entry)
XX
DE   Sequence encoding natural killer cell stimulatory factor (NKSF).
XX
KW   Natural killer cell stimulatory factor; NKSF; cancer; leukopaenia;
KW   anaemia; radiation; bone marrow transplantation; ds.
XX
OS   Homo sapiens.
XX
PN   WO9005147-A.
XX
PD   17-MAY-1990.
XX
PF   10-NOV-1988;   88US-00269945.
XX
PR   10-NOV-1988;   88US-00269945.
PR   07-FEB-1989;   89US-00307817.
XX
PA   (GEMY ) GENETICS INST INC.
PA   (WIST-) WISTAR INST.
XX
PI   Trinchieri G,  Perussia B,  Kobayashi M,  Clark SC,  Wong GG;
XX
DR   WPI; 1990-178800/23.
DR   P-PSDB; AAR05171.
XX
PT   New natural killer cell stimulatory factor - useful for treating cancer
PT   and e.g. leukopenia, bacterial and viral infections, anaemia and B or T
PT   cell deficiencies.
XX
PS   Claim 16; Page 60; 69pp; English.
XX
CC   Natural killer cell stimulatory factor (NKSF) is useful in treating
CC   cancer and other disease states which respond to NK cell activity. Such
CC   states may arise from immune or haematopoietic-cell deficiency following
CC   a bone marrow translpantation, exposure to radiation and disease.
CC   (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
CC   correct PA field.)
XX
SQ   Sequence 906 BP; 244 A; 220 C; 238 G; 204 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 2;  Length 906;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        693 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 736


RESULT 66
AAD15207
ID   AAD15207 standard; DNA; 969 BP.
XX
AC   AAD15207;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p40 encoding DNA from clone A3-48.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p40; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .969
FT                   /*tag=  a
FT                   /product= "Modified p40 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag=  b
FT   mat_peptide     67. .966
FT                   /*tag=  c
FT                   /product= "Mature modified p40 protein"
```

```
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08599.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 1; Page 137; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p40 protein encoding
CC   DNA
XX
SQ   Sequence 969 BP; 263 A; 249 C; 251 G; 206 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 5;  Length 969;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        649 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 692


RESULT 67
AAQ12149
ID   AAQ12149 standard; DNA; 979 BP.
XX
AC   AAQ12149;
XX
DT   10-SEP-1991  (first entry)
XX
DE   Cytotoxic lymphocyte maturation factor (40 kD subunit) gene.
XX
KW   Cytotoxic lymphocyte maturation factor; CLMF; probe; antitumour;
KW   monoclonal antibodies; T cell; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             41. .979
FT                   /*tag=  a
FT                   /product= "CLMF"
FT   sig_peptide     41. .106
FT                   /*tag=  b
FT                   /note= "hydrophobic signal peptide"
FT   mat_peptide     107. .979
FT                   /*tag=  c
XX
PN   EP433827-A.
XX
PD   26-JUN-1991.
XX
PF   09-DEC-1990;   90EP-00123670.
XX
PR   22-DEC-1989;   89US-00455708.
PR   09-MAY-1990;   90US-00520935.
PR   27-AUG-1990;   90US-00572284.
XX
PA   (HOFF ) HOFFMANN-LA ROCHE AG.
XX
PI   Chizzonite RA,  Gately MK,  Gubler UA,  Hulmes JD,  Pan YCE;
PI   Podlaski FJ,  Stern AS;
XX
DR   WPI; 1991-186715/26.
DR   P-PSDB; AAR12493.
XX
PT   New cytotoxic lymphocyte maturation factor - used as antitumour agent and
PT   monoclonal antibodies used in transplantation to block proliferation and
PT   activation of cytotoxic T cells.
XX
PS   Disclosure; Fig 25 (a-c); 90pp; English.
XX
CC   The natural CLMF protein is a 75 kD heterodimer comprising two
CC   polypeptide subunits, a 40 kD and a 35 kD subunit (AAQ12150). The
CC   subunits are bonded together via one or more disulfide bonds. The CLMF
CC   can interact with IL-2 to synergistically induce the cytolytic activity
CC   of Lymphokine Activated Killer (LAK) cells. It is also capable of
CC   stimulating T-cell growth. It can be used for the prepn. of LAK- and T-
CC   cell activator and antitumour compsns. and for stimulating Natural Killer
CC   (NK) cells
XX
SQ   Sequence 979 BP; 261 A; 245 C; 257 G; 216 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 2;  Length 979;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        701 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 744


RESULT 68
AAT50759
ID   AAT50759 standard; cDNA; 984 BP.
XX
AC   AAT50759;
XX
DT   17-OCT-2003  (revised)
DT   24-SEP-1997  (first entry)
XX
DE   Sequence of ovine IL-12 40 kD sununit cDNA.
XX
KW   Cytokine; ovine; sheep; interleukin-5; interleukin-12; IL-5; IL-12;
KW   livestock; cow; stress; transport; vaccine adjuvant; veterinary; cancer;
KW   immunosuppression; allergy; reproductive system; growth; early maturity;
KW   antibody; diagnosis; immunopotentiator;
KW   early haematopoietic progenitor cell; cytotoxic cell; thymocyte;
KW   secretion; IgM; IgA; bacterial endotoxin; gamma-interferon; ss.
XX
OS   Ovis aries.
XX
PN   WO9700321-A1.
XX
PD   03-JAN-1997.
XX
PF   14-JUN-1996;   96WO-AU000360.
XX
PR   14-JUN-1995;   95AU-00003502.
PR   27-OCT-1995;   95AU-00006244.
XX
PA   (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
PI   Seow H,  Wood P;
```

```
XX
DR   WPI; 1997-077528/07.
DR   P-PSDB; AAW08483.
XX
PT   Nucleic acid encoding ovine interleukin-5 or -12 - used as vaccine
PT   adjuvants and to treat or prevent microbial infections in livestock.
XX
PS   Claim 10; Page 49-51; 78pp; English.
XX
CC   The sequences given in AAT50757-59 encode ovine interleukin-12 (IL-12) 35
CC   kD subunit (partial and full length sequence) and the 40 kD subunit.
CC   Ovine IL-5 or IL-12 are used to treat and/or prevent infections in
CC   livestock (esp. cows and sheep), particularly where the animals are
CC   stressed, e.g. during transport. IL-5 and IL-12 can also be used as
CC   adjuvants in vaccines for veterinary use (partic. weakly immunogenic
CC   subunit or synthetic peptide vaccines). They may also be used to treat
CC   cancer, immunosuppression and allergy, to enhance/suppress the
CC   reproductive system and to promote growth or early maturity. Optionally
CC   interleukin can be delivered from constructs or delivery cells and
CC   antibodies are useful in enzyme immunoassays for rapid diagnosis of
CC   infection. The interleukins are immunopotentiators, especially IL-5
CC   promotes growth of early haematopoietic progenitor cells and generation
CC   of cytotoxic cells from thymocytes, also it stimulates production and
CC   secretion of IgM and IgA (in synergism with bacterial endotoxin). IL-12
CC   induces production of gamma-interferon by, and proliferation of, T and NK
CC   cells and increases the (non-)specific cytolytic lymphocyte response. The
CC   genetic constructs can also be used for in vitro production of IL-5 or -
CC   12. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ   Sequence 984 BP; 273 A; 243 C; 253 G; 215 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 2;  Length 984;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707


RESULT 69
ADG39430
ID   ADG39430 standard; DNA; 984 BP.
XX
AC   ADG39430;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human CLMF 40 kDa subunit DNA.
XX
KW   human; cytotoxic lymphocyte maturation factor; CLMF;
KW   activated T-cell stimulator; natural killer cell stimulator;
KW   immunoenhancer; antitumour; tumour; cancer; ds; gene.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             67. .984
FT                   /*tag=  a
FT                   /partial
FT                   /product= "CLMF 40 kDa subunit"
FT                   /note= "No start or stop codon given"
XX
PN   US2003204059-A1.
XX
PD   30-OCT-2003.
XX
PF   08-OCT-2002; 2002US-00267565.
XX
PR   22-DEC-1989;   89US-00455708.
PR   09-MAY-1990;   90US-00520935.
PR   27-AUG-1990;   90US-00572284.
PR   24-MAR-1992;   92US-00857023.
PR   02-MAR-1994;   94US-00205011.
PR   02-JUN-1995;   95US-00459151.
PR   22-SEP-1999;   99US-00401839.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CIE SA F.
XX
PI   Gately MK,  Gubler UA,  Hulmes JD,  Podlaski FJ,  Stern AS;
PI   Chizzonite RA,  Pan YE;
XX
DR   WPI; 2004-010534/01.
DR   P-PSDB; ADG39429.
XX
PT   Novel protein comprising cytotoxic lymphocyte maturation factor in
PT   substantially pure form or protein which exhibits cytotoxic lymphocyte
PT   maturation factor activity, useful as antitumor and immunoenhancing
PT   agent.
XX
PS   Claim 17; Page 28-29; 74pp; English.
XX
CC   The invention relates to a protein which comprises a cytotoxic lymphocyte
CC   maturation factor (CLMF). The protein is useful for stimulating activated
CC   T-cells which involves treating T-cells with the protein. The method
CC   further involves treating the activated T-cells with IL2 or its
CC   biologically active fragment. The protein is useful for stimulating
CC   natural killer cells which involves treating the natural killer cells
CC   with the protein. The protein has immunoenhancing and antitumour effects
CC   when used as single therapeutic agent in vivo. The present sequence is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 984 BP; 263 A; 243 C; 258 G; 220 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 12;  Length 984;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 70
ADK98707
ID   ADK98707 standard; DNA; 985 BP.
XX
AC   ADK98707;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human interleukin-12 (IL-12) P40 subunit DNA.
XX
KW   human; recombinant interleukin-12; IL-12; P35 subunit; P40 subunit; ds.
XX
OS   Homo sapiens.
XX
PN   CN1408727-A.
XX
PD   09-APR-2003.
XX
PF   29-SEP-2001; 2001CN-00126923.
XX
PR   29-SEP-2001; 2001CN-00126923.
XX
PA   (ZHON-) ZHONGXIN GUOJIAN PHARM CO LTD SHANGHAI.
XX
PI   Wan G,  Li C;
XX
DR   WPI; 2003-664076/63.
XX
PT   Method for efficiently expressing recombinant human interleukin 12 in
PT   eukaryotic cell.
XX
PS   Example 2; SEQ ID NO 2; 14pp; Chinese.
XX
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```
CC   The invention describes the process of producing human recombinant
CC   interleukin-12 (IL-12) includes: providing a nucleotide sequence
CC   corresponding to the P35 subunit with the first signal peptide and a
CC   nucleotide sequence corresponding to the P40 subunit; inserting the
CC   nucleotide sequences into an expression vector; converting the eukaryotic
CC   cell with the expression vector; and culturing the transfected eukaryotic
CC   cell in condition suitable for recombinant human IL-12 expression. The
CC   process balances the expression amount of both P35 and P40 subunits and
CC   thus raises the expression amount of IL-12 with bioactivity via raising
CC   the expression strength of P35 subunit. This sequence represents the
CC   human interleukin-12 (IL-12) P40 subunit polynucleotide.
XX
SQ   Sequence 985 BP; 264 A; 242 C; 258 G; 221 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 10;  Length 985;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        659 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 702


RESULT 71
AAQ97484
ID   AAQ97484 standard; cDNA; 987 BP.
XX
AC   AAQ97484;
XX
DT   25-MAR-2003  (revised)
DT   22-DEC-1995  (first entry)
XX
DE   Human interleukin-12 40 kD subunit.
XX
KW   Interleukin-12; IL-12; cytokine; gamma-interferon; T cell;
KW   natural killer cell; graft vs. host disease; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .987
FT                   /*tag=  a
XX
PN   WO9519786-A1.
XX
PD   27-JUL-1995.
XX
PF   20-JAN-1995;   95WO-US000879.
XX
PR   21-JAN-1994;   94US-00186529.
XX
PA   (GEMY ) GENETICS INST INC.
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Wolf SF,  Sykes M;
XX
DR   WPI; 1995-269273/35.
DR   P-PSDB; AAR79186.
XX
PT   Control of graft versus host disease using interleukin 12 - partic.
PT   admin. at the time of bone marrow transplant.
XX
PS   Disclosure; Page 21-22; 32pp; English.
XX
CC   AAQ97484 and AAQ97485 are from human lymphoblast cell line RMPI 8866. IL-
CC   12 is a heterodimeric cytokine which was originally identified as a
CC   factor which induces gamma-interferon from T cells and natural killer
CC   cells as set forth in PCT/US91/06332, published April 2 1992, and
CC   incorporated by reference. EP 433827, published June 26 1991, disclosed
CC   IL-12 as a cytotoxin lymphocyte maturation factor. In the patent, IL-12
CC   is defined as a heterodimeric glycoprotein comprised of two covalently
CC   linked subunits having mol. wts of about 40 kD and 35 kD. The two
CC   subunits may be disulfide-bonded. IL-12 is administered to prevent or
CC   ameliorate GVHD. Dosage is 1 ng-0.1 mg (esp. 1.0 ng-1 microg)/kg daily
CC   for 3 days, the first dose given 1 hr. after transplant. IL-12 can be
CC   used as the native heterodimer or as subunits. (Updated on 25-MAR-2003 to
CC   correct PN field.)
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 72
AAV07273
ID   AAV07273 standard; cDNA; 987 BP.
XX
AC   AAV07273;
XX
DT   25-SEP-1998  (first entry)
XX
DE   Human Interleukin-12 p40 gene.
XX
KW   IL-12 subunit; expression construct; treatment; asthma;
KW   microbial infection; viral infection; cancer; Human; Interleukin; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .987
FT                   /*tag=  a
FT                   /product= "IL-12 p40"
XX
PN   WO9817689-A2.
XX
PD   30-APR-1998.
XX
PF   10-OCT-1997;   97WO-US018779.
XX
PR   18-OCT-1996;   96US-0028676P.
XX
PA   (GENE-) GENEMEDICINE INC.
XX
PI   Nordstrom J,  Freimark B,  Deshpande D;
XX
DR   WPI; 1998-261428/23.
DR   P-PSDB; AAW51311.
XX
PT   Constructs for expression of interleukin-12 sub-units - are used for
PT   delivery of IL-12 sub-units for treating e.g. asthma, microbial or viral
PT   infections and certain cancers.
XX
PS   Claim 1; Page 34; 80pp; English.
XX
CC   The IL-12 subunits AAV07273 and AAV07274 can be expressed using an
CC   appropriate expression construct engineered into a plasmid. The plasmids
CC   can provide for efficient expression of IL-12 subunits. The products can
CC   be used for the treatment of asthma, microbial and viral infections and
CC   certain cancers
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704
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RESULT 73
AAV07217
ID   AAV07217 standard; DNA; 987 BP.
XX
AC   AAV07217;
XX
DT   12-AUG-1998  (first entry)
XX
DE   DNA encoding human interleukin-12 40kDa subunit.
XX
KW   Interleukin-12; IL-12; graft-versus-host disease;
KW   GVHD. bone marrow transplantation; graft-versus-leukemia; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .987
FT                   /*tag= a
FT                   /product= "Interleukin-12_40kDa_subunit"
XX
PN   US5756085-A.
XX
PD   26-MAY-1998.
XX
PF   30-APR-1996;   96US-00640386.
XX
PR   21-JAN-1994;   94US-00186529.
XX
PA   (GEMY ) GENETICS INST INC.
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Sykes M,  Wolf SF;
XX
DR   WPI; 1998-321459/28.
DR   P-PSDB; AAW51221.
XX
PT   Therapy of graft-versus-host disease - by administration of interleukin-
PT   12 to maintain and/or promote graft-versus-leukaemia effects.
XX
PS   Disclosure; Col 17-20; 20pp; English.
XX
CC   The invention relates to a method for the treatment or prevention of
CC   graft-versus-host disease (GVHD) which comprises the administration of
CC   interleukin-12 (IL-12) at the time of bone-marrow transplantation to
CC   maintain or promote graft-versus-leukaemia effects. Preferably, dosage is
CC   0.001-100 (preferably 1-100) mu g/kg for 3 days starting on the day of
CC   the bone marrow transplant. IL-12 is administered daily until there is an
CC   improvement in the condition. Administration is oral, cutaneous,
CC   subcutaneous, intravenous or by inhalation preferably subcutaneous, or
CC   intravenous. The present sequence encodes the human interleukin-12 40kDa
CC   subunit
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 74
AAZ40404
ID   AAZ40404 standard; DNA; 987 BP.
XX
AC   AAZ40404;
XX
DT   15-FEB-2000  (first entry)
XX
DE   Human interleukin 12 p40 subunit wild type coding sequence.
XX
KW   Wild type; human; interferon-alpha; plasmid; cytomegalovirus; CMV;
KW   promoter; growth hormone; untranslated region; UTR; mammal; disease;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9947678-A2.
XX
PD   23-SEP-1999.
XX
PF   12-MAR-1999;   99WO-US005394.
XX
PR   19-MAR-1998;   98US-0078654P.
XX
PA   (GENE-) GENEMEDICINE INC.
XX
PI   Nordstrom J,  Pericle F,  Rolland A,  Ralston R;
XX
DR   WPI; 1999-562116/47.
DR   P-PSDB; AAY42487.
XX
PT   New plasmids containing an interferon-alpha coding sequence, used for the
PT   treatment of a mammalian condition or disease, particularly cancer.
XX
PS   Claim 11; Page 43-45; 137pp; English.
XX
CC   This sequence represents the wild type coding region for the human
CC   interleukin 12 p40 subunit. The invention relates to a novel plasmid
CC   comprising a cytomegalovirus (CMV) promoter transcriptionally linked with
CC   an interferon alpha (IFN-alpha) coding sequence, and a growth hormone 3'-
CC   untranslated region (UTR). The plasmids can be used for treating a
CC   mammalian condition or disease, particularly cancer
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 75
AAV83199
ID   AAV83199 standard; DNA; 987 BP.
XX
AC   AAV83199;
XX
DT   02-MAR-1999  (first entry)
XX
DE   Interleukin (IL)-12B cDNA.
XX
KW   Mouse; immunodeficient; pathogen; tumour; lymphocyte; antigen;
KW   immunomodulator; vector; vaccine; cancer; HIV; Leishmania; Mycobacterium;
KW   Listeria; Plasmodium; retrovirus; evaluation;
KW   human immunodeficiency virus; ds.
XX
OS   Homo sapiens.
XX
PN   WO9844788-A2.
XX
PD   15-OCT-1998.
XX
PF   09-APR-1998;   98WO-US006944.
XX
PR   09-APR-1997;   97US-00838702.
PR   01-MAY-1997;   97US-00848760.
PR   09-DEC-1997;   97US-0069163P.
XX
PA   (CHAN/) CHANG L.
```

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XX
PI   Chang L;
XX
DR   WPI; 1999-024005/02.
XX
PT   Use of immunodeficient mice comprising human cells - particularly
PT   SCTD/beige mice comprising human immune cells for evaluating vaccines
PT   against cancers or human pathogens, e.g. HIV.
XX
PS   Example 10(c)(i); Page 110; 154pp; English.
XX
CC   Immunodeficient mice comprising human cells can be used for exposure to
CC   human pathogens and/or their components or human tumour cells and human
CC   peripheral blood lymphocytes. Also claimed is a vaccine comprising a cell
CC   modified to express an antigen and an immune-modulating protein, this is
CC   preferably an expression vector comprising a polynucleotide sequence that
CC   encodes the antigen and immune-modulating protein. Such vectors can be
CC   used to treat a subject having a tumour by transferring the expression
CC   vector into the tumour so that the antigen and the immune-modulator are
CC   expressed by at least the tumour. The methods can be used for producing
CC   and evaluating vaccines including cancer vaccines and vaccines directed
CC   against human pathogens, e.g. HIV, Leishmania, Mycobacterium, Listeria or
CC   Plasmodium. Two primers (AAV83197, AAV83198) were used to amplify the IL-
CC   12B for insertion into expression vectors of the invention
XX
SQ   Sequence 987 BP; 264 A; 245 C; 257 G; 221 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 76
AAD15210
ID   AAD15210 standard; DNA; 987 BP.
XX
AC   AAD15210;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Human cytokine p40 DNA.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection; AIDS;
KW   diabetic retinopathy; cancer; vaccine; cell-mediated immunity; human;
KW   p40; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .987
FT                   /*tag= a
FT                   /product= "p40 protein precursor"
FT   sig_peptide     1. .66
FT                   /*tag= b
FT   mat_peptide     67. .984
FT                   /*tag= c
FT                   /product= "Mature p40 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US032664.
XX
PR   02-DEC-1999;   99US-0169035P.
PR   28-NOV-2000; 2000US-00725324.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08603.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified p40
PT   and p35 polypeptides), useful for treating various diseases e.g. diabetic
PT   retinopathy and cancer.
XX
PS   Claim 5; Page 142; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is human p40 protein encoding DNA
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 5;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 77
ACC47592
ID   ACC47592 standard; DNA; 987 BP.
XX
AC   ACC47592;
XX
DT   12-JUN-2003  (first entry)
XX
DE   Human interleukin 12 (hIL-12) P40 subunit gene.
XX
KW   Human; interleukin 12; hIL-12; baculovirus vector;
KW   recombinant production; AcNPV-hIL12;
KW   Autographa california nuclear polyhedrosis virus; tumour; cancer;
KW   infection; bacterial; viral; cytostatic; P40 subunit; gene; ds.
XX
OS   Homo sapiens.
XX
PN   CN1357622-A.
XX
PD   10-JUL-2002.
XX
PF   02-NOV-2001; 2001CN-00133631.
XX
PR   02-NOV-2001; 2001CN-00133631.
XX
PA   (UYWU-) UNIV WUHAN.
XX
PI   Meng X,  Xu J,  Yu Z;
XX
DR   WPI; 2002-741792/81.
XX
PT   Human interleukin-12 recombinant insect virus strain and its preparation.
XX
PS   Claim 5; Fig 7; 17pp; Chinese.
XX
CC   The invention relates to a recombinant baculovirus comprising DNA
CC   encoding human interleukin 12 (hIL-12) and methods for its preparation.
CC   The recombinant baculovirus strain is designated Autographa california
CC   nuclear polyhedrosis virus AcNPV-hIL12 (CCTCC No. 2 V200108). This strain
CC   contains two human IL-12 subunit genes, the IL-12 P35 subunit gene
CC   (ACC47589) and the IL-12 P40 subunit gene (ACC47592) which are
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CC   respectively under the control of the viral polyhedrin and P10 promoters.
CC   The baculovirus can be used in the recombinant production of human IL-12
CC   which is suitable for treating tumours and bacterial, viral and other
CC   infections. The present sequence represents the human IL-12 P40 subunit
CC   gene used in construction of the baculovirus vector of the invention
XX
SQ   Sequence 987 BP; 264 A; 245 C; 257 G; 221 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 6;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 78
ADF77276
ID   ADF77276 standard; DNA; 987 BP.
XX
AC   ADF77276;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human IL-12 p40 subunit DNA.
XX
KW   ds; human; interferon alpha expression plasmid; tumour; IL-12.
XX
OS   Homo sapiens.
XX
PN   US2003181405-A1.
XX
PD   25-SEP-2003.
XX
PF   29-APR-2002; 2002US-00136837.
XX
PR   12-MAR-1999;   99US-00268135.
XX
PA   (NORD/) NORDSTROM J L.
PA   (PERI/) PERICLE F.
PA   (ROLL/) ROLLAND A.
PA   (RALS/) RALSTON R O.
XX
PI   Nordstrom JL,  Pericle F,  Rolland A,  Ralston RO;
XX
DR   WPI; 2004-020834/02.
XX
PT   A mammalian interferon alpha expression plasmid is useful in gene therapy
PT   to deliver interferon alpha to cells to modulate tumor activity in the
PT   treatment of cancer.
XX
PS   Disclosure; Page 14-15; 65pp; English.
XX
CC   The invention relates to a mammalian interferon alpha expression plasmid,
CC   comprising a promoter and a synthetic 5' intron transcriptionally linked
CC   with an interferon alpha coding sequence and a 3' untranslated region.
CC   The mammalian interferon alpha expression plasmid is useful for treating
CC   tumour growth. The present sequence is used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 987 BP; 264 A; 243 C; 258 G; 221 T; 0 U; 1 Other;

  Query Match             4.5%;  Score 44;  DB 12;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 79
ADO07653
ID   ADO07653 standard; DNA; 987 BP.
XX
AC   ADO07653;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Human interleukin-12 40kDa coding sequence.
XX
KW   cytostatic; virucide; anti-HIV; hepatotropic; neuroprotective;
KW   immunostimulant; expression cassette; viral vector; interleukin-12;
KW   co-stimulatory protein; cancer; infection; ds; gene; human.
XX
OS   Homo sapiens.
XX
PN   WO2004035799-A2.
XX
PD   29-APR-2004.
XX
PF   10-OCT-2003; 2003WO-EP011252.
XX
PR   11-OCT-2002; 2002DE-01048141.
XX
PA   (UYHA-) UNIV HAMBURG-EPPENDORF KLINIKUM.
XX
PI   Waehler R,  Schnieders F;
XX
DR   WPI; 2004-357221/33.
XX
PT   Viral vector that expresses single-chain interleukin-12 and costimulator,
PT   useful for treatment of tumors, viral infections, e.g. human
PT   immunodeficiency virus, and prion diseases.
XX
PS   Claim 4; Fig 19; 129pp; German.
XX
CC   The present invention relates to a viral vector that includes a nucleic
CC   acid encoding a single-chain interleukin-12 (IL-12) and a co-stimulatory
CC   protein. Viral vectors and virus particles derived from them are useful
CC   for treatment of tumours, infectious diseases (e.g. HIV, hepatitis A, B
CC   or C, cytomegalovirus or human papilloma virus), or prion diseases. The
CC   present sequence is a human interleukin-12 coding sequence used in the
CC   exemplification of the invention.
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 12;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 80
ADS00006
ID   ADS00006 standard; DNA; 987 BP.
XX
AC   ADS00006;
XX
DT   16-DEC-2004  (first entry)
XX
DE   Human interleukin-23 (IL-23) p40 subunit DNA.
XX
KW   tumour; interleukin-23; IL-23; cytostatic; immunostimulant; cancer;
KW   p40 subunit; ds; gene.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .987
FT                   /*tag=  a
FT                   /product= "Human interleukin-23 (IL-23) p40 subunit
```

```
FT                   protein"
XX
PN   JP2004262797-A.
XX
PD   24-SEP-2004.
XX
PF   28-FEB-2003; 2003JP-00052999.
XX
PR   28-FEB-2003; 2003JP-00052999.
XX
PA   (CHIB-) CHIBA PREFECTURE.
XX
DR   WPI; 2004-665614/65.
DR   P-PSDB; ADS00010.
XX
PT   Novel anti-tumor agent comprising interleukin-23 gene, or cell transduced
PT   with interleukin-23 gene, as active ingredient, useful for activating
PT   anti-tumor immune response and treating tumor.
XX
PS   Disclosure; SEQ ID NO 2; 23pp; Japanese.
XX
CC   The invention relates to a novel anti-tumour agent comprising an
CC   interleukin-23 (IL-23) gene, or a cell transduced with an IL-23 gene, as
CC   an active ingredient. The molecules of the invention demonstrate
CC   cytostatic and immunostimulant activities and may be useful within an
CC   anti-tumour agent which activates an anti-tumour immune response. The
CC   agent is safe when used in cancer treatment, may be combined with other
CC   treatments and induces tumour-specific acquired immunity. The current
CC   sequence is that of the human interleukin-23 (IL-23) p40 subunit DNA of
CC   the invention.
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 13;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 81
ADV42753
ID   ADV42753 standard; cDNA; 987 BP.
XX
AC   ADV42753;
XX
DT   10-MAR-2005  (first entry)
XX
DE   Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 381.
XX
KW   microarray; psychoneuroendocrinimmune; chronic fatigue;
KW   non-insulin dependent diabetes; allergy; immune disorder; inflammation;
KW   cancer; neoplasm; infection; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO2004108899-A2.
XX
PD   16-DEC-2004.
XX
PF   04-JUN-2004; 2004WO-US017686.
XX
PR   04-JUN-2003; 2003US-0475915P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Nicholson A,  Vernon SD;
XX
DR   WPI; 2005-031682/03.
XX
PT   New microarray comprising probes for genes involved in
PT   psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a
PT   condition associated with PNI activity, e.g., inflammatory or infectious
PT   diseases.
XX
PS   Claim 1; SEQ ID NO 381; 254pp; English.
XX
CC   The invention relates to a new microarray which comprises probes for
CC   genes involved in psychoneuroendocrinimmune (PNI) activity. The
CC   microarray is useful in diagnosing a condition associated with PNI
CC   activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
CC   cancer and infection. The present sequence represents a
CC   psychoneuroendocrinimmune gene expressed sequence tag. Note the
CC   specificatio mentions SEQ ID NO of up to 3314 but only sequences up to
CC   SEQ ID NO 1829 are provided.
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 14;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 82
ADW97242
ID   ADW97242 standard; DNA; 987 BP.
XX
AC   ADW97242;
XX
DT   19-MAY-2005  (first entry)
XX
DE   Human p40 gene that inhibits IL-23 immune response Seq 1a.
XX
KW   immune inhibition; transplant rejection; immune disorder;
KW   autoimmune disease; allergy; immunosuppressive; antiallergic; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .987
FT                   /*tag=  a
FT                   /product= "P40 protein"
XX
PN   JP2005060313-A.
XX
PD   10-MAR-2005.
XX
PF   13-AUG-2003; 2003JP-00292937.
XX
PR   13-AUG-2003; 2003JP-00292937.
XX
PA   (CHIB-) CHIBA PREFECTURE.
XX
DR   WPI; 2005-200132/21.
DR   P-PSDB; ADW97244.
XX
PT   Pharmaceutical formulation for inhibiting immune response generated by
PT   interleukin-23 (IL-23) and treating e.g. autoimmune diseases, comprises
PT   p40 molecules or gene encoding p40 molecules.
XX
PS   Claim 3; SEQ ID NO 1; 12pp; Japanese.
XX
CC   This invention relates to a novel pharmaceutical formulation used for
CC   inhibiting the immune response generated by interleukin-23 (IL-23).
CC   Specifically, it refers to a formulation comprising the p40 protein or
CC   the gene encoding this protein thereof. The present invention describes
CC   the p40 gene contained in the form of a viral or non-viral vector that is
CC   capable of expressing and secreting the p40 protein. This vector can be
CC   introduced into a cell such that it can in turn inhibit the immune
CC   response generated by the production of IL-23. Accordingly, this method
```

```
CC   is useful for suppressing organ transplant rejection or treating
CC   immunological disorders associated with abnormal immune response with
CC   regard to IL-23. Furthermore, it can be used to treat autoimmune diseases
CC   and allergy. As such, compositions exhibit immunosuppressive and
CC   antiallergic activities. This polynucleotide sequence is the human p40
CC   gene of the invention.
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 14;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 83
AEB48822
ID   AEB48822 standard; cDNA to mRNA; 987 BP.
XX
AC   AEB48822;
XX
DT   22-SEP-2005  (first entry)
XX
DE   Human interleukin-12 p40 domain coding sequence.
XX
KW   Interleukin-12; cytokine; lymphokine; cancer; tumor; glioblastoma;
KW   neoplasm; neurological disease; cytostatic; therapy; immunoconjugate;
KW   fusion protein; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .987
FT                   /*tag=  b
FT   sig_peptide     1. .66
FT                   /*tag=  a
FT   mat_peptide     67. .984
FT                   /*tag=  c
FT                   /product= "Mature interleukin-12 p40 subunit"
XX
PN   WO2005066348-A2.
XX
PD   21-JUL-2005.
XX
PF   05-JAN-2005; 2005WO-GB000007.
XX
PR   05-JAN-2004; 2004US-0534307P.
XX
PA   (EMDL-) EMD LEXIGEN RES CENT CORP.
PA   (ANTI-) ANTISOMA PLC.
XX
PI   Gillies S,  Lo K,  Lan Y,  Verma R;
XX
DR   WPI; 2005-512669/52.
XX
PT   Novel compound comprising target specific portion having monoclonal
PT   antibody having specificity for oncofetal fibronectin and effector
PT   portion having interleukin-12, useful for treating cancer e.g.
PT   glioblastoma.
XX
PS   Claim 36; SEQ ID NO 10; 83pp; English.
XX
CC   The invention provides a compound comprising a target specific portion
CC   and an effector portion, in which the target specific portion comprises
CC   or consists of a monoclonal antibody having specificity for oncofetal
CC   fibronectin, or its fragment or variant which retains the antigen binding
CC   specificity of the parent monoclonal antibody, and the effector portion
CC   comprises or consists of interleukin-12, or its functional fragment or
CC   variant. The monoclonal antibody binds to a region of oncofetal
CC   fibronectin other than the extra-domain B region. Preferably, the
CC   compound comprises a target specific portion that is capable of binding
CC   to an amino acid sequence present in fibronectin expressed in both fetal
CC   and normal adult tissue, especially the repeat 7 domain of fibronectin,
CC   and is preferably specific for human oncofetal fibronectin. The
CC   monoclonal antibody is preferably a BC1 antibody. The invention also
CC   provides nucleic acids encoding the compounds of the invention and
CC   methods of their use in the production of these compounds, as well as
CC   methods of using the compounds in medicine, especially for the treatment
CC   of cancer in a patient, where the patient is a mammal, preferably a
CC   human, and the patient has a solid tumor. The cancer is a glioblastoma
CC   (claimed) or ovarian, gastric, colorectal or pancreatic cancer. The
CC   present sequence is the coding sequence of the p40 domain of human
CC   interleukin-12. In a claimed compound, the effector portion consists of a
CC   single chain interleukin-12 comprising or consisting of an interleukin-12
CC   p40 domain conjugated to the interleukin-12 and p35 domain AEB48815 via a
CC   disulfide bond. A further claimed compound comprises the p40 sequence
CC   linked by disulfide bond to a fusion protein AEB48818 comprising the BC1
CC   heavy chain fused to human interleukin-12 p35.
XX
SQ   Sequence 987 BP; 264 A; 243 C; 259 G; 221 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 14;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 84
AAD18585
ID   AAD18585 standard; DNA; 1007 BP.
XX
AC   AAD18585;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human interleukin-12 (IL-12) p40 subunit DNA.
XX
KW   Human; interleukin-12; IL-12; p40 subunit; cytostatic; virucide; AIDS;
KW   Acquired Immune Deficiency Syndrome; immunisation; hepatitis; malaria;
KW   tuberculosis; vaccine; gene therapy; cancer; influenza; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             7. .993
FT                   /*tag=  a
FT                   /product= "Human IL-12p40 subunit protein"
XX
PN   WO200168802-A2.
XX
PD   20-SEP-2001.
XX
PF   15-MAR-2001; 2001WO-KR000408.
XX
PR   15-MAR-2000; 2000KR-00013133.
PR   13-MAR-2001; 2001KR-00012987.
XX
PA   (UYPO-) UNIV POHANG SCI & TECHNOLOGY.
PA   (PROG-) PROGEN CO LTD.
XX
PI   Sung YC,  Lee SH,  Ha SJ,  Song MK,  Chang J;
XX
DR   WPI; 2001-596904/67.
DR   P-PSDB; AAE11198.
XX
PT   Novel human or mouse interleukin (IL)-12p40 subunit mutant genes, that
PT   inhibit secretion of IL-12p40, but normally secrete IL-12p70, useful as
PT   adjuvant for DNA vaccination and gene therapy to AIDS, cancer, malaria.
XX
PS   Claim 1; Page 89-90; 103pp; English.
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XX
CC   The invention relates to mutant interleukin (IL)-12p40 subunit genes
CC   which produces highly active human or mouse IL-12p40 sequence. IL-12p40
CC   DNA is useful for DNA immunisation or gene therapy for treating diseases
CC   such as cancer, AIDS, hepatitis C, hepatitis B or influenza, malaria or
CC   tuberculosis, as an therapeutic or prophylactic adjuvant. IL-12p40 DNA
CC   induces immune response by increasing the hydrolysis activity of
CC   cytotoxic T lymphocytes when IL-12p40 subunit gene is injected with the
CC   DNA vaccine, or increasing secretion of interferon (IFN)-gamma from T
CC   helper cells or CD8+ T cells when IL-12p40 subunit gene is injected with
CC   DNA vaccine. IL-12p40 DNA is useful in gene therapy and as a DNA vaccine.
CC   The present sequence is a DNA encoding human Interleukin (IL)-12p40
CC   subunit protein
XX
SQ   Sequence 1007 BP; 270 A; 247 C; 265 G; 225 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 5;  Length 1007;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        667 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 710


RESULT 85
AAQ67879
ID   AAQ67879 standard; DNA; 1018 BP.
XX
AC   AAQ67879;
XX
DT   25-MAR-2003  (revised)
DT   23-MAR-1995  (first entry)
XX
DE   EPV 42 kD promoter/Human IL-12 p40 subunit expression cassette.
XX
KW   Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant;
KW   murine; interleukin-2; IL-2; pRW825; pmut-1; pBS-SK; pMM151; TK vector;
KW   plasmid; vaccinia; H6 promoter; amplify; primer; antigenic response;
KW   polymerase chain reaction; poxvirus; pSD542; immunological response;
KW   pathogen; human; interferon; IFN; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   promoter        1. .31
FT                   /*tag=  a
FT                   /note= "EPV 42 kD promoter"
FT   CDS             32. .1018
FT                   /*tag=  b
FT                   /product= "Human IL-12 p40"
XX
PN   WO9416716-A1.
XX
PD   04-AUG-1994.
XX
PF   21-JAN-1994;   94WO-US000888.
XX
PR   21-JAN-1993;   93US-00007115.
PR   19-JAN-1994;   94US-00184009.
XX
PA   (VIRO-) VIROGENETICS CORP.
XX
PI   Paoletti E,  Tartaglia J,  Cox WI;
XX
DR   WPI; 1994-263767/32.
XX
PT   Attenuated recombinant virus used for cancer therapy - comprises DNA
PT   encoding cytokine and/or tumour associated antigen.
XX
PS   Example 27; Fig 33; 232pp; English.
XX
CC   The sequences given in AAQ67879-80 are expression cassettes which contain
CC   the p40 and p35 subunits of human interleukin-12 (IL-12) under the
CC   control of the entomopox virus (EPV) promoter and the vaccinia E3L
CC   promoter, respectively. These sequences were used in the construction of
CC   an ALVAC-based recombinant virus containing the genes for the two
CC   subunits of human IL-12. The p40 subunit was amplified using primers
CC   JP202 and JP189 and placed under the control of the entomopox virus (EPV)
CC   42 kD promoter in plasmid PBSHIL12p40II. The p35 subunit was amplified
CC   using primers JP186 and JP201 and placed under the control of the
CC   vaccinia E3L promoter using primers JP218 and JP220. The expression
CC   cassette was isolated and ligated with pBSSK+ generating plasmid
CC   PBSHIL12p35II. The p35 and p40 expression cassettes were excised and
CC   assembled in pBSSK+ to give PBSHIL12 in which the two expression
CC   cassettes are orientated head-to-head relative to each other. The
CC   combination casette containing the poxvirus promoted genes for both IL-12
CC   subunits was excised from PBSHIL12 and cloned in to ALVAC C6 vector
CC   plasmid pC6L to give pC6HIL12. Recombination between this donor plasmid
CC   and ALVAC rescuing virus produced recombinant virus ALVAC+IL12, which
CC   contains both the human IL-12 genes in the C6 locus. The resulting virus
CC   may be used in a composition for inducing an antigenic or immunological
CC   response, ie. for immunisation against pathogens. (Updated on 25-MAR-2003
CC   to correct PN field.)
XX
SQ   Sequence 1018 BP; 283 A; 245 C; 260 G; 230 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 2;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 86
AAZ08510
ID   AAZ08510 standard; DNA; 1018 BP.
XX
AC   AAZ08510;
XX
DT   19-OCT-1999  (first entry)
XX
DE   EPV 42 kDa/human IL-12 P40 expression cassette.
XX
KW   Attenuated recombinant virus; cytokine; tumour associated antigen;
KW   NYVAC recombinant virus; ALVAC recombinant virus; gene therapy; rabies;
KW   cancer; tumour necrosis factor; nuclear phosphoprotein; p53; IL-2; GMCSF;
KW   interleukin; interferon; IFN-gamma; IL-4; melanoma associated antigen;
KW   carcinoembryonic antigen; immunisation; antigenic; poxvirus; influenza;
KW   immunological response; immunotherapy; vaccine; Newcastle Disease; ss.
XX
OS   Synthetic.
OS   pox virus.
OS   Homo sapiens.
OS   Unidentified.
XX
PN   US5942235-A.
XX
PD   24-AUG-1999.
XX
PF   02-JUN-1995;   95US-00458356.
XX
PR   24-DEC-1981;   81US-00334456.
PR   08-DEC-1982;   82US-00446824.
PR   19-JUN-1984;   84US-00622135.
PR   27-AUG-1987;   87US-00090209.
PR   28-AUG-1987;   87US-00090711.
PR   20-OCT-1987;   87US-00110335.
PR   25-APR-1988;   88US-00186054.
PR   23-AUG-1988;   88US-00234390.
PR   14-JUN-1990;   90US-00537882.
PR   14-JUN-1990;   90US-00537890.
PR   16-DEC-1991;   91US-00805567.
PR   03-MAR-1992;   92US-00847977.
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PR   06-MAR-1992;   92US-00847951.
PR   04-MAY-1992;   92US-00881995.
PR   22-JUL-1992;   92US-00918278.
PR   20-JAN-1993;   93US-00007115.
PR   19-JAN-1994;   94US-00184009.
PR   14-APR-1994;   94US-00228926.
PR   13-SEP-1994;   94US-00306259.
XX
PA   (HEAL-) HEALTH RES INC.
XX
PI   Paoletti E;
XX
DR   WPI; 1999-493494/41.
XX
PT   Recombinant poxviruses comprising exogenous DNA encoding antigenic
PT   determinants useful in immunotherapy to immunize against cancers and
PT   other diseases such as influenza, Newcastle Disease and rabies.
XX
PS   Example 27; Fig 33; 163pp; English.
XX
CC   The present invention describes a recombinant poxvirus (I), comprising
CC   exogenous DNA encoding an antigenic determinant of a pathogen which is
CC   then expressed in vivo in infected host cells after administration to a
CC   patient and therefore induces an immunological response. (I) may be used
CC   to vaccinate patients against a wide range of diseases and disorders
CC   depending on the type of antigen encoded by the exogenous DNA. (I) may be
CC   used to vaccinate against diseases such as rabies, influenza and
CC   Newcastle Disease. It is particularly useful for immunising against
CC   cancers. The poxvirus (I) also provides a means of manipulating
CC   lymphocytes and tumour cells for use in cell-based immunotherapeutic
CC   modalities for cancer. (I) also have enhanced safety compared to
CC   unattenuated viruses (attenuation reduces the virulence of the viruses)
CC   and known recombinant poxvirus vaccines. This increased level of safety
CC   reduces the possibility of a 'runaway' infection in the host and reduces
CC   the chance of transmission from vaccinated to unvaccinated individuals
CC   and contamination of the environment. The present sequence represents a
CC   EPV 42 kDa/human IL-12 P40 expression cassette used in the
CC   exemplification of the present invention
XX
SQ   Sequence 1018 BP; 283 A; 245 C; 260 G; 230 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 2;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 87
ADR21886
ID   ADR21886 standard; DNA; 1018 BP.
XX
AC   ADR21886;
XX
DT   04-NOV-2004  (first entry)
XX
DE   EPV 42kDa/human IL-12 expression cassette.
XX
KW   Cytostatic; Vaccine; recombinant poxvirus; nonessential region;
KW   attenuated avipox Virus; carcinoembryonic antigen; B7 protein;
KW   cancer therapy; ds; human; IL-12; EPV 42kDa; expression cassette.
XX
OS   Heliothis armigera entomopoxvirus.
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US6780407-B1.
XX
PD   24-AUG-2004.
XX
PF   15-SEP-2000; 2000US-00663667.
XX
PR   08-MAR-1989;   89US-00320471.
PR   14-FEB-1990;   90US-00478179.
PR   07-JAN-1991;   91US-00638080.
PR   07-MAR-1991;   91US-00666056.
PR   11-JUN-1991;   91US-00713967.
PR   16-DEC-1991;   91US-00805567.
PR   03-MAR-1992;   92US-00847977.
PR   06-MAR-1992;   92US-00847951.
PR   21-JAN-1993;   93US-00007115.
PR   19-JAN-1994;   94US-00184009.
PR   30-AUG-1995;   95US-00521016.
XX
PA   (AVET ) AVENTIS PASTEUR.
XX
PI   Paoletti E,  Tartaglia J,  Cox WI;
XX
DR   WPI; 2004-601998/58.
XX
PT   New recombinant poxvirus which is an attenuated avipox Virus that
PT   expresses an exogenous DNA encoding carcinoembryonic antigen and an
PT   exogenous DNA encoding B7 protein, useful for cancer therapy.
XX
PS   Example 27; SEQ ID NO 194; 181pp; English.
XX
CC   The invention describes a recombinant poxvirus containing exogenous DNA
CC   in a nonessential region of the poxvirus, where the poxvirus is an
CC   attenuated avipox Virus that expresses an exogenous DNA encoding
CC   carcinoembryonic antigen and an exogenous DNA encoding B7 protein. Also
CC   described are: a composition comprising a poxvirus above in admixture
CC   with a carrier; and expressing carcinoembryonic antigen and B7 protein in
CC   vivo comprising administering to a mammal the composition above.
CC   Disclosed are: making recombinant poxvirus defined above; recombinant
CC   poxvirus vaccine having an increased level of safety compared to known
CC   recombinant poxvirus vaccines; and a modified vector for expressing a
CC   gene product in a host. The recombinant poxvirus is useful for providing
CC   a recombinant poxvirus vaccine having an increased level of safety
CC   compared to known recombinant poxvirus vaccines. The recombinant poxvirus
CC   is useful for cancer therapy. This sequence represents a human IL-12
CC   expression cassette used in the creation of NYVAC rescue virus and
CC   canarypox virus vector ALVAC comprising the human IL-12 gene.
XX
SQ   Sequence 1018 BP; 283 A; 245 C; 260 G; 230 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 13;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 88
AAA70709
ID   AAA70709 standard; DNA; 1019 BP.
XX
AC   AAA70709;
XX
DT   15-DEC-2000  (first entry)
XX
DE   Bovine interleukin-12 p40 subunit gene.
XX
KW   Antiinfective; bovine; interleukin 12; IL12; heterodimer; infection; ss.
XX
OS   Bos taurus.
XX
FH   Key             Location/Qualifiers
FT   CDS             12. .995
FT                   /*tag=  a
FT                   /product= "IL-12 p40 subunit"
XX
PN   JP2000157274-A.
```

XX
PD 13-JUN-2000.
XX
PF 20-NOV-1998; 98JP-00331052.
XX
PR 20-NOV-1998; 98JP-00331052.
XX
PA (DAUC) DAIICHI PHARM CO LTD.
XX
DR WPI; 2000-468201/41.
DR P-PSDB; AAB15391.
XX
PT Preparation of bovine interleukin 12 comprising using a vector containing
PT the gene encoding it, useful for the prevention and treatment of chronic
PT and opportunistic infections.
XX
PS Example 1; Page 8-9; 11pp; Japanese.
XX
CC The invention relates to a method for the preparation of bovine
CC interleukin 12 (BoIL12). BoIL12 consists of a heterodimer of p35 and p40
CC subunits. BoIL12 is produced by introducing into a host cell, recombinant
CC vectors containing genes encoding the p35 and p40 subunits. This sequence
CC represents the coding region for the bovine IL12 p40 subunit. Interleukin
CC 12 is used for the prevention and treatment of chronic infections and
CC opportunistic infections
XX
SQ Sequence 1019 BP; 273 A; 248 C; 271 G; 227 T; 0 U; 0 Other;

Query Match 4.5%; Score 44; DB 3; Length 1019;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
||||||||||||||||||||||||||||||||||||||||||||
Db 675 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 718

RESULT 89
ADP88402
ID ADP88402 standard; cDNA; 1029 BP.
XX
AC ADP88402;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human interleukin-12 beta chain coding sequence.
XX
KW antiinflammatory; antiasthmatic; antiallergic; immunosuppressive;
KW antibacterial; protozoacide; gene therapy; expression vector;
KW interleukin; ecdysone-inducible promoter; ss; gene; interleukin-12;
KW human.
XX
OS Homo sapiens.
XX
PN WO2004052929-A2.
XX
PD 24-JUN-2004.
XX
PF 08-DEC-2003; 2003WO-IB006404.
XX
PR 06-DEC-2002; 2002GB-00028465.
XX
PA (UYBE-) UNIV QUEENS BELFAST.
XX
PI Vandenbroeck K, Alloza I;
XX
DR WPI; 2004-487887/46.
XX
PT New expression vector comprising DNA encoding a subunit of a dimeric form
PT of interleukin under transcriptional control of an ecdysone-inducible
PT promoter, useful in preparing a composition for treating e.g.,
PT inflammatory disease.
XX
PS Disclosure; Page 86-87; 87pp; English.
XX
CC The present invention relates to an expression vector comprising DNA
CC encoding a subunit of a dimeric form of interleukin under transcriptional
CC control of an ecdysone-inducible promoter. The expression vector is
CC useful in preparing a composition for treating a disease having a
CC pathogenesis which includes endogenous production of cytokine IL-12, IL-
CC 23 or IL-27, e.g., infectious diseases, bacterial, protozoal or virus-
CC induced inflammation, epithelial airway inflammation such as asthma,
CC allergic disease, or autoimmune disease such as multiple sclerosis or
CC inflammatory bowel disease. The present sequence is the coding sequence
CC of the human interleukin-12 beta chain used in the exemplification of the
CC invention.
XX
SQ Sequence 1029 BP; 275 A; 261 C; 267 G; 226 T; 0 U; 0 Other;

Query Match 4.5%; Score 44; DB 12; Length 1029;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
||||||||||||||||||||||||||||||||||||||||||||
Db 676 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 719

RESULT 90
AAF76880
ID AAF76880 standard; DNA; 1389 BP.
XX
AC AAF76880;
XX
DT 15-MAY-2001 (first entry)
XX
DE Human p40-IL-2 coding sequence.
XX
KW Human; p40-IL-2; interleukin-2; IL-2; antiviral; antibacterial;
KW antifungal; cytostatic; antiparasitic; vaccine; gene therapy;
KW fusion protein; protein complex; cytokine; immunoglobulin; cancer;
KW infection; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200110912-A1.
XX
PD 15-FEB-2001.
XX
PF 09-AUG-2000; 2000WO-US021715.
XX
PR 09-AUG-1999; 99US-0147924P.
XX
PA (LEXI-) LEXIGEN PHARM CORP.
XX
PI Gillies SD, Lo KM;
XX
DR WPI; 2001-191523/19.
XX
PT Novel multifunctional fusion protein or protein complexes useful for
PT treating cancer and viral infections, comprise two different cytokine
PT molecules and a targeting group.
XX
PS Example 1; Page 75-76; 90pp; English.
XX
CC The present sequence is given in a specification relating to
CC multifunctional fusion proteins and protein complexes comprising at least
CC two different cytokine molecules and a targeting group such as an
CC immunoglobulin. The fusion proteins and protein complexes are useful for
CC treating cancers, and bacterial, viral, fungal and parasitic infections.
CC They are also useful in gene therapy and as vaccines to prevent or treat
CC various diseases
XX
SQ Sequence 1389 BP; 413 A; 325 C; 327 G; 324 T; 0 U; 0 Other;

```
  Query Match             4.5%;  Score 44;  DB 4;  Length 1389;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 91
AAT77849
ID   AAT77849 standard; DNA; 1397 BP.
XX
AC   AAT77849;
XX
DT   25-MAR-2003  (revised)
DT   18-MAR-1998  (first entry)
XX
DE   40 kDa subunit of human cytotoxic lymphocyte maturation factor DNA.
XX
KW   Cytotoxic lymphocyte maturation factor; CLMF; 40 kDa subunit;
KW   interleukin-2; T-cell growth; antibody; lymphokine activated killer cell;
KW   CLMF bioactivity inhibition; affinity ligand; transplantation;
KW   cytotoxic T cell proliferation; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             41. .1027
FT                   /*tag=  a
XX
PN   EP790255-A2.
XX
PD   20-AUG-1997.
XX
PF   09-DEC-1990;   97EP-00104656.
XX
PR   22-DEC-1989;   89US-00455708.
PR   09-MAY-1990;   90US-00520935.
PR   27-AUG-1990;   90US-00572284.
PR   09-DEC-1990;   90EP-00123670.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Chizzonite RA,  Gately MK,  Gubler UA,  Hulmes JD,  Pan YE;
PI   Podlanski FJ,  Stern AS;
XX
DR   WPI; 1997-404698/38.
DR   P-PSDB; AAW24235.
XX
PT   Antibodies to cytotoxic lymphocyte maturation factor protein - useful as
PT   affinity ligands, assay reagents and medicaments.
XX
PS   Disclosure; Fig 25; 80pp; English.
XX
CC   The present DNA sequence encodes the 40 kDa subunit of cytotoxic
CC   lymphocyte maturation factor (CLMF) protein. The natural CLMF protein is
CC   a 75 kDa heterodimer, where the 2 subunits (see AAT77850 for the 35 kDa
CC   subunit) are bonded together via one or more disulphide bonds. CLMF
CC   protein is produced by a human B lyphoblastoid cell line. CLMF
CC   synergistically induces, in the presence of interleukin-2, the cytolytic
CC   activity of lymphokine activated killer cells. CLMF is also capable of
CC   stimulating T-cell growth. A novel antibody directed against an epitope
CC   of CLMF protein (see AAW24237 for epitope) is capable of neutralising
CC   and/or inhibiting CLMF bioactivity. This antibody may be used as an
CC   affinity ligand for purifying the CLMF protein. The antibody can also be
CC   used as an assay reagent for detecting the CLMF protein, and as a
CC   medicament for selectively blocking the proliferation and activation of
CC   cytotoxic T cells, e.g. in transplantation. (Updated on 25-MAR-2003 to
CC   correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 1397 BP; 390 A; 307 C; 333 G; 367 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 2;  Length 1397;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        701 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 744


RESULT 92
AAT97969
ID   AAT97969 standard; DNA; 1397 BP.
XX
AC   AAT97969;
XX
DT   25-MAR-2003  (revised)
DT   18-MAR-1998  (first entry)
XX
DE   40 kDa subunit of human cytotoxic lymphocyte maturation factor DNA.
XX
KW   Cytotoxic lymphocyte maturation factor; CLMF; 40 kDa subunit;
KW   interleukin-2; T-cell growth; antibody; lymphokine activated killer cell;
KW   CLMF bioactivity inhibition; affinity ligand; transplantation;
KW   cytotoxic T cell proliferation; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             41. .1027
FT                   /*tag=  a
XX
PN   EP790308-A1.
XX
PD   20-AUG-1997.
XX
PF   09-DEC-1990;   97EP-00104682.
XX
PR   22-DEC-1989;   89US-00455708.
PR   09-MAY-1990;   90US-00520935.
PR   27-AUG-1990;   90US-00572284.
PR   09-DEC-1990;   90EP-00123670.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Chizzonite RA,  Gately MK,  Gubler UA,  Hulmes JD,  Pan YE;
PI   Podlanski FJ,  Stern AS;
XX
DR   WPI; 1997-404733/38.
DR   P-PSDB; AAW36939.
XX
PT   Sub-unit of cytotoxic lymphocyte maturation factor protein - useful for
PT   producing protein and as antitumour agent.
XX
PS   Disclosure; Fig 25; 83pp; English.
XX
CC   The present DNA sequence encodes a 40 kDa subunit of cytotoxic lymphocyte
CC   maturation factor (CLMF) protein. The natural CLMF protein is a 75 kDa
CC   heterodimer, where the 2 subunits (see AAT97970 for the 35 kDa subunit)
CC   are bonded together via one or more disulphide bonds. CLMF protein is
CC   produced by a human B lyphoblastoid cell line. CLMF synergistically
CC   induces, in the presence of interleukin-2, the cytolytic activity of
CC   lymphokine activated killer cells. CLMF is also capable of stimulating T-
CC   cell growth. The subunits may be used for preparing the CLMF protein and
CC   for preparing medicants for antitumour therapy. (Updated on 25-MAR-2003
CC   to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 1397 BP; 390 A; 307 C; 333 G; 367 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 2;  Length 1397;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
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                    ||||||||||||||||||||||||||||||||||||||||||||
Db        701 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 744


RESULT 93
AAV00401
ID   AAV00401 standard; DNA; 1397 BP.
XX
AC   AAV00401;
XX
DT   25-MAR-2003  (revised)
DT   18-MAR-1998  (first entry)
XX
DE   40 kDa subunit of human cytotoxic lymphocyte maturation factor DNA.
XX
KW   Cytotoxic lymphocyte maturation factor; CLMF; 40 kDa subunit;
KW   interleukin-2; T-cell growth; antibody; lymphokine activated killer cell;
KW   CLMF bioactivity inhibition; affinity ligand; transplantation;
KW   cytotoxic T cell proliferation; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             41. .1027
FT                   /*tag=  a
XX
PN   EP790309-A1.
XX
PD   20-AUG-1997.
XX
PF   09-DEC-1990;   97EP-00104860.
XX
PR   22-DEC-1989;   89US-00455708.
PR   09-MAY-1990;   90US-00520935.
PR   27-AUG-1990;   90US-00572284.
PR   09-DEC-1990;   90EP-00123670.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Chizzonite RA,  Gately MK,  Gubler UA,  Hulmes J,  Pan YE;
PI   Podlanski FJ,  Stern AS,  Witte H;
XX
DR   WPI; 1997-404734/38.
DR   P-PSDB; AAW36941.
XX
PT   Sub-unit of cytotoxic lymphocyte maturation factor protein - useful for
PT   producing CLMF protein and as an antitumour agent.
XX
PS   Disclosure; Fig 25; 83pp; English.
XX
CC   The present DNA sequence encodes a novel 40 kDa subunit of cytotoxic
CC   lymphocyte maturation factor (CLMF) protein. The natural CLMF protein is
CC   a 75 kDa heterodimer, where the 2 subunits (see AAV00402 for the 35 kDa
CC   subunit) are bonded together via one or more disulphide bonds. CLMF
CC   protein is produced by a human B lyphoblastoid cell line. CLMF
CC   synergistically induces, in the presence of interleukin-2, the cytolytic
CC   activity of lymphokine activated killer cells. CLMF is also capable of
CC   stimulating T-cell growth. The subunits may be used for preparing the
CC   CLMF protein and for preparing medicants for antitumour therapy. (Updated
CC   on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC   PR field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 1397 BP; 390 A; 307 C; 333 G; 367 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 2;  Length 1397;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        701 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 744


RESULT 94
AAV37767
ID   AAV37767 standard; cDNA; 1397 BP.
XX
AC   AAV37767;
XX
DT   17-SEP-1998  (first entry)
XX
DE   Cytotoxic lymphocyte maturation factor 40 kD subunit encoding cDNA.
XX
KW   Cytotoxic lymphocyte maturation factor; CLMF; cytokine; synergize;
KW   interleukin 2; IL-2; human; lymphoblastoid cell; detection; purifying;
KW   proliferation; cytotoxic T cell; transplantation; antibody; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             41. .1027
FT                   /*tag=  a
FT                   /product= "CLMF 40 kD subunit"
XX
PN   US5780597-A.
XX
PD   14-JUL-1998.
XX
PF   02-JUN-1995;   95US-00460061.
XX
PR   22-DEC-1989;   89US-00455708.
PR   09-MAY-1990;   90US-00520935.
PR   27-AUG-1990;   90US-00572284.
PR   24-MAR-1992;   92US-00857023.
PR   02-MAR-1994;   94US-00205011.
XX
PA   (HOFF ) HOFFMANN LA ROCHE INC.
XX
PI   Podlaski FJ,  Stern AS,  Gately MK,  Pan YE,  Hulmes JD;
PI   Chizzonite RA,  Gubler UA;
XX
DR   WPI; 1998-413150/35.
DR   P-PSDB; AAW58725.
XX
PT   New antibodies to cytotoxic lymphocyte maturation factor - useful for
PT   detecting, purifying, and/or blocking proliferation and activation of
PT   cytotoxic T cells, such as in transplantation(s).
XX
PS   Example 10; Fig 25; 71pp; English.
XX
CC   An isolated antibody has been developed which binds specifically to
CC   cytotoxic lymphocyte maturation factor (CLMF) and neutralises CLMF
CC   induced proliferation by more than 50% in a CLMF dependent T cell growth
CC   assay and/or inhibits binding of at least 60% of the factor to
CC   phytohaemagglutinin (PHA) activated peripheral blood lymphocyte (PBL)
CC   blasts as determined in a CLMF receptor binding assay. CLMF is a
CC   heterodimeric protein having a molecular weight band of 75 kD, determined
CC   by sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE)
CC   under non-reducing and/or reducing conditions, providing a first subunit
CC   having a molecular weight band of 40 kD and a second subunit having a
CC   molecular weight of 35 kD. The present sequence encodes the CLMF 40 kD
CC   subunit, from an example of the present invention. The antibody can be
CC   used for the purification and/or detection of CLMF. It is also used in
CC   therapeutic treatments which require selective blocking of proliferation
CC   and activation of cytotoxic T cells (CTLs) such as in transplantation
XX
SQ   Sequence 1397 BP; 390 A; 309 C; 333 G; 365 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 2;  Length 1397;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        701 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 744
```

```
RESULT 95
ADG39387
ID   ADG39387 standard; DNA; 1397 BP.
XX
AC   ADG39387;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human cytotoxic lymphocyte maturation factor, CLMF, 40 kDa subunit DNA.
XX
KW   ds; gene; human; cytotoxic lymphocyte maturation factor; CLMF;
KW   activated T-cell stimulator; natural killer cell stimulator;
KW   immunoenhancer; antitumour; tumour; cancer.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             41. .1027
FT                   /*tag=  a
FT                   /product= "CLMF 40 kDa subunit"
XX
PN   US2003204059-A1.
XX
PD   30-OCT-2003.
XX
PF   08-OCT-2002; 2002US-00267565.
XX
PR   22-DEC-1989;   89US-00455708.
PR   09-MAY-1990;   90US-00520935.
PR   27-AUG-1990;   90US-00572284.
PR   24-MAR-1992;   92US-00857023.
PR   02-MAR-1994;   94US-00205011.
PR   02-JUN-1995;   95US-00459151.
PR   22-SEP-1999;   99US-00401839.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CIE SA F.
XX
PI   Gately MK,  Gubler UA,  Hulmes JD,  Podlaski FJ,  Stern AS;
PI   Chizzonite RA,  Pan YE;
XX
DR   WPI; 2004-010534/01.
DR   P-PSDB; ADG39388.
XX
PT   Novel protein comprising cytotoxic lymphocyte maturation factor in
PT   substantially pure form or protein which exhibits cytotoxic lymphocyte
PT   maturation factor activity, useful as antitumor and immunoenhancing
PT   agent.
XX
PS   Disclosure; Fig 25; 74pp; English.
XX
CC   The invention relates to a protein which comprises a cytotoxic lymphocyte
CC   maturation factor (CLMF). The protein is useful for stimulating activated
CC   T-cells which involves treating T-cells with the protein. The method
CC   further involves treating the activated T-cells with IL2 or its
CC   biologically active fragment. The protein is useful for stimulating
CC   natural killer cells which involves treating the natural killer cells
CC   with the protein. The protein has immunoenhancing and antitumour effects
CC   when used as single therapeutic agent in vivo. The present sequence is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 1397 BP; 390 A; 309 C; 333 G; 365 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 12;  Length 1397;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        701 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 744
```

```
RESULT 96
ADO03758
ID   ADO03758 standard; cDNA; 1397 BP.
XX
AC   ADO03758;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human CLMF 40kDa subunit cDNA.
XX
KW   pharmaceutical composition; T cell growth factor assay; cytokine;
KW   cytokine lymphocyte maturation factor; CLMF; interleukin-12; IL-12;
KW   NC-37 B lymphoblastoid cell; T-cell growth stimulator; human; gene; ss;
KW   40 kDa subunit.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             41. .1027
FT                   /*tag=  b
FT                   /product= "CLMF 40 kDa subunit"
FT                   /note= "Cytotoxic Lymphocyte Maturation Factor"
FT   sig_peptide     41. .106
FT                   /*tag=  a
FT   mat_peptide     107. .1024
FT                   /*tag=  c
FT                   /note= "Mature CLMF 40 kDa subunit"
XX
PN   US6683046-B1.
XX
PD   27-JAN-2004.
XX
PF   02-JUN-1995;   95US-00459151.
XX
PR   22-DEC-1989;   89US-00455708.
PR   09-MAY-1990;   90US-00520935.
PR   27-AUG-1990;   90US-00572284.
PR   24-MAR-1992;   92US-00857023.
PR   02-MAR-1994;   94US-00205011.
XX
PA   (HOFF ) HOFFMANN LA ROCHE INC.
XX
PI   Gately MK,  Gubler UA,  Hulmes JD,  Podlaski FJ,  Stern AS;
PI   Chizzonite RA,  Pan YE;
XX
DR   WPI; 2004-118577/12.
DR   P-PSDB; ADO03759, ADO03795.
XX
PT   Pharmaceutical composition useful for activating T cell growth factors in
PT   assays comprises heterodimeric protein comprising first and second
PT   subunits and carrier.
XX
PS   Disclosure; Fig 25; 72pp; English.
XX
CC   The invention describes a pharmaceutical composition active in a T cell
CC   growth factor assay. The pharmaceutical composition comprises a
CC   heterodimeric protein having a molecular weight of 75 kDa as determined
CC   by Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE)
CC   under non-reducing conditions, and under reducing conditions, providing a
CC   first subunit having a molecular weight of 40 kDa as determined by (SDS-
CC   PAGE), and having a fully defined sequence of 306 amino acids as given in
CC   the specification, and second subunit having a molecular weight of 35 kDa
CC   as determined by (SDS-PAGE). Also described are: a novel cytokine protein
CC   called Cytokine lymphocyte maturation factor (CLMF) or interleukin-12 (IL
CC   -12) synthesised by mammalian cells, particularly human NC-37 B
CC   lymphoblastoid cells, and capable of stimulating T-cell growth; and
CC   monoclonal antibodies directed against (CLMF). (I) is useful as a
CC   pharmaceutical composition which is active in a T cell growth factor
CC   assay. This sequence encodes human cytotoxic lymphocyte maturation factor
CC   (CLMF) 40 kDa subunit.
XX
SQ   Sequence 1397 BP; 390 A; 309 C; 333 G; 365 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 12;  Length 1397;
```

```
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        701 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 744


RESULT 97
AAZ40021
ID   AAZ40021 standard; DNA; 1399 BP.
XX
AC   AAZ40021;
XX
DT   14-FEB-2000  (first entry)
XX
DE   Human p40 coding sequence.
XX
KW   Interleukin-12; IL-12; fusion protein; IL-12 p35 subunit; B7 protein;
KW   IL-12 p40 subunit; gene therapy; tumour; leukaemia; ss.
XX
OS   Homo sapiens.
XX
PN   US5994104-A.
XX
PD   30-NOV-1999.
XX
PF   08-NOV-1996;   96US-00751767.
XX
PR   08-NOV-1996;   96US-00751767.
XX
PA   (UNLO ) ROYAL FREE HOSPITAL SCHOOL MED.
XX
PI   Anderson RJ,  Prentice HG,  Macdonald ID;
XX
DR   WPI; 2000-038261/03.
DR   P-PSDB; AAY54919.
XX
PT   Nucleic acid constructs encoding interleukin-12 fusion proteins useful
PT   for treating leukemia and other cancers.
XX
PS   Example; Fig 9; 73pp; English.
XX
CC   This sequence encodes the human p40 protein sequence. The invention
CC   relates to an isolated nucleic acid construct (I) comprising a region
CC   encoding an interleukin-12 (IL-12) fusion protein (comprising an IL-12
CC   p35 subunit, an IL-12 p40 subunit and a linker peptide (joining the
CC   subunits)) and a region encoding a B7 protein. (I) may be used to produce
CC   IL-12 fusion proteins according to standard recombinant DNA
CC   methodologies. The fusion proteins may be produced either in vitro in a
CC   fermentation culture or in vivo as part of a gene therapy protocol (in
CC   this case (I) is used to transform a patients cells, which then secrete
CC   the functional polypeptide to supplement the patients own production of
CC   IL-12 or to rectify mutations which lead to the expression of inactive
CC   polypeptides). The fusion proteins produced in this way may be used to
CC   treat any disease which responds to IL-12 such as tumours (both solid and
CC   dispersed of the kidney, breast, colon, ovarian and cervical tumours and
CC   melanomas) and in particular, tumours of the blood such as leukaemia.
CC   Alternatively, the polypeptides may be used as antigens in the production
CC   of antibodies to IL-12 and to assay for agonists and antagonists of its
CC   activity. The antibodies and antagonists may be used to inhibit the
CC   activity of IL-12. (I) may also be used diagnostically as a probe which
CC   hybridizes to sequences encoding IL-12 and the antibodies may be used to
CC   detect the presence of IL-12 polypeptides in samples. They may be used
CC   diagnostically to quantitate the expression of the polypeptide by
CC   patients and hence which subjects may be in need of restorative therapy.
XX
SQ   Sequence 1399 BP; 390 A; 310 C; 333 G; 366 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 3;  Length 1399;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        703 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 746


RESULT 98
ADY86632
ID   ADY86632 standard; DNA; 1399 BP.
XX
AC   ADY86632;
XX
DT   02-JUN-2005  (first entry)
XX
DE   Human interleukin-12 40 kDa (IL-12 p40) subunit gene.
XX
KW   Gene expression; screening; multiple sclerosis; neuroprotective;
KW   immune disorder; neurological disease; DNA microarray; gene; ds;
KW   interleukin-12; lymphokine; cytokine.
XX
OS   Homo sapiens.
XX
PN   US2005064483-A1.
XX
PD   24-MAR-2005.
XX
PF   30-AUG-2004; 2004US-00929182.
XX
PR   28-AUG-2003; 2003US-0498731P.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   Zang JZ,  Hong J;
XX
DR   WPI; 2005-252668/26.
DR   GENBANK; M65272.
XX
PT   Monitoring multiple sclerosis patient taking beta-interferon or
PT   glatiramer acetate to predict treatment response by determining
PT   expression profile of inflammatory nucleic acids using RNA of patient and
PT   comparing to control.
XX
PS   Claim 1; SEQ ID NO 22; 73pp; English.
XX
CC   The present invention relates to gene expression profiling technology to
CC   quantatively measure the expression profiles of genes selected based on
CC   their role in inflammation and their susceptibility to regulation by
CC   current multiple sclerosis (MS) treatment agents by isolating RNA from
CC   peripheral blood mononuclear cells (PBMC) of patient. The invention is
CC   particularly useful for monitoring a multiple sclerosis patient taking
CC   interferon-beta (IFN-beta) or glatiramer acetate (GA) in order to predict
CC   treatment response. The present sequence is human interleukin-12 40 kDa
CC   (IL-12 p40) subunit gene. This gene is used to illustrate the evaluation
CC   of PBMC responses to in Vitro treatment with IFN-beta or GA agents by
CC   gene expression profiling technology.
XX
SQ   Sequence 1399 BP; 390 A; 310 C; 333 G; 366 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 14;  Length 1399;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        703 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 746


RESULT 99
ADQ14472
ID   ADQ14472 standard; DNA; 1580 BP.
XX
AC   ADQ14472;
XX
DT   07-OCT-2004  (first entry)
```

```
XX
DE   DNA encoding human hyperkine protein.
XX
KW   Wound healing; agonist; antagonist; interleukin-23; IL-23; vulnerary;
KW   cytokine; human; hyperkine; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             7. .1572
FT                   /*tag=  a
FT                   /product= "Human hyperkine protein"
XX
PN   WO2004058178-A2.
XX
PD   15-JUL-2004.
XX
PF   18-DEC-2003; 2003WO-US040937.
XX
PR   23-DEC-2002; 2002US-0436274P.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Bowman EP,  Chen S,  Cua DJ;
XX
DR   WPI; 2004-525781/50.
DR   P-PSDB; ADQ14473.
XX
PT   Treating inflammatory skin disorders or improving wound healing comprises
PT   administering to a subject an agonist or antagonist of Interleukin-23.
XX
PS   Example; SEQ ID NO 7; 52pp; English.
XX
CC   The invention relates to a novel method for treating or improving wound
CC   healing. The method comprises administering to a subject an agonist or
CC   antagonist of interleukin (IL)-23. The invention further comprises: an
CC   agonist of IL-23 derived from the binding site of an antibody that
CC   specifically binds to an IL-23 receptor; and a kit comprising the agonist
CC   and a compartment or instructions for use or disposal. The interleukin-23
CC   agents have vulnerary activity. The method is useful for treating or
CC   improving wound healing. This polynucleotide sequence represents the
CC   nucleic acid encoding a hyperkine protein used in the wound healing
CC   method of the invention.
XX
SQ   Sequence 1580 BP; 399 A; 411 C; 426 G; 344 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 12;  Length 1580;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        673 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 716


RESULT 100
AAA92406
ID   AAA92406 standard; cDNA; 2300 BP.
XX
AC   AAA92406;
XX
DT   15-JAN-2001  (first entry)
XX
DE   Human interleukin 2 encoding p35 and p40 proteins.
XX
KW   Human; interleukin 2; IL-2; p35; p40; immune response; tumour;
KW   infectious disease; bacteria; virus; parasite; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             19. .678
FT                   /*tag=  a
FT                   /product= "p35"
FT   CDS             1304. .2290
FT                   /*tag=  b
FT                   /product= "p40"
XX
PN   CN1258740-A.
XX
PD   05-JUL-2000.
XX
PF   31-DEC-1998;   98CN-00126748.
XX
PR   31-DEC-1998;   98CN-00126748.
XX
PA   (HUAC-) HUACHEN BIOLOGICAL TECHNOLOGY INST SHANG.
XX
PI   Cao X,  Zhang W,  Ju D;
XX
DR   WPI; 2000-558956/52.
DR   P-PSDB; AAB23795, AAB23796.
XX
PT   Recombinant adenovirus expressing human interleukin-12 and its
PT   preparation and use.
XX
PS   Example 3; Fig 4; 27pp; Chinese.
XX
CC   The present invention describes a recombinant adenovirus and its
CC   preparation and use, as well as medicine composite containing the
CC   recombinant adenovirus. The recombinant adenovirus is used clinically,
CC   has the advantages of low cost, easy use and high efficiency and is
CC   especially suitable for immune treatment of tumour and infectious
CC   diseases caused by bacteria, virus and parasite. The present sequence
CC   represents human interleukin 2 (IL-2) cDNA which encodes the p35 and p40
CC   proteins, which is used in an example from the present invention
XX
SQ   Sequence 2300 BP; 598 A; 591 C; 571 G; 540 T; 0 U; 0 Other;

  Query Match             4.5%;  Score 44;  DB 3;  Length 2300;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db       1964 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 2007


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OM nucleic - nucleic search, using sw model

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Searched: 48236798 seqs, 27959665780 residues

Word size : 1

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	4	44	4.5	736	5	CD559453	CD559453 AGENCOURT
c	5	44	4.5	762	5	CD559451	CD559451 AGENCOURT
c	6	44	4.5	766	5	CD559449	CD559449 AGENCOURT
c	7	44	4.5	772	5	CD559450	CD559450 AGENCOURT
c	8	44	4.5	785	5	CD559448	CD559448 AGENCOURT
	9	41	4.2	772	5	CD559604	CD559604 AGENCOURT
	10	39	4.0	724	5	CD559603	CD559603 AGENCOURT
	11	39	4.0	745	5	CD559602	CD559602 AGENCOURT
	12	39	4.0	747	5	CD559607	CD559607 AGENCOURT
c	13	39	4.0	754	5	CD559452	CD559452 AGENCOURT
	14	39	4.0	756	5	CK130264	CK130264 AGENCOURT
	15	39	4.0	1042	5	CD559606	CD559606 AGENCOURT
	16	33	3.3	252	10	DV799576	DV799576 est_t_tru
	17	30	3.0	1839	6	AK162981	AK162981 Mus muscu
	18	30	3.0	2908	6	AK155593	AK155593 Mus muscu
	19	29	2.9	346	4	BY164658	BY164658 BY164658
	20	29	2.9	355	4	BY221814	BY221814 BY221814
	21	29	2.9	375	4	BY222535	BY222535 BY222535
	22	29	2.9	387	4	BY167742	BY167742 BY167742
	23	29	2.9	417	8	CO949904	CO949904 UMC-pd12c
	24	29	2.9	423	4	BY218447	BY218447 BY218447
	25	29	2.9	432	4	BY154173	BY154173 BY154173
	26	29	2.9	475	7	BF704417	BF704417 MI-P-E6-a
c	27	29	2.9	569	11	AZ853726	AZ853726 2M0157M01
	28	29	2.9	649	5	CJ134671	CJ134671 CJ134671
	29	29	2.9	666	4	BY749553	BY749553 BY749553
	30	28	2.8	535	11	AZ441303	AZ441303 1M0232M24
c	31	27	2.7	668	14	AG079702	AG079702 Pan trogl
	32	26	2.6	672	13	DU179885	DU179885 109855349
c	33	24	2.4	414	13	CW885638	CW885638 RPCI42_10
c	34	21	2.1	330	13	CW047416	CW047416 104_285_1
c	35	21	2.1	374	10	T99581	T99581 ye65d08.r1
c	36	21	2.1	508	8	CN071927	CN071927 1021022B0
c	37	21	2.1	509	5	CF059708	CF059708 QCS15g07.
c	38	21	2.1	509	5	CF060247	CF060247 QCS5b05.y
c	39	21	2.1	510	5	CF059885	CF059885 QCS18b04.
c	40	21	2.1	521	2	BI431328	BI431328 949071E08
c	41	21	2.1	523	1	AI491671	AI491671 486020E06
c	42	21	2.1	553	7	AW566435	AW566435 660074D12
	43	21	2.1	566	3	BQ294193	BQ294193 1091026G0
c	44	21	2.1	588	4	CA627255	CA627255 w11n.pk15
	45	21	2.1	594	7	AW573354	AW573354 660074D12
	46	21	2.1	599	2	BI478972	BI478972 949071E08
c	47	21	2.1	632	4	CA293522	CA293522 SCSGLV100
c	48	21	2.1	633	9	DN207344	DN207344 MEST847_H
c	49	21	2.1	637	3	BQ294192	BQ294192 1091026G0
c	50	21	2.1	692	9	DN222336	DN222336 MEST1126_
c	51	21	2.1	693	9	DN220924	DN220924 MEST1104_
c	52	21	2.1	694	9	DN219584	DN219584 MEST1083_
c	53	21	2.1	716	10	DV622355	DV622355 IV-1091-4
c	54	21	2.1	724	6	AY112414	AY112414 Zea mays
c	55	21	2.1	743	12	CL163765	CL163765 104_357_1
	56	21	2.1	755	14	AG462380	AG462380 Mus muscu
c	57	21	2.1	762	12	CC698019	CC698019 OGWBY19TH
	58	21	2.1	803	12	CG122646	CG122646 PUIMH25TB
c	59	21	2.1	837	12	CG134486	CG134486 PUFSJ61TD
c	60	21	2.1	853	12	CC927699	CC927699 ZMMBBc053
c	61	21	2.1	895	7	BF241716	BF241716 601879850
c	62	21	2.1	983	12	CG033595	CG033595 PUKDR51TB
	63	21	2.1	987	12	BZ782656	BZ782656 PUFDX77TB
c	64	21	2.1	999	12	BZ782662	BZ782662 PUFDX77TD
	65	20	2.0	366	12	CE034167	CE034167 tigr-gss-
	66	20	2.0	376	9	DN901347	DN901347 naq18f07.
	67	20	2.0	454	11	BH772784	BH772784 4CTF CTSS
	68	20	2.0	460	3	BM849607	BM849607 K-EST0129
c	69	20	2.0	467	9	DN504486	DN504486 HL0100090
	70	20	2.0	479	2	BI983815	BI983815 fu08a02.x
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	72	20	2.0	488	1	AI292392	AI292392 NYZ036 Ap
	73	20	2.0	496	2	BI476340	BI476340 fq26h04.x
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	75	20	2.0	515	4	CB179502	CB179502 EST0595 Z
	76	20	2.0	520	2	BM270069	BM270069 sak24b12.
	77	20	2.0	526	3	BQ777940	BQ777940 il39a02.y
c	78	20	2.0	528	13	CW070565	CW070565 104_321_1
	79	20	2.0	535	5	CK902268	CK902268 il39a02.x
c	80	20	2.0	555	8	CO854235	CO854235 LM_SH5_00
	81	20	2.0	556	2	BI785024	BI785024 saf96h10.
	82	20	2.0	563	1	AL956562	AL956562 AL956562
	83	20	2.0	564	2	BJ030774	BJ030774 BJ030774
	84	20	2.0	570	1	AI666909	AI666909 fd16d08.x
	85	20	2.0	571	2	BJ032049	BJ032049 BJ032049
	86	20	2.0	578	2	BJ627752	BJ627752 BJ627752
c	87	20	2.0	621	9	CX600301	CX600301 CT020026A
	88	20	2.0	633	1	AL900775	AL900775 AL900775
c	89	20	2.0	646	12	CE454520	CE454520 tigr-gss-
	90	20	2.0	649	13	CZ709509	CZ709509 OC__Ba003
	91	20	2.0	654	2	BM096034	BM096034 fv29g12.x
	92	20	2.0	667	2	BJ042592	BJ042592 BJ042592

	93	20	2.0	667	14	CT167835 CT167835 Sus scrof
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c	95	20	2.0	690	11	AZ424475 AZ424475 1M0204A12
c	96	20	2.0	696	11	BZ240832 BZ240832 CH230-272
	97	20	2.0	698	2	BG740695 BG740695 602631544
c	98	20	2.0	701	10	DT267303 DT267303 JGI_CAAV1
	99	20	2.0	701	10	DT267304 DT267304 JGI_CAAV1
c	100	20	2.0	719	10	DT283860 DT283860 JGI_CAAV1
c	101	20	2.0	724	13	CZ313704 ZMMBF0012
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	103	20	2.0	752	9	CX474004 CX474004 JGI_XZG49
	104	20	2.0	760	9	CX401138 CX401138 JGI_XZT49
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c	106	20	2.0	777	14	AG472962 AG472962 Mus muscu
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c	110	20	2.0	794	12	CC526964 CC526964 CH240_401
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	112	20	2.0	819	12	CG433498 CG433498 ZMMBBc004
	113	20	2.0	837	12	CG424739 CG424739 ZMMBBc004
	114	20	2.0	862	9	CX490517 CX490517 JGI_XZG33
	115	20	2.0	866	4	BX719908 BX719908 BX719908
	116	20	2.0	876	11	BZ274756 BZ274756 CH230-450
c	117	20	2.0	879	3	BU134895 BU134895 603121826
	118	20	2.0	879	12	CG419488 CG419488 ZMMBBc002
	119	20	2.0	881	8	CR579278 CR579278 CR579278
	120	20	2.0	884	12	CG152443 CG152443 PUFQD62TB
	121	20	2.0	885	9	CX414760 CX414760 JGI_XZT55
	122	20	2.0	890	9	CX375663 CX375663 JGI_XZT59
	123	20	2.0	893	4	CA792037 CA792037 AGENCOURT
	124	20	2.0	893	12	CC969890 CC969890 ZUAGO82TV
c	125	20	2.0	897	11	BZ169807 BZ169807 CH230-463
c	126	20	2.0	900	12	CC001138 CC001138 PUEAP48TD
	127	20	2.0	905	7	BE533710 BE533710 601232852
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	129	20	2.0	927	14	DX042542 DX042542 KBrB042P0
	130	20	2.0	947	12	CG701262 CG701262 ZMMBBc017
c	131	20	2.0	956	10	DW611860 DW611860 CLJ265-F0
c	132	20	2.0	960	12	CG152445 CG152445 PUFQD62TD
	133	20	2.0	965	13	CL304216 CL304216 ZMMBBb009
c	134	20	2.0	985	10	DW657589 DW657589 CLJ397-G1
c	135	20	2.0	998	14	DU878040 DU878040 279669 To
c	136	20	2.0	1003	12	CG222548 CG222548 OG0DT06TV
	137	20	2.0	1048	12	CG698770 CG698770 ZMMBBc011
	138	20	2.0	1049	10	DW611861 DW611861 CLJ265-F0
	139	20	2.0	1082	12	CC175278 CC175278 ZMMBBc029
c	140	20	2.0	1204	9	DN661975 DN661975 CFW06-B07
	141	20	2.0	1595	2	BG256021 BG256021 602367310
c	142	19	1.9	224	12	BZ779302 BZ779302 ih87h11.g
	143	19	1.9	234	4	CD131385 CD131385 MG1-0012T
c	144	19	1.9	236	8	CO314283 CO314283 EK235626.
c	145	19	1.9	255	8	CV827114 CV827114 EST001412
	146	19	1.9	293	3	BP949628 BP949628 BP949628
c	147	19	1.9	300	1	AA714194 AA714194 nw05h05.s
c	148	19	1.9	328	14	CNS00P65 AL084107 Arabidops
c	149	19	1.9	346	2	BJ694940 BJ694940 BJ694940
c	150	19	1.9	368	3	BU661053 BU661053 cl67c12.z
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	152	19	1.9	369	11	AZ884788 AZ884788 RPCI-23-1
c	153	19	1.9	373	5	CK045056 CK045056 51163rsic
	154	19	1.9	377	4	CA362220 CA362220 636256 NC
c	155	19	1.9	378	2	BI594826 BI594826 As_tgz_44
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	157	19	1.9	382	8	CN921966 CN921966 000409AEL
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c	159	19	1.9	394	7	AW042400 AW042400 614028B11
	160	19	1.9	394	9	DR059212 DR059212 RTNIT1_16
	161	19	1.9	413	9	DR177926 DR177926 RTMNUT1_8
c	162	19	1.9	415	5	CF917109 CF917109 Bflor498.
	163	19	1.9	429	14	CR204657 CR204657 Reverse s
c	164	19	1.9	434	4	CB793439 CB793439 AMGNNUC:S
c	165	19	1.9	434	4	CB793440 CB793440 AMGNNUC:S
	166	19	1.9	434	12	CE700465 CE700465 tigr-gss-
c	167	19	1.9	439	2	BI385075 BI385075 BFLG2_003
	168	19	1.9	444	9	CX646589 CX646589 COLD1_10_
c	169	19	1.9	448	5	CI357610 CI357610 CI357610
	170	19	1.9	493	8	CN619918 CN619918 TgESTzym9
	171	19	1.9	496	1	AI871624 AI871624 we28d11.x
c	172	19	1.9	505	11	AZ635629 AZ635629 1M0493D09
	173	19	1.9	510	10	DR446638 DR446638 AR1034E03
c	174	19	1.9	511	12	CG991849 CG991849 CH240_151
c	175	19	1.9	512	5	CK057894 CK057894 61316rsic
c	176	19	1.9	512	13	CL955283 CL955283 OsIRUA000
c	177	19	1.9	517	10	DR787178 DR787178 ZM_BFb000
	178	19	1.9	523	14	AG956728 AG956728 Drosophil
c	179	19	1.9	526	8	CO783019 CO783019 BL016D_D1
	180	19	1.9	530	13	CL259985 CL259985 ZMMBBb061
c	181	19	1.9	533	5	CI183750 CI183750 CI183750
	182	19	1.9	534	5	CK737831 CK737831 TgESTzyj8
	183	19	1.9	535	2	BF922172 BF922172 MR4-NT014
	184	19	1.9	536	7	AW073130 AW073130 wy94a10.x
	185	19	1.9	537	7	BF394460 BF394460 UI-R-CA0-
	186	19	1.9	541	3	BP949994 BP949994 BP949994
	187	19	1.9	543	9	DA100433 DA100433 DA100433
	188	19	1.9	543	9	DA100435 DA100435 DA100435
c	189	19	1.9	543	14	CT107392 CT107392 Sus scrof
	190	19	1.9	551	4	BW536306 BW536306 BW536306
c	191	19	1.9	555	8	CO700056 CO700056 DG32-170e
c	192	19	1.9	562	2	BJ692987 BJ692987 BJ692987
	193	19	1.9	566	3	BQ906981 BQ906981 M023C03 O
	194	19	1.9	571	2	BJ524824 BJ524824 BJ524824
	195	19	1.9	573	9	DA674546 DA674546 DA674546
	196	19	1.9	577	14	AG961043 AG961043 Drosophil
	197	19	1.9	582	3	BP280239 BP280239 BP280239
	198	19	1.9	583	3	BP280282 BP280282 BP280282
c	199	19	1.9	587	10	DR787069 DR787069 ZM_BFb000
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ALIGNMENTS

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LOCUS       CE093997                700 bp    DNA     linear   GSS 24-SEP-2003
DEFINITION  tigr-gss-dog-17000359883851 Dog Library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION   CE093997
VERSION     CE093997.1  GI:35160844
KEYWORDS    GSS.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 700)
  AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
            Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
            Venter,J.C.
  TITLE     The dog genome: survey sequencing and comparative analysis
  JOURNAL   Science 301 (5641), 1898-1903 (2003)
   PUBMED   14512627
COMMENT     Contact: Kirkness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirknes@tigr.org
            Class: shotgun.
FEATURES             Location/Qualifiers
     source          1. .700
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /strain="Standard Poodle"
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                     /db_xref="taxon:9615"
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                     peripheral blood"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 3.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        360 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 419

Qy        597 CTGCCC 602
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Db        420 CTGCCC 425


RESULT 2
CD559454/c
LOCUS       CD559454                725 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14497089 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971868 5', mRNA sequence.
ACCESSION   CD559454
VERSION     CD559454.2  GI:38453478
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 725)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585522.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: g  column: 11
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            High quality sequence stop: 573.
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971868"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             4.5%;  Score 44;  DB 5;  Length 725;
  Best Local Similarity   100.0%;  Pred. No. 5.2e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db        426 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 383


RESULT 3
CD559605
LOCUS       CD559605                735 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496534 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971870 5', mRNA sequence.
ACCESSION   CD559605
VERSION     CD559605.2  GI:38558937
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 735)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585673.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 01
            High quality sequence stop: 709.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971870"
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                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
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a Note: this is a NIH_MGC Library."
ORIGIN

Query Match 4.5%; Score 44; DB 5; Length 735;
Best Local Similarity 100.0%; Pred. No. 5.3e-12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db 677 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 720

RESULT 4
CD559453/c
LOCUS CD559453 736 bp mRNA linear EST 19-NOV-2003
DEFINITION AGENCOURT_14497154 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971869 5', mRNA sequence.
ACCESSION CD559453
VERSION CD559453.2 GI:38453475
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 736)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585521.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: g column: 12
High quality sequence stop: 683.
FEATURES Location/Qualifiers
source 1. .736
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971869"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."
ORIGIN

Query Match 4.5%; Score 44; DB 5; Length 736;
Best Local Similarity 100.0%; Pred. No. 5.3e-12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db 401 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 358

RESULT 5
CD559451/c
LOCUS CD559451 762 bp mRNA linear EST 19-NOV-2003
DEFINITION AGENCOURT_14496580 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971871 5', mRNA sequence.
ACCESSION CD559451
VERSION CD559451.2 GI:38453471
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 762)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585519.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: h column: 02
High quality sequence start: 38
High quality sequence stop: 761.
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971871"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."
ORIGIN

Query Match 4.5%; Score 44; DB 5; Length 762;
Best Local Similarity 100.0%; Pred. No. 5.3e-12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        422 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 379


RESULT 6
CD559449/c
LOCUS       CD559449                766 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496649 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971873 5', mRNA sequence.
ACCESSION   CD559449
VERSION     CD559449.2  GI:38453467
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 766)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585517.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 04
            High quality sequence stop: 641.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971873"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             4.5%;  Score 44;  DB 5;  Length 766;
  Best Local Similarity   100.0%;  Pred. No. 5.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db        414 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 371


RESULT 7
CD559450/c
LOCUS       CD559450                772 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496612 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971872 5', mRNA sequence.
ACCESSION   CD559450
VERSION     CD559450.2  GI:38453469
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 772)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585518.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 03
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            High quality sequence stop: 753.
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                     /clone="IMAGE:6971872"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             4.5%;  Score 44;  DB 5;  Length 772;
  Best Local Similarity   100.0%;  Pred. No. 5.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db        425 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 382


RESULT 8
CD559448/c
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LOCUS       CD559448                785 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496712 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971874 5', mRNA sequence.
ACCESSION   CD559448
VERSION     CD559448.2  GI:38453466
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 785)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585516.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 05
            High quality sequence stop: 696.
FEATURES             Location/Qualifiers
     source          1. .785
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971874"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             4.5%;  Score 44;  DB 5;  Length 785;
  Best Local Similarity   100.0%;  Pred. No. 5.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        416 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 373


RESULT 9
CD559604
LOCUS       CD559604                772 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496598 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971872 5', mRNA sequence.
ACCESSION   CD559604
VERSION     CD559604.2  GI:38558934
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 772)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585672.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 03
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            High quality sequence stop: 750.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971872"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             4.2%;  Score 41;  DB 5;  Length 772;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-10;
  Matches   41;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAA 704
              |||||||||||||||||||||||||||||||||||||||||
Db        698 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAA 738


RESULT 10
CD559603
LOCUS       CD559603                724 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496630 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971873 5', mRNA sequence.
ACCESSION   CD559603
VERSION     CD559603.2  GI:38558932
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
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```
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 724)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585671.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 04
            High quality sequence stop: 525.
FEATURES             Location/Qualifiers
     source          1. .724
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971873"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             4.0%;  Score 39;  DB 5;  Length 724;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-09;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        400 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 438
              |||||||||||||||||||||||||||||||||||||||
Db        413 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 451


RESULT 11
CD559602
LOCUS       CD559602                 745 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496684 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971874 5', mRNA sequence.
ACCESSION   CD559602
VERSION     CD559602.2  GI:38558930
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 745)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585670.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 05
            High quality sequence start: 2
            High quality sequence stop: 644.
FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             4.0%;  Score 39;  DB 5;  Length 745;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-09;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        400 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 438
              |||||||||||||||||||||||||||||||||||||||
Db        405 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 443


RESULT 12
CD559607
LOCUS       CD559607                 747 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14497061 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971868 5', mRNA sequence.
ACCESSION   CD559607
VERSION     CD559607.2  GI:38558941
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 747)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
```

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  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585675.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: g  column: 11
            High quality sequence start: 14
            High quality sequence stop: 671.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             4.0%;  Score 39;  DB 5;  Length 747;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-09;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        400 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 438
              |||||||||||||||||||||||||||||||||||||||
Db        428 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 466


RESULT 13
CD559452/c
LOCUS       CD559452                754 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496548 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971870 5', mRNA sequence.
ACCESSION   CD559452
VERSION     CD559452.2  GI:38453473
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 754)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585520.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 01
            High quality sequence start: 130
            High quality sequence stop: 572.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971870"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             4.0%;  Score 39;  DB 5;  Length 754;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-09;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        400 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 438
              |||||||||||||||||||||||||||||||||||||||
Db        682 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 644


RESULT 14
CK130264
LOCUS       CK130264                756 bp    mRNA    linear   EST 02-DEC-2003
DEFINITION  AGENCOURT_14496566 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971871 5', mRNA sequence.
ACCESSION   CK130264
VERSION     CK130264.1  GI:38622200
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 756)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
```

Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: IRBK2 row: h column: 02
High quality sequence start: 5
High quality sequence stop: 731.

FEATURES Location/Qualifiers
source 1. .756
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971871"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.data Note: this is a NIH_MGC Library."

ORIGIN

Query Match 4.0%; Score 39; DB 5; Length 756;
Best Local Similarity 100.0%; Pred. No. 3.1e-09;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        400 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 438
              |||||||||||||||||||||||||||||||||||||||
Db        433 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 471
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RESULT 15
CD559606
LOCUS CD559606 1042 bp mRNA linear EST 11-JUN-2003
DEFINITION AGENCOURT_14497125 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971869 5', mRNA sequence.
ACCESSION CD559606
VERSION CD559606.1 GI:31585674
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1042)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: IRBK2 row: g column: 12
High quality sequence stop: 386.

FEATURES Location/Qualifiers
source 1. .1042
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971869"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.data Note: this is a NIH_MGC Library."

ORIGIN

Query Match 4.0%; Score 39; DB 5; Length 1042;
Best Local Similarity 100.0%; Pred. No. 3.2e-09;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        400 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 438
              |||||||||||||||||||||||||||||||||||||||
Db        403 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 441
```

RESULT 16
DV799576
LOCUS DV799576 252 bp mRNA linear EST 23-NOV-2005
DEFINITION est_t_truncatus2262 HML_TuTr_IL-2_PBL Tursiops truncatus cDNA, mRNA sequence.
ACCESSION DV799576
VERSION DV799576.1 GI:82652485
KEYWORDS EST.
SOURCE Tursiops truncatus (bottlenosed dolphin)
ORGANISM Tursiops truncatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae; Tursiops.
REFERENCE 1 (bases 1 to 252)
AUTHORS Mancia,A., Gefroh,H.A., Lundqvist,M.L., Romano,T.A., Almeida,J.S., Chen,Y., McKillen,D.J., Trent,H.F., Wu,S. and Warr,G.W.
TITLE Construction and validation of T. truncatus immunospecific cDNA microarray at marinegenomics.org
JOURNAL Unpublished (2005)
COMMENT Contact: Annalaura Mancia
Hollings Marine Lab
Medical University of South Carolina
Hollings Marine Lab, 331 Ft. Johnson Rd., Charleston, SC 29412, USA
Tel: (843) 762 8962
Fax: (843) 762 8737
Email: mancia@musc.edu.

FEATURES Location/Qualifiers
source 1. .252
/organism="Tursiops truncatus"
/mol_type="mRNA"
/db_xref="taxon:9739"

/tissue_type="PBL"
/cell_type="PBL"
/clone_lib="HML_TuTr_IL-2_PBL"
/note="Vector: pCR2.1TOPO; Site_1: GAATTC"
ORIGIN

Query Match 3.3%; Score 33; DB 10; Length 252;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 320 AGGAAGATGGAATTTGGTCCACTGATATCTTAA 352
||||||||||||||||||||||||||||||||
Db 1 AGGAAGATGGAATTTGGTCCACTGATATCTTAA 33

RESULT 17
AK162981
LOCUS AK162981 1839 bp mRNA linear HTC 21-SEP-2005
DEFINITION Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430014H12 product:interleukin 12b, full insert sequence.
ACCESSION AK162981
VERSION AK162981.1 GI:74188061
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
CONSRTM RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
PUBMED 11217851
REFERENCE 5
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
CONSRTM FANTOM Consortium
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420 (6915), 563-573 (2002)
PUBMED 12466851
REFERENCE 6
AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M.,

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            Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M.,
            Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K.,
            Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.
  CONSRTM   FANTOM Consortium
  TITLE     The transcriptional landscape of the mammalian genome
  JOURNAL   Science 309 (5740), 1559-1563 (2005)
  PUBMED    16141072
REFERENCE   7
  AUTHORS   Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M.,
            Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H.,
            Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T.,
            Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L.,
            Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A.,
            Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and
            Wahlestedt,C.
  CONSRTM   RIKEN Genome Exploration Research Group
  TITLE     Antisense transcription in the mammalian transcriptome
  JOURNAL   Science 309 (5740), 1564-1566 (2005)
  PUBMED    16141073
REFERENCE   8  (bases 1 to 1839)
  AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K.,
            Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S.,
            Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N.,
            Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D.,
            Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
     source          1. .1839
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
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                     /db_xref="taxon:10090"
                     /clone="A430014H12"
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                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="0 day neonate"
     CDS             58. .1065
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                     putative"
                     /codon_start=1
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                     /db_xref="GI:74188062"
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                     LLHKKENGIWSTEILKNFKNKTFLKCEAPNYSGRFTCSWLVQRNMDLKFNIKSSSSSP
                     DSRAVTCGMASLSAEKVTLDQRDYEKYSVSCQEDVTCPTAEETLPIELALEARQQNKY
                     ENYSTSFFIRDIIKPDPPKNLQMKPLKNSQVEVSWEYPDSWSTPHSYFSLKFFVRIQR
                     KKEKMKETEEGCNQKGAFLVEKTSTEVQCKGGNVCVQAQDRYYNSSCSKWACVPCRVR
                     S"
ORIGIN

  Query Match             3.0%;  Score 30;  DB 6;  Length 1839;
  Best Local Similarity   100.0%;  Pred. No. 0.00032;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||
Db        726 CAGCTTCTTCATCAGGGACATCATCAAACC 755


RESULT 18
AK155593
LOCUS       AK155593               2908 bp    mRNA    linear   HTC 21-SEP-2005
DEFINITION  Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN
            full-length enriched library, clone:F730005O03 product:interleukin
            12b, full insert sequence.
ACCESSION   AK155593
VERSION     AK155593.1  GI:74212721
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  PUBMED    10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  PUBMED    11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  PUBMED    11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
            Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
            Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
            Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
            Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
            Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
            Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
            Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
            Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  CONSRTM   RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
  PUBMED    11217851
REFERENCE   5
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
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Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420 (6915), 563-573 (2002)

PUBMED 12466851

REFERENCE 6

AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE The transcriptional landscape of the mammalian genome

JOURNAL Science 309 (5740), 1559-1563 (2005)

PUBMED 16141072

REFERENCE 7

AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.

CONSRTM RIKEN Genome Exploration Research Group

TITLE Antisense transcription in the mammalian transcriptome

JOURNAL Science 309 (5740), 1564-1566 (2005)

PUBMED 16141073

REFERENCE 8 (bases 1 to 2908)

AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

source 1. .2908
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/cell_type="B6-derived CD11 +ve dendritic cells"
/clone_lib="RIKEN full-length enriched mouse cDNA library"

misc_feature 1. .2908
/note="interleukin 12b (MGD|MGI:96540 GB|M86671, evidence: BLASTN, 99%, match=1807) putative"

ORIGIN

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Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db       1130 CAGCTTCTTCATCAGGGACATCATCAAACC 1159
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RESULT 19
BY164658
LOCUS BY164658 346 bp mRNA linear EST 10-DEC-2002
DEFINITION BY164658 RIKEN full-length enriched, bone marrow macrophage Mus musculus cDNA clone I830052P21 5', mRNA sequence.
ACCESSION BY164658
VERSION BY164658.1 GI:26301304
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 346)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
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Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by David A. Hume (Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane,Q 4072 Australia) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
FEATURES Location/Qualifiers
source 1. .346
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/mol_type="mRNA"
/strain="C57BL/6J"
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/clone="I830052P21"
/tissue_type="bone marrow"
/cell_type="macrophage"
/clone_lib="RIKEN full-length enriched, bone marrow macrophage"
ORIGIN

Query Match 2.9%; Score 29; DB 4; Length 346;
Best Local Similarity 100.0%; Pred. No. 0.00096;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 157 CCTGAAGAAGATGACATCACCTGGACCTC 185
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Db 214 CCTGAAGAAGATGACATCACCTGGACCTC 242

RESULT 20
BY221814
LOCUS BY221814 355 bp mRNA linear EST 10-DEC-2002
DEFINITION BY221814 RIKEN full-length enriched, activated spleen Mus musculus cDNA clone F830223O08 5', mRNA sequence.
ACCESSION BY221814
VERSION BY221814.1 GI:26402917
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 355)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,

Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

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FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             2.9%;  Score 29;  DB 4;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 0.00096;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        157 CCTGAAGAAGATGACATCACCTGGACCTC 185
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RESULT 21
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ACCESSION   BY222535
VERSION     BY222535.1  GI:26403638
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
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            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 375)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
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            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
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            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
            Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
            Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
            Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
            Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
            Hayashizaki,Y. Direct Submission
            Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
            Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
            RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
            Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
            Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
            Trust/MRC building Addenbrookes Hospital Cambridge) whose
            assistance we gratefully acknowledge.
            Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .375
                     /organism="Mus musculus"
                     /mol_type="mRNA"
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                     /db_xref="taxon:10090"
                     /clone="F830228K06"
                     /tissue_type="activated spleen"
                     /clone_lib="RIKEN full-length enriched, activated spleen"
ORIGIN

  Query Match             2.9%;  Score 29;  DB 4;  Length 375;
  Best Local Similarity   100.0%;  Pred. No. 0.00097;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        157 CCTGAAGAAGATGACATCACCTGGACCTC 185
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Db        213 CCTGAAGAAGATGACATCACCTGGACCTC 241
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RESULT 22
BY167742
LOCUS BY167742 387 bp mRNA linear EST 10-DEC-2002
DEFINITION BY167742 RIKEN full-length enriched, bone marrow macrophage Mus musculus cDNA clone I830068I17 5', mRNA sequence.
ACCESSION BY167742
VERSION BY167742.1 GI:26304388
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 387)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by David A. Hume (Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane,Q 4072 Australia) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
FEATURES Location/Qualifiers
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/mol_type="mRNA"
/strain="C57BL/6J"
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/clone="I830068I17"
/tissue_type="bone marrow"
/cell_type="macrophage"
/clone_lib="RIKEN full-length enriched, bone marrow macrophage"
ORIGIN

Query Match 2.9%; Score 29; DB 4; Length 387;
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Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 157 CCTGAAGAAGATGACATCACCTGGACCTC 185
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RESULT 23
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DEFINITION UMC-pd12cl-003-b07 Day 12 Corpus Luteum pd12cl Sus scrofa cDNA 3', mRNA sequence.
ACCESSION CO949904
VERSION CO949904.1 GI:51326849
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 417)
AUTHORS Jiang,H., Whitworth,K.M., Bivens,N.J., Ries,J.E., Woods,R.J., Forrester,L.J., Springer,G.K., Mathialagan,N., Agca,C., Prather,R.S. and Lucy,M.C.
TITLE Large-scale Generation and Analysis of Expressed Sequence Tags from Porcine Ovary
JOURNAL Unpublished (2004)
COMMENT Contact: DNA Core Facility (Swine Project)
Animal Science - RS Prather
University of Missouri-Columbia
M616 Medical Sciences Bldg., Columbia, MO 65212, USA
Tel: (573)882-0428
Fax: (573)884-5552
Email: porcine@rnet.missouri.edu
POLYA=No.
FEATURES Location/Qualifiers
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/note="Vector: T3T7PAC; Funding: A grant from the Monsanto Company to the University of Missouri. Genetic Source: Ovarian tissue (whole ovary, dissected follicles, or corpora lutea) was collected from crossbred pigs (Sus scrofa domestica), frozen in liquid nitrogen shortly after collection, and stored at -80 degrees Celsius until RNA

extraction. The tissue from several individual pigs was pooled for the purpose of RNA extraction. The specific tissues collected were fetal whole ovary; neonatal whole ovary; prepubutal whole ovary; 2, 4, 6 and 8 mm growing follicles; Day 0 follicles; Day 5 small antral follicles and corpora lutea; Day 12 corpora lutea and Day 12 follicles. More information regarding the methods can be found at:
http://genome.rnet.missouri.edu/Swine/Methods.html.
Library Construction (Standard Protocol): All procedures discussed in this section have been described in detail elsewhere (Soares et al., 1994; Bonaldo et al., 1996; Jiang et al., 2001). Total cellular RNA from each sample was isolated by using STAT-60 reagent (Tel-Test, Friendswood, TX) and the poly(A)+ RNA was obtained by two rounds of purification with the Oligotex mRNA isolation kit (Qiagen) according to the manufacturer's instructions. The libraries were constructed essentially as described by the manufacturer's instructions provided with the SuperScript Plasmid System (Invitrogen, cat. no. 18248-013). Briefly, 1mg of poly(A)+ RNA will be annealed at 37 degrees Celsius with 10mg of NotI-tag-dT18 oligonucleotide (GCTGCTCGCGGCCGC-tag-T18) and reverse transcribed at 37 degrees Celsius with SuperScript II (Invitrogen) reverse transcriptase (Jiang et al., 2001). The 'tag' represents a tissue/stage-specific ten-base sequence identifier (http://genome.uiowa.edu/pubsoft/software.html) present in the oligonucleotide used to prime first-strand synthesis. Second strand synthesis was performed with T4 DNA polymerase in the presence of DNA ligase and RNase H. After second strand synthesis, the double-stranded cDNAs was ligated to SalI adapters (Invitrogen-Life Technologies) and digested with NotI. The cDNAs will be size selected by passage through cDNA size fractionation columns (Invitrogen-Life technologies). The cDNAs derived from each developmental stage of a particular tissue were mixed on an equimolar basis and ligated directionally into the NotI and SalI sites of the pSPORT1 vector (Invitrogen). After ligation of the inserts, the plasmids will be electroporated into DH10B bacteria. Preliminary Library Characterization: Randomly chosen clones from each library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (~4 96-well plates) to confirm library quality [e.g. the presence of short polyA+ tails, genomic DNA contamination (must be <1%), ribosomal RNA clones (must be <1%), etc.] and to provide a sequence database representing the predominant clones in each library. The clones were sequenced at the University of Missouri-Columbia DNA Core Facility. Bioinformatics work was performed by GK Springer's bioinformatics group (WG Spollen, JE Ries, A Guillen, AA Khambati, RV Patel, CM Topinka, SB Bhuiyan) in Computer Science and Health Management and Informatics Departments at the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri DNA Core facility at: porcine@rnet.missouri.edu. Citations: 1. Bonaldo MF, Lennon G, Soares MB. Normalization and Subtraction: Two approaches to facilitate gene discovery. Genome Res, 1996; 6:791-806. 2. Jiang H, Bivens NJ, Ries JE, Whitworth KM, Green JA, Forrester LJ, Springer GK, Didion BA, Mathialagan N, Prather RS, Lucy MC (2001) Constructing cDNA libraries with fewer clones that contain long poly(dA) tails. Biotechniques 31:38-42. 3. Soares MB, MF Banaldo, P Jelene, L Su, L Lawton, A Efstrantiadis. 1994. Construction and characterization of a normalized cDNA library. Proc Natl Acad Sci, 91:9228-9232.
TAG_TISSUE=Day 12 Corpus Luteum
TAG_SEQ=Not found"

ORIGIN

Query Match 2.9%; Score 29; DB 8; Length 417;
Best Local Similarity 100.0%; Pred. No. 0.00098;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      157 CCTGAAGAAGATGACATCACCTGGACCTC 185
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Db      201 CCTGAAGAAGATGACATCACCTGGACCTC 229
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RESULT 24
BY218447
LOCUS BY218447 423 bp mRNA linear EST 10-DEC-2002
DEFINITION BY218447 RIKEN full-length enriched, activated spleen Mus musculus cDNA clone F830107N16 5', mRNA sequence.
ACCESSION BY218447
VERSION BY218447.1 GI:26399344
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 423)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

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FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             2.9%;  Score 29;  DB 4;  Length 423;
  Best Local Similarity   100.0%;  Pred. No. 0.00098;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        157 CCTGAAGAAGATGACATCACCTGGACCTC 185
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RESULT 25
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DEFINITION  BY154173 RIKEN full-length enriched, bone marrow macrophage Mus
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ACCESSION   BY154173
VERSION     BY154173.1  GI:26290747
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 432)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
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            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
            Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
            Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
            Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
            Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
            Hayashizaki,Y. Direct Submission
            Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
            Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
            RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
            Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Tissues were provided by David A. Hume ( Depts. of Biochemistry
            and Microbiology/Parasitology Institute for Molecular Bioscience
            University of Queensland Brisbane,Q 4072 Australia ) whose
            assistance we gratefully acknowledge.
            Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
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                     /cell_type="macrophage"
                     /clone_lib="RIKEN full-length enriched, bone marrow
                     macrophage"
ORIGIN

  Query Match             2.9%;  Score 29;  DB 4;  Length 432;
  Best Local Similarity   100.0%;  Pred. No. 0.00098;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        157 CCTGAAGAAGATGACATCACCTGGACCTC 185
              ||||||||||||||||||||||||||||||
Db        214 CCTGAAGAAGATGACATCACCTGGACCTC 242


RESULT 26
BF704417
LOCUS       BF704417                475 bp    mRNA    linear   EST 22-DEC-2000
DEFINITION  MI-P-E6-acc-g-09-1-UM.s1 MI-P-E6 Sus scrofa cDNA clone
            MI-P-E6-acc-g-09-1-UM 3', mRNA sequence.
ACCESSION   BF704417
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VERSION     BF704417.1  GI:11989825
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 475)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
   PUBMED   8889548
COMMENT     Contact: Tuggle CK
            Molecular Genetics Laboratory, Department of Animal Science
            Iowa State University
            201 Kildee Hall, Ames, IA 50011-3150, USA
            Tel: 5152944252
            Fax: 5152942401
            Email: cktuggle@iastate.edu
            Oligo-dT track not found, Not I site shown in beginning of sequence
            is likely internal to the message. cDNA Library Preparation: RJ
            Woods, JA Green, RS Prather S142 Animal Science Research Center,
            Department of Animal Science, University of Missouri-Columbia,
            65211 Clone distribution: clones will be available through Research
            Genetics (www.resgen.com)
            Seq primer: M13 Forward
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .475
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /strain="crossbreed"
                     /db_xref="taxon:9823"
                     /clone="MI-P-E6-acc-g-09-1-UM"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="MI-P-E6"
                     /note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: EcoRI;
                     The MI-P-E6 library is derived from fetus at gestational
                     day 20.  For a detailed description of the  library from
                     which this clone was derived, please visit our web site at
                     http://pigest.genome.iastate.edu/.
                     TAG_SEQ=None found"
ORIGIN

  Query Match             2.9%;  Score 29;  DB 7;  Length 475;
  Best Local Similarity   100.0%;  Pred. No. 0.00099;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        157 CCTGAAGAAGATGACATCACCTGGACCTC 185
              ||||||||||||||||||||||||||||
Db        202 CCTGAAGAAGATGACATCACCTGGACCTC 230


RESULT 27
AZ853726/c
LOCUS       AZ853726                569 bp    DNA     linear   GSS 21-FEB-2001
DEFINITION  2M0157M01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0157M01 F, genomic survey sequence.
ACCESSION   AZ853726
VERSION     AZ853726.1  GI:13042136
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 569)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0157  row: M  column: 01
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 569.
FEATURES             Location/Qualifiers
     source          1. .569
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0157M01"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             2.9%;  Score 29;  DB 11;  Length 569;
  Best Local Similarity   100.0%;  Pred. No. 0.001;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        157 CCTGAAGAAGATGACATCACCTGGACCTC 185
              ||||||||||||||||||||||||||||
Db        214 CCTGAAGAAGATGACATCACCTGGACCTC 186


RESULT 28
CJ134671
LOCUS       CJ134671                649 bp    mRNA    linear   EST 23-SEP-2005
DEFINITION  CJ134671 RIKEN full-length enriched mouse cDNA library, C57BL/6J
            bone marrow macrophage Mus musculus cDNA clone G530135F14 5', mRNA
            sequence.
ACCESSION   CJ134671
VERSION     CJ134671.1  GI:76234999
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 649)
  AUTHORS   The FANTOM Consortium and RIKEN Genome Exploration Research Group
            and Genome Science Group (Genome Network Project Core Group).
  TITLE     The transcriptional landscape of the mammalian genome
```

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  JOURNAL   Science 309 (5740), 1559-1563 (2005)
   PUBMED   16141072
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. Tissues were provided by David A. Hume (
            Depts. of Biochemistry and Microbiology/Parasitology Institute for
            Molecular Bioscience University of Queensland Brisbane,Q 4072
            Australia ) whose assistance we gratefully acknowledge.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/.
FEATURES             Location/Qualifiers
     source          1. .649
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="G530135F14"
                     /tissue_type="bone marrow"
                     /cell_type="macrophage"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library,
                     C57BL/6J bone marrow macrophage"
ORIGIN

  Query Match             2.9%;  Score 29;  DB 5;  Length 649;
  Best Local Similarity   100.0%;  Pred. No. 0.001;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        157 CCTGAAGAAGATGACATCACCTGGACCTC 185
              |||||||||||||||||||||||||||||
Db        214 CCTGAAGAAGATGACATCACCTGGACCTC 242


RESULT 29
BY749553
LOCUS       BY749553                 666 bp    mRNA    linear   EST 17-DEC-2002
DEFINITION  BY749553 RIKEN full-length enriched, B6-derived CD11 +ve dendritic
            cells Mus musculus cDNA clone F730005O03 5', mRNA sequence.
ACCESSION   BY749553
VERSION     BY749553.1  GI:27179008
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
            Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
            Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
            Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
            Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
            Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
            Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
            Direct Submission
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
             cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
             Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
            Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
            Trust/MRC building Addenbrookes Hospital Cambridge) whose
            assistance we gratefully acknowledge.
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="F730005O03"
                     /cell_type="B6-derived CD11 +ve dendritic cells"
                     /clone_lib="RIKEN full-length enriched, B6-derived CD11
                     +ve dendritic cells"
ORIGIN

  Query Match             2.9%;  Score 29;  DB 4;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 0.001;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        157 CCTGAAGAAGATGACATCACCTGGACCTC 185
              |||||||||||||||||||||||||||||
Db        614 CCTGAAGAAGATGACATCACCTGGACCTC 642
```

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RESULT 30
AZ441303
LOCUS       AZ441303                 535 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0232M24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0232M24 R, genomic survey sequence.
ACCESSION   AZ441303
VERSION     AZ441303.1  GI:10565316
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 535)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0232  row: M  column: 24
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 535.
FEATURES             Location/Qualifiers
     source          1. .535
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0232M24"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             2.8%;  Score 28;  DB 11;  Length 535;
  Best Local Similarity   100.0%;  Pred. No. 0.0036;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        158 CTGAAGAAGATGACATCACCTGGACCTC 185
              ||||||||||||||||||||||||||||
Db        157 CTGAAGAAGATGACATCACCTGGACCTC 184
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RESULT 31
AG079702/c
LOCUS       AG079702                 668 bp    DNA     linear   GSS 03-NOV-2001
DEFINITION  Pan troglodytes DNA, clone: PTB-075I07.R, genomic survey sequence.
ACCESSION   AG079702
VERSION     AG079702.1  GI:16631504
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     BAC end sequences of Library PTB
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 668)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the chimpanzee BAC library PTB This BAC end
            was generated during the R&D process and may have higher chance of
            clone tracking errors.
             PRIMERS
                 Sequencing: M13Rev
             LIBRARY
                 Vector    : pKS145
                 R.Site 1  : SacI
                 R.Site 2  : SacI.
FEATURES             Location/Qualifiers
     source          1. .668
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
                     /clone="PTB-075I07.R"
                     /sex="male"
                     /cell_type="lymphoblast"
                     /clone_lib="PTB Chimpanzee Male BAC Library"
ORIGIN

  Query Match             2.7%;  Score 27;  DB 14;  Length 668;
  Best Local Similarity   100.0%;  Pred. No. 0.013;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        412 GGACGTTTCACCTGCTGGTGGCTGACG 438
              |||||||||||||||||||||||||||
Db        494 GGACGTTTCACCTGCTGGTGGCTGACG 468
```

```
RESULT 32
DU179885
LOCUS       DU179885                 672 bp    DNA     linear   GSS 03-OCT-2005
DEFINITION  1098553497457 CHORI-243 Ovis aries genomic clone CH243-410B4,
            genomic survey sequence.
ACCESSION   DU179885
VERSION     DU179885.1  GI:76820406
KEYWORDS    GSS.
SOURCE      Ovis aries (sheep)
  ORGANISM  Ovis aries
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Caprinae; Ovis.
REFERENCE   1  (bases 1 to 672)
  AUTHORS   Kirkness,E., Shetty,J., de Jong,P., McEwan,J.C., Oddy,H. and
            Cockett,N.
  TITLE     Ovine BAC End Sequences from Library CHORI-243
```

```
  JOURNAL   Unpublished (2004)
COMMENT     Other_GSSs: 1098553723711
            Contact: Ewen Kirkness
            The Institute for Genomic Research (TIGR; www.tigr.org)
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-795-7536
            Email: ekirknes@tigr.org
            Sequences generated at the J. Craig Venter Institute Joint
            Technology Center (JCVIJTC; http://www.venterinstitute.org/).
            Original Trace: 1098553497457 Trace TI: gnl|ti|918706746
            Insert Length: 184000   Std Error: 0.00  row: B  column: 4
            Seq primer: SP6
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .672
                     /organism="Ovis aries"
                     /mol_type="genomic DNA"
                     /strain="Texel breed"
                     /db_xref="taxon:9940"
                     /clone="CH243-410B4"
                     /sex="Male"
                     /cell_type="Blood"
                     /clone_lib="CHORI-243"
                     /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
                     The CHORI-243 sheep (M) (Ovis aries) BAC library produced
                     by Pieter de Jong's lab at CHORI
                     http://bacpac.chori.org/library.php?id=162"
ORIGIN

  Query Match             2.6%;  Score 26;  DB 13;  Length 672;
  Best Local Similarity   100.0%;  Pred. No. 0.047;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         26 CCTGGTTTTCCCTGGTTTTGCTGGCA 51
              |||||||||||||||||||||||||
Db        108 CCTGGTTTTCCCTGGTTTTGCTGGCA 133


RESULT 33
CW885638/c
LOCUS       CW885638                414 bp    DNA     linear   GSS 08-DEC-2004
DEFINITION  RPCI42_102G16.TV RPCI-42 Bos taurus genomic clone RPCI42_102G16,
            genomic survey sequence.
ACCESSION   CW885638
VERSION     CW885638.1  GI:56424578
KEYWORDS    GSS.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 414)
  AUTHORS   Larkin,D.M., Donthu,K., LeDuc,R., Ryan,K., Liu,L., de Jong,P.J. and
            Lewin,H.A.
  TITLE     End sequencing of Holstein BAC library RPCI-42
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Harris Lewin
            Department of Animal Sciences
            University of Illinois at Urbana Champaign
            1201 W. Gregory Dr., Urbana, IL 61801, USA
            Tel: 217 333 5998
            Fax: 217 244 5617
            Email: h-lewin@uiuc.edu
            Clones are derived from the bovine BAC library RPCI-42
            (http://bacpac.chori.org/mbovine42.htm). For BAC library
            availability, please contact Pieter de Jong
            (pdejong@mail.cho.org).Clones may be purchased from BACPAC
            Resources (http://www.chori.org/bacpac/ordering_information.htm).
            Funding was provided in part by grant no. AG2004-34480-14417 from
            USDA-CSREES (Livestock Genome Sequencing Initiative) and
            AG58-5438-2-313 from USDA-ARS
            Plate: 102  row: G  column: 16
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .414
                     /organism="Bos taurus"
                     /mol_type="genomic DNA"
                     /strain="Holstein"
                     /db_xref="taxon:9913"
                     /clone="RPCI42_102G16"
                     /sex="male"
                     /cell_type="blood"
                     /clone_lib="RPCI-42"
                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     RPCI-42 Bovine BAC library (Male) produced by Pieter de
                     Jong"
ORIGIN

  Query Match             2.4%;  Score 24;  DB 13;  Length 414;
  Best Local Similarity   100.0%;  Pred. No. 0.57;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        709 GACCCACCCAAGAACCTGCAACTG 732
              ||||||||||||||||||||||||
Db         24 GACCCACCCAAGAACCTGCAACTG 1


RESULT 34
CW047416/c
LOCUS       CW047416                330 bp    DNA     linear   GSS 28-OCT-2004
DEFINITION  104_285_10512716_115_30217 Sorghum methylation filtered library
            (LibID: 104) Sorghum bicolor genomic clone 10512716, genomic survey
            sequence.
ACCESSION   CW047416
VERSION     CW047416.1  GI:54724146
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 330)
  AUTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
            Martienssen,R.A.
  TITLE     Sorghum genome sequencing by methylation filtration
  JOURNAL   PLoS Biol. 3 (1), e13 (2005)
   PUBMED   15660154
COMMENT     Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: 285  row: e  column: 18
            Seq primer: M13/pUC Reverse
            Class: methylation filtered
            High quality sequence stop: 330.
FEATURES             Location/Qualifiers
     source          1. .330
                     /organism="Sorghum bicolor"
                     /mol_type="genomic DNA"
                     /cultivar="ATx623"
                     /db_xref="taxon:4558"
                     /clone="10512716"
                     /clone_lib="Sorghum methylation filtered library (LibID:
                     104)"
                     /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                     prepared from purified nuclei was randomly sheared,
                     end-repaired, size fractionated to enrich for the 0.5 to 5
                     kb fraction, ligated into HincII-digested pBCSK(-) vector
                     and electroporated into E. coli cells. This is a
                     methylation filtered library."
```

```
ORIGIN

  Query Match             2.1%;  Score 21;  DB 13;  Length 330;
  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        441 AATCAGTACCGATTTGAAATT 461
              |||||||||||||||||||||
Db        100 AATCAGTACCGATTTGAAATT 80


RESULT 35
T99581/c
LOCUS       T99581                  374 bp    mRNA    linear   EST 31-MAR-1995
DEFINITION  ye65d08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone
            IMAGE:122607 5', mRNA sequence.
ACCESSION   T99581
VERSION     T99581.1  GI:749318
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 374)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 954
            High qality sequence stops: 243 Source: IMAGE Consortium, LLNL This
            clone is available royalty-free through LLNL ; contact the IMAGE
            Consortium (info@image.llnl.gov) for further information.
            Insert Length: 954   Std Error: 0.00
            Seq primer: M13RP1
            High quality sequence stop: 243.
FEATURES             Location/Qualifiers
     source          1. .374
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:475152"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:122607"
                     /sex="male"
                     /dev_stage="20 week-post conception fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares fetal liver spleen 1NFLS"
                     /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                     with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                     1st strand cDNA was primed with a Pac I - oligo(dT) primer
                     [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Pac I and cloned into the Pac I
                     and Eco RI sites of the modified pT7T3 vector.  Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
ORIGIN

  Query Match             2.1%;  Score 21;  DB 10;  Length 374;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        387 AAAATGTGAGGCAAAGAATTA 407
              |||||||||||||||||||||
Db         84 AAAATGTGAGGCAAAGAATTA 64


RESULT 36
CN071927/c
LOCUS       CN071927                508 bp    mRNA    linear   EST 30-MAR-2004
DEFINITION  1021022B08.x2 1021 - Unigene II from Maize Genome Project Zea mays
            cDNA, mRNA sequence.
ACCESSION   CN071927
VERSION     CN071927.1  GI:45847984
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 508)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 1021022  row: B  column: 08.
FEATURES             Location/Qualifiers
     source          1. .508
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /db_xref="dbEST:949071E08.x1"
                     /db_xref="taxon:4577"
                     /clone_lib="1021 - Unigene II from Maize Genome Project"
                     /note="This library represents the unique genes found in
                     the second round of EST sequencing at Stanford University
                     for the maize genome project. Sequences are present from
                     library 949. Contigs were assembled using ZmDBAssembler
                     and 2 representatives from each contig were selected for
                     the Unigene set. All singlets were also selected. Library
                     947, also part of Unigene II, was submitted under NAME
                     '1020 - Unigene II from Maize Genome Project'."
ORIGIN

  Query Match             2.1%;  Score 21;  DB 8;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        314 TACTCCTGAAGAAGATGACAT 294


RESULT 37
CF059708/c
LOCUS       CF059708                509 bp    mRNA    linear   EST 21-JUL-2003
DEFINITION  QCS15g07.yg QCS Zea mays cDNA clone QCS15g07, mRNA sequence.
ACCESSION   CF059708
VERSION     CF059708.1  GI:33099748
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 509)
  AUTHORS   Genoplante.
  TITLE     Genoplante, a major partnership french program in plant genomics
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Genoplante
            Genoplante
```

```
            93, rue Henri Rochefort 91025 EVRY CEDEX France
            Tel: 33 1 69 47 54 00
            Fax: 33 1 69 47 54 10
            This sequence has been generated in the framework of the french
            plant genomics programme 'Genoplante' (http://www.genoplante.com
            and http://genoplante-info.infobiogen.fr).
FEATURES              Location/Qualifiers
     source           1. .509
                      /organism="Zea mays"
                      /mol_type="mRNA"
                      /cultivar="F2"
                      /db_xref="taxon:4577"
                      /clone="QCS15g07"
                      /tissue_type="whole plant"
                      /clone_lib="QCS"
ORIGIN

  Query Match             2.1%;  Score 21;  DB 5;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        362 TACTCCTGAAGAAGATGACAT 342


RESULT 38
CF060247/c
LOCUS       CF060247                509 bp    mRNA    linear   EST 21-JUL-2003
DEFINITION  QCS5b05.yg QCS Zea mays cDNA clone QCS5b05, mRNA sequence.
ACCESSION   CF060247
VERSION     CF060247.1  GI:33100287
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 509)
  AUTHORS   Genoplante.
  TITLE     Genoplante, a major partnership french program in plant genomics
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Genoplante
            Genoplante
            93, rue Henri Rochefort 91025 EVRY CEDEX France
            Tel: 33 1 69 47 54 00
            Fax: 33 1 69 47 54 10
            This sequence has been generated in the framework of the french
            plant genomics programme 'Genoplante' (http://www.genoplante.com
            and http://genoplante-info.infobiogen.fr).
FEATURES              Location/Qualifiers
     source           1. .509
                      /organism="Zea mays"
                      /mol_type="mRNA"
                      /cultivar="F2"
                      /db_xref="taxon:4577"
                      /clone="QCS5b05"
                      /tissue_type="whole plant"
                      /clone_lib="QCS"
ORIGIN

  Query Match             2.1%;  Score 21;  DB 5;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        362 TACTCCTGAAGAAGATGACAT 342


RESULT 39
CF059885/c
LOCUS       CF059885                510 bp    mRNA    linear   EST 21-JUL-2003
DEFINITION  QCS18b04.yg QCS Zea mays cDNA clone QCS18b04, mRNA sequence.
ACCESSION   CF059885
VERSION     CF059885.1  GI:33099925
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 510)
  AUTHORS   Genoplante.
  TITLE     Genoplante, a major partnership french program in plant genomics
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Genoplante
            Genoplante
            93, rue Henri Rochefort 91025 EVRY CEDEX France
            Tel: 33 1 69 47 54 00
            Fax: 33 1 69 47 54 10
            This sequence has been generated in the framework of the french
            plant genomics programme 'Genoplante' (http://www.genoplante.com
            and http://genoplante-info.infobiogen.fr).
FEATURES              Location/Qualifiers
     source           1. .510
                      /organism="Zea mays"
                      /mol_type="mRNA"
                      /cultivar="F2"
                      /db_xref="taxon:4577"
                      /clone="QCS18b04"
                      /tissue_type="whole plant"
                      /clone_lib="QCS"
ORIGIN

  Query Match             2.1%;  Score 21;  DB 5;  Length 510;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        363 TACTCCTGAAGAAGATGACAT 343


RESULT 40
BI431328/c
LOCUS       BI431328                521 bp    mRNA    linear   EST 20-AUG-2001
DEFINITION  949071E08.x1 949 - Juvenile leaf and shoot cDNA from Steve Moose
            Zea mays cDNA, mRNA sequence.
ACCESSION   BI431328
VERSION     BI431328.1  GI:15215523
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 521)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 949071  row: E  column: 08.
FEATURES              Location/Qualifiers
     source           1. .521
                      /organism="Zea mays"
                      /mol_type="mRNA"
                      /cultivar="W64A"
                      /db_xref="taxon:4577"
```

```
                     /tissue_type="immature leaf primordium and vegetative
                     meristem"
                     /dev_stage="4 stages from 3-13 days after imbibing"
                     /lab_host="E. coli XLOLR"
                     /clone_lib="949 - Juvenile leaf and shoot cDNA from Steve
                     Moose"
                     /note="Organ: juvenile vegetative shoots; Vector:
                     pAD-GAL4-2.1; Site_1: EcoRI; Site_2: XhoI; Equal amounts
                     of total RNA by weight from 4 tissue sources (see below)
                     were pooled, polyA+ RNA isolated, and cDNA synthesized for
                     EcoRI (5') and XhoI (3') directional cloning into lambda
                     Hybrizap vector from Stratagene. Tissue Sources: 1. Whole
                     shoots 3 days after sowing/imbibing in wet soil. 2. Basal
                     1.5 cm shoots 6 days after sowing - includes yellow
                     portions of developing leaves 1-5, primordia from 6-8, and
                     the vegetative apex. 3. Non-green portions of developing
                     leaves 4-5 and the vegetative apex,  including adult leaf
                     primordia, 9 days after sowing. 4. Partially expanded and
                     greening leaves 4-5 at 13 days after sowing."
ORIGIN

  Query Match             2.1%;  Score 21;  DB 2;  Length 521;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        351 TACTCCTGAAGAAGATGACAT 331


RESULT 41
AI491671/c
LOCUS       AI491671                523 bp    mRNA    linear   EST 22-APR-1999
DEFINITION  486020E06.x2 486 - leaf primordia cDNA library from Hake lab Zea
            mays cDNA, mRNA sequence.
ACCESSION   AI491671
VERSION     AI491671.2  GI:4646526
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 523)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     On Mar 8, 1999 this sequence version replaced gi:4388499.
            Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 486020  row: E  column: 06.
FEATURES             Location/Qualifiers
     source          1. .523
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="B73"
                     /db_xref="taxon:4577"
                     /tissue_type="leaf primordia"
                     /dev_stage="P7-P11 leaf"
                     /lab_host="E.coli XL1-Blue MFR'"
                     /clone_lib="486 - leaf primordia cDNA library from Hake
                     lab"
                     /note="Organ: shoot; Vector: Lambda zap; Hake lab cDNA
                     library."
ORIGIN

  Query Match             2.1%;  Score 21;  DB 1;  Length 523;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        408 TACTCCTGAAGAAGATGACAT 388


RESULT 42
AW566435/c
LOCUS       AW566435                553 bp    mRNA    linear   EST 10-MAR-2000
DEFINITION  660074D12.x1 660 - Mixed stages of anther and pollen Zea mays cDNA,
            mRNA sequence.
ACCESSION   AW566435
VERSION     AW566435.1  GI:7227794
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 553)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 660074  row: D  column: 12.
FEATURES             Location/Qualifiers
     source          1. .553
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="Ohio43"
                     /db_xref="taxon:4577"
                     /tissue_type="whole premieotic anthers to pollen shed"
                     /dev_stage="premieotic anthers to pollen shed"
                     /lab_host="XLOLR"
                     /clone_lib="660 - Mixed stages of anther and pollen"
                     /note="Organ: anthers; Vector: Lambda Zap; Site_1: EcoRI;
                     Site_2: XhoI; Anther and pollen cDNA library.
                     Directionally sequenced with 5' end at the EcoRI site.
                     Created by Amie Franklin."
ORIGIN

  Query Match             2.1%;  Score 21;  DB 7;  Length 553;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        324 TACTCCTGAAGAAGATGACAT 304


RESULT 43
BQ294193
LOCUS       BQ294193                566 bp    mRNA    linear   EST 15-MAY-2002
DEFINITION  1091026G08.y2 1091 - Immature ear with common ESTs screened by
            Schmidt lab Zea mays cDNA, mRNA sequence.
ACCESSION   BQ294193
VERSION     BQ294193.1  GI:20803143
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 566)
```

```
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 1091026  row: G  column: 08.
FEATURES             Location/Qualifiers
     source          1. .566
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="OH43"
                     /db_xref="taxon:4577"
                     /tissue_type="Inflorescence meristem - floral organ
                     primordia"
                     /dev_stage="0.5 cm to 2 cm"
                     /lab_host="Stratagene XLOLR"
                     /clone_lib="1091 - Immature ear with common ESTs screened
                     by Schmidt lab"
                     /note="Organ: Immature ear; Vector: pAD-GAL4; Site_1:
                     EcoRI; Site_2: XhoI; RNA from library 606 was filtered for
                     common ESTs found in 606."
ORIGIN

  Query Match             2.1%;  Score 21;  DB 3;  Length 566;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        500 TACTCCTGAAGAAGATGACAT 520


RESULT 44
CA627255/c
LOCUS       CA627255                588 bp    mRNA    linear   EST 23-NOV-2002
DEFINITION  w11n.pk154.e4 w11n Triticum aestivum cDNA clone w11n.pk154.e4 5'
            end, mRNA sequence.
ACCESSION   CA627255
VERSION     CA627255.1  GI:25205551
KEYWORDS    EST.
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 588)
  AUTHORS   Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,
            Miao,G., Caraher,N. and Hanafey,M.K.
  TITLE     DuPont Wheat cDNA Sequence
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Scott V. Tingey
            Crop Genetics
            E. I. DuPont de Nemours and Company
            1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
            Tel: 302-631-2602
            Fax: 302-631-2607
            Email: Scott.V.Tingey@USA.dupont.com
            Seq primer: M13.
FEATURES             Location/Qualifiers
     source          1. .588
                     /organism="Triticum aestivum"
                     /mol_type="mRNA"
                     /db_xref="taxon:4565"
                     /clone="w11n.pk154.e4"
                     /tissue_type="leaf"
                     /clone_lib="w11n"
                     /note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
                     XhoI; Wheat (Triticum aestivum L.) leaf 7 day old
                     seedling, light grown (normalized)"
ORIGIN

  Query Match             2.1%;  Score 21;  DB 4;  Length 588;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        357 TACTCCTGAAGAAGATGACAT 337


RESULT 45
AW573354
LOCUS       AW573354                594 bp    mRNA    linear   EST 13-MAR-2000
DEFINITION  660074D12.y1 660 - Mixed stages of anther and pollen Zea mays cDNA,
            mRNA sequence.
ACCESSION   AW573354
VERSION     AW573354.1  GI:7238132
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 594)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 660074  row: D  column: 12.
FEATURES             Location/Qualifiers
     source          1. .594
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="Ohio43"
                     /db_xref="taxon:4577"
                     /tissue_type="whole premieotic anthers to pollen shed"
                     /dev_stage="premieotic anthers to pollen shed"
                     /lab_host="XLOLR"
                     /clone_lib="660 - Mixed stages of anther and pollen"
                     /note="Organ: anthers; Vector: Lambda Zap; Site_1: EcoRI;
                     Site_2: XhoI; Anther and pollen cDNA library.
                     Directionally sequenced with 5' end at the EcoRI site.
                     Created by Amie Franklin."
ORIGIN

  Query Match             2.1%;  Score 21;  DB 7;  Length 594;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        336 TACTCCTGAAGAAGATGACAT 356


RESULT 46
BI478972
LOCUS       BI478972                599 bp    mRNA    linear   EST 27-AUG-2001
DEFINITION  949071E08.y1 949 - Juvenile leaf and shoot cDNA from Steve Moose
            Zea mays cDNA, mRNA sequence.
ACCESSION   BI478972
VERSION     BI478972.1  GI:15313824
KEYWORDS    EST.
SOURCE      Zea mays
```

```
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 599)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 949071  row: E  column: 08.
FEATURES             Location/Qualifiers
     source          1. .599
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="W64A"
                     /db_xref="taxon:4577"
                     /tissue_type="immature leaf primordium and vegetative
                     meristem"
                     /dev_stage="4 stages from 3-13 days after imbibing"
                     /lab_host="E. coli XLOLR"
                     /clone_lib="949 - Juvenile leaf and shoot cDNA from Steve
                     Moose"
                     /note="Organ: juvenile vegetative shoots; Vector:
                     pAD-GAL4-2.1; Site_1: EcoRI; Site_2: XhoI; Equal amounts
                     of total RNA by weight from 4 tissue sources (see below)
                     were pooled, polyA+ RNA isolated, and cDNA synthesized for
                     EcoRI (5') and XhoI (3') directional cloning into lambda
                     Hybrizap vector from Stratagene. Tissue Sources: 1. Whole
                     shoots 3 days after sowing/imbibing in wet soil. 2. Basal
                     1.5 cm shoots 6 days after sowing - includes yellow
                     portions of developing leaves 1-5, primordia from 6-8, and
                     the vegetative apex. 3. Non-green portions of developing
                     leaves 4-5 and the vegetative apex,  including adult leaf
                     primordia, 9 days after sowing. 4. Partially expanded and
                     greening leaves 4-5 at 13 days after sowing."
ORIGIN

  Query Match             2.1%;  Score 21;  DB 2;  Length 599;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        471 TACTCCTGAAGAAGATGACAT 491


RESULT 47
CA293522/c
LOCUS       CA293522                632 bp    mRNA    linear   EST 26-SEP-2003
DEFINITION  SCSGLV1005G05.g LV1 Saccharum officinarum cDNA clone SCSGLV1005G05
            5', mRNA sequence.
ACCESSION   CA293522
VERSION     CA293522.1  GI:36054204
KEYWORDS    EST.
SOURCE      Saccharum officinarum
  ORGANISM  Saccharum officinarum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
            complex.
REFERENCE   1  (bases 1 to 632)
  AUTHORS   Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
  TITLE     The libraries that made SUCEST
  JOURNAL   Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT     Contact: Arruda P
            Centro de Biologia Molecular e Engenharia Genetica
            Universidade Estadual de Campinas
            Caixa Postal 6010, 13083-970, Campinas SP, Brazil
            Tel: 55 19 3788 1137
            Fax: 55 19 3788 1089
            Email: parruda@unicamp.br
            Clone distribution: clone distribution information can be found
            through the Brazilian Clone Collection Center (BCCC) at
            http://www.bcccenter.fcav.unesp.br
            Plate: 005  row: G  column: 05
            Seq primer: T7 Promoter Primer.
FEATURES             Location/Qualifiers
     source          1. .632
                     /organism="Saccharum officinarum"
                     /mol_type="mRNA"
                     /db_xref="taxon:4547"
                     /clone="SCSGLV1005G05"
                     /lab_host="DH10B"
                     /clone_lib="LV1"
                     /note="Organ: Etiolated leaves from in vitro grown
                     sedlings; Vector: pSport1; Site_1: SalI; Site_2: NotI; An
                     unidirectional cDNA library generated from [Etiolated
                     leaves from in  vitro grown sedlings]. cDNA was prepared
                     from polyA+ mRNA using  SuperScript Plasmid System Kit
                     (Invitrogen). The double-strand cDNAs were  fractionated
                     in a sepharose CL-2B 40cm-columns and fragments sizing
                     between 0.8 and 1.5 Kb were directionally cloned into the
                     vector. Details  of each source of RNA and library
                     construction can be obtained at
                     http://sucest.lad.ic.unicamp.br/public"
ORIGIN

  Query Match             2.1%;  Score 21;  DB 4;  Length 632;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        441 AATCAGTACCGATTTGAAATT 461
              |||||||||||||||||||||
Db        620 AATCAGTACCGATTTGAAATT 600


RESULT 48
DN207344/c
LOCUS       DN207344                633 bp    mRNA    linear   EST 28-FEB-2005
DEFINITION  MEST847_H05.T7-1 UGA-ZmSAM-XZ2 Zea mays cDNA, mRNA sequence.
ACCESSION   DN207344
VERSION     DN207344.1  GI:60340371
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 633)
  AUTHORS   Chen,H.D., Zhang,X., Zhou,R.L., Arias L,A.C., Shendelman,J.M.,
            Zazubovits,N., Borsuk,L.A., Emrich,S.J., Ashlock,D.A., Scanlon,M.J.
            and Schnable,P.S.
  TITLE     Expressed Sequence Tags from B73 Maize Shoot Apical Meristems
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Patrick S. Schnable
            Schnable Laboratory
            Iowa State University
            2035B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA
            Tel: 515-294-0975
            Fax: 515-294-5256
            Email: schnable@iastate.edu.
FEATURES             Location/Qualifiers
     source          1. .633
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="inbred B73"
                     /db_xref="taxon:4577"
                     /tissue_type="Vegetative Shoot Apical Meristem (SAM) and
                     leaf primordia staged P1-P4"
```

/lab_host="XL1-Blue"
/clone_lib="UGA-ZmSAM-XZ2"
/note="Organ: Shoot apex; Vector: Uni-Zap XR; Site_1: EcoRI; Site_2: XhoI; This library was constructed by Xiaolan Zhang. Vegetative Shoot Apical Meristem (SAM) and leaf primordia staged P1-P4 from 14-17 day-after germination seedlings were quickly dissected into dry ice under a light microscope. Total RNA was isolated using Trizol and mRNA was purified with Dynal Oligo-DT25. ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with an XhoI oligo-dT primer (5'-GAGAGAGAGAGAGAGAGAACTAGTCTCGAGTTTTTTTTTTTTTTTT). The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with XhoI and size-selected to be >600 bp. The resulting molecules were directionally cloned into the EcoRI and XhoI sites of the Uni-Zap XR vector. The lambda library was packaged with Gigapack III Gold packaging extract and was mass excised by XL1-Blue cells and ExAssist helper phage. Excised phagemids were titered in SOLR cells and plated onto LB-ampicillin agar plates. Base calling was conducted using Phred. Trimming was performed using Lucy with the following criteria: (-minimum 200 -error 0.01 0.01 -bracket 10 0.01). A low complexity filter was applied and additional trimming was conducted to remove E. coli, vector, and organelle contamination. After processing ~30% of the sequences contained a minimum of 10 Ts at the beginning of the sequence. For reasons that are not understood many of the clones in this library lack an XhoI site at their 3' ends."
ORIGIN

Query Match 2.1%; Score 21; DB 9; Length 633;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 153 TACTCCTGAAGAAGATGACAT 173
||||||||||||||||||||
Db 456 TACTCCTGAAGAAGATGACAT 436

RESULT 49
BQ294192/c
LOCUS BQ294192 637 bp mRNA linear EST 15-MAY-2002
DEFINITION 1091026G08.x2 1091 - Immature ear with common ESTs screened by Schmidt lab Zea mays cDNA, mRNA sequence.
ACCESSION BQ294192
VERSION BQ294192.1 GI:20803142
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 637)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 1091026 row: G column: 08.
FEATURES Location/Qualifiers
source 1. .637
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="OH43"
/db_xref="taxon:4577"
/tissue_type="Inflorescence meristem - floral organ primordia"
/dev_stage="0.5 cm to 2 cm"
/lab_host="Stratagene XLOLR"
/clone_lib="1091 - Immature ear with common ESTs screened by Schmidt lab"
/note="Organ: Immature ear; Vector: pAD-GAL4; Site_1: EcoRI; Site_2: XhoI; RNA from library 606 was filtered for common ESTs found in 606."
ORIGIN

Query Match 2.1%; Score 21; DB 3; Length 637;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 153 TACTCCTGAAGAAGATGACAT 173
||||||||||||||||||||
Db 359 TACTCCTGAAGAAGATGACAT 339

RESULT 50
DN222336/c
LOCUS DN222336 692 bp mRNA linear EST 28-FEB-2005
DEFINITION MEST1126_F09.T7-1 UGA-ZmSAM-XZ2 Zea mays cDNA, mRNA sequence.
ACCESSION DN222336
VERSION DN222336.1 GI:60355363
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 692)
AUTHORS Chen,H.D., Zhang,X., Zhou,R.L., Arias L,A.C., Shendelman,J.M., Zazubovits,N., Borsuk,L.A., Emrich,S.J., Ashlock,D.A., Scanlon,M.J. and Schnable,P.S.
TITLE Expressed Sequence Tags from B73 Maize Shoot Apical Meristems
JOURNAL Unpublished (2004)
COMMENT Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
2035B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA
Tel: 515-294-0975
Fax: 515-294-5256
Email: schnable@iastate.edu.
FEATURES Location/Qualifiers
source 1. .692
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="inbred B73"
/db_xref="taxon:4577"
/tissue_type="Vegetative Shoot Apical Meristem (SAM) and leaf primordia staged P1-P4"
/lab_host="XL1-Blue"
/clone_lib="UGA-ZmSAM-XZ2"
/note="Organ: Shoot apex; Vector: Uni-Zap XR; Site_1: EcoRI; Site_2: XhoI; This library was constructed by Xiaolan Zhang. Vegetative Shoot Apical Meristem (SAM) and leaf primordia staged P1-P4 from 14-17 day-after germination seedlings were quickly dissected into dry ice under a light microscope. Total RNA was isolated using Trizol and mRNA was purified with Dynal Oligo-DT25. ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with an XhoI oligo-dT primer (5'-GAGAGAGAGAGAGAGAGAACTAGTCTCGAGTTTTTTTTTTTTTTTT). The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with XhoI and size-selected to be

>600 bp. The resulting molecules were directionally cloned into the EcoRI and XhoI sites of the Uni-Zap XR vector. The lambda library was packaged with Gigapack III Gold packaging extract and was mass excised by XL1-Blue cells and ExAssist helper phage. Excised phagemids were titered in SOLR cells and plated onto LB-ampicillin agar plates. Base calling was conducted using Phred. Trimming was performed using Lucy with the following criteria: (-minimum 200 -error 0.01 0.01 -bracket 10 0.01). A low complexity filter was applied and additional trimming was conducted to remove E. coli, vector, and organelle contamination. After processing ~30% of the sequences contained a minimum of 10 Ts at the beginning of the sequence. For reasons that are not understood many of the clones in this library lack an XhoI site at their 3' ends."

ORIGIN

```
  Query Match             2.1%;  Score 21;  DB 9;  Length 692;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        388 TACTCCTGAAGAAGATGACAT 368
```

RESULT 51
DN220924/c

```
LOCUS       DN220924                693 bp    mRNA    linear   EST 28-FEB-2005
DEFINITION  MEST1104_C12.T7-1 UGA-ZmSAM-XZ2 Zea mays cDNA, mRNA sequence.
ACCESSION   DN220924
VERSION     DN220924.1  GI:60353951
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 693)
  AUTHORS   Chen,H.D., Zhang,X., Zhou,R.L., Arias L,A.C., Shendelman,J.M.,
            Zazubovits,N., Borsuk,L.A., Emrich,S.J., Ashlock,D.A., Scanlon,M.J.
            and Schnable,P.S.
  TITLE     Expressed Sequence Tags from B73 Maize Shoot Apical Meristems
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Patrick S. Schnable
            Schnable Laboratory
            Iowa State University
            2035B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA
            Tel: 515-294-0975
            Fax: 515-294-5256
            Email: schnable@iastate.edu.
FEATURES             Location/Qualifiers
     source          1. .693
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="inbred B73"
                     /db_xref="taxon:4577"
                     /tissue_type="Vegetative Shoot Apical Meristem (SAM) and
                     leaf primordia staged P1-P4"
                     /lab_host="XL1-Blue"
                     /clone_lib="UGA-ZmSAM-XZ2"
                     /note="Organ: Shoot apex; Vector: Uni-Zap XR; Site_1:
                     EcoRI; Site_2: XhoI; This library was constructed by
                     Xiaolan Zhang. Vegetative Shoot Apical Meristem (SAM) and
                     leaf primordia staged P1-P4 from 14-17 day-after
                     germination seedlings were quickly dissected into dry ice
                     under a light microscope. Total RNA was isolated using
                     Trizol and mRNA was purified with Dynal Oligo-DT25.
                     ds-cDNA molecules were generated as follows. First-strand
                     cDNA was prepared from oligo-dT selected mRNA by priming
                     with an XhoI oligo-dT primer
                     (5'-GAGAGAGAGAGAGAGAGAACTAGTCTCGAGTTTTTTTTTTTTTTTT).
```

The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with XhoI and size-selected to be >600 bp. The resulting molecules were directionally cloned into the EcoRI and XhoI sites of the Uni-Zap XR vector. The lambda library was packaged with Gigapack III Gold packaging extract and was mass excised by XL1-Blue cells and ExAssist helper phage. Excised phagemids were titered in SOLR cells and plated onto LB-ampicillin agar plates. Base calling was conducted using Phred. Trimming was performed using Lucy with the following criteria: (-minimum 200 -error 0.01 0.01 -bracket 10 0.01). A low complexity filter was applied and additional trimming was conducted to remove E. coli, vector, and organelle contamination. After processing ~30% of the sequences contained a minimum of 10 Ts at the beginning of the sequence. For reasons that are not understood many of the clones in this library lack an XhoI site at their 3' ends."

ORIGIN

```
  Query Match             2.1%;  Score 21;  DB 9;  Length 693;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        359 TACTCCTGAAGAAGATGACAT 339
```

RESULT 52
DN219584/c

```
LOCUS       DN219584                694 bp    mRNA    linear   EST 28-FEB-2005
DEFINITION  MEST1083_C10.T7-1 UGA-ZmSAM-XZ2 Zea mays cDNA, mRNA sequence.
ACCESSION   DN219584
VERSION     DN219584.1  GI:60352611
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 694)
  AUTHORS   Chen,H.D., Zhang,X., Zhou,R.L., Arias L,A.C., Shendelman,J.M.,
            Zazubovits,N., Borsuk,L.A., Emrich,S.J., Ashlock,D.A., Scanlon,M.J.
            and Schnable,P.S.
  TITLE     Expressed Sequence Tags from B73 Maize Shoot Apical Meristems
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Patrick S. Schnable
            Schnable Laboratory
            Iowa State University
            2035B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA
            Tel: 515-294-0975
            Fax: 515-294-5256
            Email: schnable@iastate.edu.
FEATURES             Location/Qualifiers
     source          1. .694
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="inbred B73"
                     /db_xref="taxon:4577"
                     /tissue_type="Vegetative Shoot Apical Meristem (SAM) and
                     leaf primordia staged P1-P4"
                     /lab_host="XL1-Blue"
                     /clone_lib="UGA-ZmSAM-XZ2"
                     /note="Organ: Shoot apex; Vector: Uni-Zap XR; Site_1:
                     EcoRI; Site_2: XhoI; This library was constructed by
                     Xiaolan Zhang. Vegetative Shoot Apical Meristem (SAM) and
                     leaf primordia staged P1-P4 from 14-17 day-after
                     germination seedlings were quickly dissected into dry ice
                     under a light microscope. Total RNA was isolated using
                     Trizol and mRNA was purified with Dynal Oligo-DT25.
```

ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with an XhoI oligo-dT primer (5'-GAGAGAGAGAGAGAGAGAACTAGTCTCGAGTTTTTTTTTTTTTTTT). The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with XhoI and size-selected to be >600 bp. The resulting molecules were directionally cloned into the EcoRI and XhoI sites of the Uni-Zap XR vector. The lambda library was packaged with Gigapack III Gold packaging extract and was mass excised by XL1-Blue cells and ExAssist helper phage. Excised phagemids were titered in SOLR cells and plated onto LB-ampicillin agar plates. Base calling was conducted using Phred. Trimming was performed using Lucy with the following criteria: (-minimum 200 -error 0.01 0.01 -bracket 10 0.01). A low complexity filter was applied and additional trimming was conducted to remove E. coli, vector, and organelle contamination. After processing ~30% of the sequences contained a minimum of 10 Ts at the beginning of the sequence. For reasons that are not understood many of the clones in this library lack an XhoI site at their 3' ends."

ORIGIN

Query Match 2.1%; Score 21; DB 9; Length 694;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        456 TACTCCTGAAGAAGATGACAT 436
```

RESULT 53
DV622355/c
LOCUS DV622355 716 bp mRNA linear EST 01-NOV-2005
DEFINITION IV-1091-403D-A11.T7-1 UGIV-1091-Reseq Zea mays cDNA, mRNA sequence.
ACCESSION DV622355
VERSION DV622355.1 GI:78544857
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 716)
AUTHORS Zhou,R.L., Shendelman,J.M., Borsuk,L.A., Chen,H.D., Chen,Y.R. and Schnable,P.S.
TITLE Resequencing Unigene IV-1091 EST set
JOURNAL Unpublished (2005)
COMMENT Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
2035B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA
Tel: 515-294-0975
Fax: 515-294-5256
Email: schnable@iastate.edu.
FEATURES Location/Qualifiers
source 1. .716
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="taxon:4577"
/clone_lib="UGIV-1091-Reseq"

ORIGIN

Query Match 2.1%; Score 21; DB 10; Length 716;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        409 TACTCCTGAAGAAGATGACAT 389
```

RESULT 54
AY112414/c
LOCUS AY112414 724 bp mRNA linear HTC 01-MAR-2005
DEFINITION Zea mays CL8984_1 mRNA sequence.
ACCESSION AY112414
VERSION AY112414.1 GI:21217004
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 724)
AUTHORS Gardiner,J., Schroeder,S., Polacco,M.L., Sanchez-Villeda,H., Fang,Z., Morgante,M., Landewe,T., Fengler,K., Useche,F., Hanafey,M., Tingey,S., Chou,H., Wing,R., Soderlund,C. and Coe,E.H. Jr.
TITLE Anchoring 9,371 maize expressed sequence tagged unigenes to the bacterial artificial chromosome contig map by two-dimensional overgo hybridization
JOURNAL Plant Physiol. 134 (4), 1317-1326 (2004)
PUBMED 15020742
REFERENCE 2 (bases 1 to 724)
AUTHORS Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 3 (bases 1 to 724)
AUTHORS Coe,E.H.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.
FEATURES Location/Qualifiers
source 1. .724
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="MaizeGDB:633032"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Cornsensus Library"
/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN

Query Match 2.1%; Score 21; DB 6; Length 724;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        391 TACTCCTGAAGAAGATGACAT 371
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RESULT 55
CL163765/c
LOCUS CL163765 743 bp DNA linear GSS 06-JAN-2004
DEFINITION 104_357_10807387_116_31813_139 Sorghum methylation-filtered library (LibID: 104) Sorghum bicolor genomic clone 10807387, genomic survey

```
            sequence.
ACCESSION   CL163765
VERSION     CL163765.1  GI:40671650
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 743)
  AUTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
            Martienssen,R.A.
  TITLE     Sorghum genome sequencing by methylation filtration
  JOURNAL   PLoS Biol. 3 (1), e13 (2005)
   PUBMED   15660154
COMMENT     Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: 357  row: f  column: 19
            Seq primer: T3 Reverse
            Class: methylation filtered
            High quality sequence stop: 743.
FEATURES             Location/Qualifiers
     source          1. .743
                     /organism="Sorghum bicolor"
                     /mol_type="genomic DNA"
                     /cultivar="ATx623"
                     /db_xref="taxon:4558"
                     /clone="10807387"
                     /clone_lib="Sorghum methylation-filtered library (LibID:
                     104)"
                     /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                     prepared from purified nuclei was randomly sheared,
                     end-repaired, size fractionated to enrich for the 0.5 to 5
                     kb fraction, ligated into HincII-digested pBCSK(-) vector
                     and electroporated into E. coli cells. This is a
                     methylation-filtered library."
ORIGIN

  Query Match             2.1%;  Score 21;  DB 12;  Length 743;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        441 AATCAGTACCGATTTGAAATT 461
              |||||||||||||||||||||
Db         77 AATCAGTACCGATTTGAAATT 57


RESULT 56
AG462380
LOCUS       AG462380                755 bp    DNA     linear   GSS 22-DEC-2004
DEFINITION  Mus musculus molossinus DNA, clone:MSMg01-350N23.T7, genomic survey
            sequence.
ACCESSION   AG462380
VERSION     AG462380.1  GI:48159636
KEYWORDS    GSS.
SOURCE      Mus musculus molossinus (Japanese wild mouse)
  ORGANISM  Mus musculus molossinus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T.,
            Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and
            Shiroishi,T.
  TITLE     Contribution of Asian mouse subspecies Mus musculus molossinus to
            genomic constitution of strain C57BL/6J, as defined by BAC-end
            sequence-SNP analysis
  JOURNAL   Genome Res. 14 (12), 2439-2447 (2004)
   PUBMED   15574823
REFERENCE   2  (bases 1 to 755)
  AUTHORS   Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
            (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the mouse BAC library MSMg01. For BAC
            library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
            Tsukuba Institude, Bio Resource Center,
            The Institute of Physical and Chemical Research (RIKEN) 3-1-1
            Koyadai, Tsukuba, 305-0074 Japan
            phone: 81-298-36-9189, fax: 81-298-36-9199
            e-mail: abe@rtc.riken.jp
            PRIMERS
            Sequencing : T7
            LIBRARY
            Vector     : pBACe3.6
            R.Site 1   : EcoRI
            R.Site 2   : EcoRI.
FEATURES             Location/Qualifiers
     source          1. .755
                     /organism="Mus musculus molossinus"
                     /mol_type="genomic DNA"
                     /sub_species="molossinus"
                     /db_xref="taxon:57486"
                     /clone="MSMg01-350N23.T7"
                     /sex="male"
                     /tissue_type="mixture of kidney and spleen"
                     /clone_lib="MSMg01 Mouse Male BAC Library"
ORIGIN

  Query Match             2.1%;  Score 21;  DB 14;  Length 755;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        346 ATCTTAAGGGAACAGAAAGAA 366
              |||||||||||||||||||||
Db        102 ATCTTAAGGGAACAGAAAGAA 122


RESULT 57
CC698019/c
LOCUS       CC698019                762 bp    DNA     linear   GSS 19-JUN-2003
DEFINITION  OGWBY19TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0532D13,
            genomic survey sequence.
ACCESSION   CC698019
VERSION     CC698019.1  GI:32102795
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
            Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
  TITLE     Consortium for Maize Genomics
  JOURNAL   Unpublished (2002)
COMMENT     Other_GSSs: OGWBY19TV
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TR
            Class: methylation filtered.
```

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FEATURES             Location/Qualifiers
     source          1. .762
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBMa0532D13"
                     /clone_lib="ZM_0.7_1.5_KB"
                     /note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
                     methylation filtered genomic DNA library"
ORIGIN

  Query Match             2.1%;  Score 21;  DB 12;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        308 TACTCCTGAAGAAGATGACAT 288


RESULT 58
CG122646
LOCUS       CG122646                803 bp    DNA     linear   GSS 20-AUG-2003
DEFINITION  PUIMH25TB ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0615F02,
            genomic survey sequence.
ACCESSION   CG122646
VERSION     CG122646.1  GI:34006083
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 803)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
  TITLE     Maize Genomics Consortium
  JOURNAL   Unpublished (2003)
COMMENT     Other_GSSs: PUIMH25TD
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TR
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .803
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBTa0615F02"
                     /clone_lib="ZM_0.6_1.0_KB"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
                     CoT selected genomic DNA library"
ORIGIN

  Query Match             2.1%;  Score 21;  DB 12;  Length 803;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        252 TACTCCTGAAGAAGATGACAT 272


RESULT 59
CG134486/c
LOCUS       CG134486                837 bp    DNA     linear   GSS 21-AUG-2003
DEFINITION  PUFSJ61TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0722K02,
            genomic survey sequence.
ACCESSION   CG134486
VERSION     CG134486.1  GI:34021933
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 837)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
  TITLE     Maize Genomics Consortium
  JOURNAL   Unpublished (2003)
COMMENT     Other_GSSs: PUFSJ61TB
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .837
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBTa0722K02"
                     /clone_lib="ZM_0.6_1.0_KB"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
                     CoT selected genomic DNA library"
ORIGIN

  Query Match             2.1%;  Score 21;  DB 12;  Length 837;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        441 AATCAGTACCGATTTGAAATT 461
              |||||||||||||||||||||
Db        401 AATCAGTACCGATTTGAAATT 381


RESULT 60
CC927699/c
LOCUS       CC927699                853 bp    DNA     linear   GSS 11-AUG-2003
DEFINITION  ZMMBBc0532M21r ZMMBBc Zea mays genomic clone ZMMBBc0532M21 3',
            genomic survey sequence.
ACCESSION   CC927699
VERSION     CC927699.1  GI:33578797
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 853)
  AUTHORS   Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
            Rouzard,K., Fuks,G., Yu,Y., Wing,R. and Messing,J.
  TITLE     Sequencing of the maize genome at PGIR (2003b)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Bharti,A.K.
            Dr.Joachim Messing's lab
            The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
            University
            190 Frelinghuysen Road, Piscataway, NJ 08854, USA
            Tel: 732 445 3801
            Fax: 732 445 5735
            Email: bharti@waksman.rutgers.edu
            Seq primer: SP6
```

```
            Class: BAC ends
            High quality sequence start: 431.
FEATURES             Location/Qualifiers
     source          1. .853
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /cultivar="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBBc0532M21"
                     /lab_host="E. coli DH10B"
                     /clone_lib="ZMMBBc"
                     /note="Vector: pTARBAC1.3; Site_1: BamHI; Site_2: BamHI"
ORIGIN

  Query Match             2.1%;  Score 21;  DB 12;  Length 853;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        708 GGACCCACCCAAGAACCTGCA 728
              |||||||||||||||||||||
Db         86 GGACCCACCCAAGAACCTGCA 66


RESULT 61
BF241716/c
LOCUS       BF241716                 895 bp    mRNA    linear   EST 14-NOV-2000
DEFINITION  601879850F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108381 5',
            mRNA sequence.
ACCESSION   BF241716
VERSION     BF241716.1  GI:11155642
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 895)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: CLONETECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM991  row: d  column: 14
            High quality sequence stop: 588.
FEATURES             Location/Qualifiers
     source          1. .895
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4108381"
                     /tissue_type="from acute myelogenous leukemia"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_55"
                     /note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
                     Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI
                     (ggccattatggcc); Double-stranded cDNA was prepared from
                     cell line RNA.  5' and 3' adaptors were used in cloning as
                     follows: 5' adaptor sequence:  5'-CACGGCCATTATGGCC-3' and
                     3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).   Average insert size
                     1.65 kb (range 0.9-4.0 kb).  14/15 colonies contained
                     inserts by PCR. This library was enriched for full-length
                     clones and was constructed by Clontech  Laboratories (Palo
                     Alto, CA)."
ORIGIN

  Query Match             2.1%;  Score 21;  DB 7;  Length 895;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        593 GTGCCTGCCCGGCTGCCGAGG 613
              |||||||||||||||||||||
Db        813 GTGCCTGCCCGGCTGCCGAGG 793


RESULT 62
CG033595/c
LOCUS       CG033595                 983 bp    DNA     linear   GSS 19-AUG-2003
DEFINITION  PUKDR51TB ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0795J06,
            genomic survey sequence.
ACCESSION   CG033595
VERSION     CG033595.1  GI:33905751
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 983)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
  TITLE     Maize Genomics Consortium
  JOURNAL   Unpublished (2003)
COMMENT     Other_GSSs: PUKDR51TD
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TR
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .983
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBTa0795J06"
                     /clone_lib="ZM_0.6_1.0_KB"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
                     CoT selected genomic DNA library"
ORIGIN

  Query Match             2.1%;  Score 21;  DB 12;  Length 983;
  Best Local Similarity   100.0%;  Pred. No. 29;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        267 TACTCCTGAAGAAGATGACAT 247


RESULT 63
BZ782656
LOCUS       BZ782656                 987 bp    DNA     linear   GSS 17-MAR-2003
DEFINITION  PUFDX77TB ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa297M10,
            genomic survey sequence.
ACCESSION   BZ782656
VERSION     BZ782656.1  GI:28976253
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 987)
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  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
  TITLE     Maize Genomics Consortium
  JOURNAL   Unpublished (2003)
COMMENT     Other_GSSs: PUFDX77TD
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TR
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBTa297M10"
                     /clone_lib="ZM_0.6_1.0_KB"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
                     CoT selected genomic DNA library"
ORIGIN

  Query Match             2.1%;  Score 21;  DB 12;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 29;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        463 TACTCCTGAAGAAGATGACAT 483


RESULT 64
BZ782662/c
LOCUS       BZ782662                 999 bp    DNA     linear   GSS 17-MAR-2003
DEFINITION  PUFDX77TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa297M10,
            genomic survey sequence.
ACCESSION   BZ782662
VERSION     BZ782662.1  GI:28976259
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 999)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
  TITLE     Maize Genomics Consortium
  JOURNAL   Unpublished (2003)
COMMENT     Other_GSSs: PUFDX77TB
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .999
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBTa297M10"
                     /clone_lib="ZM_0.6_1.0_KB"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
                     CoT selected genomic DNA library"
ORIGIN

  Query Match             2.1%;  Score 21;  DB 12;  Length 999;
  Best Local Similarity   100.0%;  Pred. No. 29;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 TACTCCTGAAGAAGATGACAT 173
              |||||||||||||||||||||
Db        686 TACTCCTGAAGAAGATGACAT 666


RESULT 65
CE034167
LOCUS       CE034167                 366 bp    DNA     linear   GSS 24-SEP-2003
DEFINITION  tigr-gss-dog-17000348379744 Dog Library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION   CE034167
VERSION     CE034167.1  GI:35059603
KEYWORDS    GSS.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 366)
  AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
            Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
            Venter,J.C.
  TITLE     The dog genome: survey sequencing and comparative analysis
  JOURNAL   Science 301 (5641), 1898-1903 (2003)
   PUBMED   14512627
COMMENT     Contact: Kirkness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirknes@tigr.org
            Class: shotgun.
FEATURES             Location/Qualifiers
     source          1. .366
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /strain="Standard Poodle"
                     /db_xref="taxon:9615"
                     /clone_lib="Dog Library"
                     /note="Site_1: BstXI; Libraries were prepared from
                     peripheral blood"
ORIGIN

  Query Match             2.0%;  Score 20;  DB 12;  Length 366;
  Best Local Similarity   100.0%;  Pred. No. 92;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        314 ACAAAAAGGAAGATGGAATT 333
              ||||||||||||||||||||
Db         58 ACAAAAAGGAAGATGGAATT 77


RESULT 66
DN901347
LOCUS       DN901347                 376 bp    mRNA    linear   EST 25-APR-2005
DEFINITION  naq18f07.y1 Zebrafish retina. Unnormalized (naq) Danio rerio cDNA
            clone naq18f07 5', mRNA sequence.
ACCESSION   DN901347
VERSION     DN901347.1  GI:62886110
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 376)
```

```
  AUTHORS   Wistow,G.
  TITLE     NEIBank analysis of Zebrafish retina
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Wistow G
            Section on Molecular Structure and Function
            National Eye Institute
            6/331, NIH, Bethesda, MD 20892-2740, USA
            Tel: 301 402 3452
            Fax: 301 496 0078
            Email: graeme@helix.nih.gov
            Plate: 18  row: f  column: 07
            Seq primer: Universal M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .376
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="naq18f07"
                     /tissue_type="Retina"
                     /dev_stage="Adult"
                     /lab_host="EMDH10B"
                     /clone_lib="Zebrafish retina. Unnormalized (naq)"
                     /note="Organ: Eye; Vector: pCMVSport6; RNA was extracted
                     from Zebrafish retina tissue. A directionally cloned cDNA
                     library in the pCMVSPORT6 vector (Invitrogen) was
                     constructed at Bioserve Biotechnology (Laurel MD)
                     essentially following the protocols of the SuperScript
                     Plasmid System, full details of which are contained in the
                     manufacturer's Instruction manual
                     (http://www.lifetech.com/). First strand synthesis was
                     carried out using a Not I primer-adapter
                     [5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)15-3']. cDNA was
                     cloned in Not I/Sal I sites. EST analysis was performed at
                     the NIH Intramural Sequencing Center (NISC). Analyzed data
                     available through http://neibank.nei.nih.gov."
ORIGIN

  Query Match             2.0%;  Score 20;  DB 9;  Length 376;
  Best Local Similarity   100.0%;  Pred. No. 92;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        842 AGAACAACAGAGAAAAGAAA 861
              ||||||||||||||||||||
Db         72 AGAACAACAGAGAAAAGAAA 91


RESULT 67
BH772784
LOCUS       BH772784                454 bp    DNA     linear   GSS 01-AUG-2002
DEFINITION  4CTF CTSSR-PCRlibrary Biomphalaria glabrata genomic clone 4-CTF,
            genomic survey sequence.
ACCESSION   BH772784
VERSION     BH772784.1  GI:22038714
KEYWORDS    GSS.
SOURCE      Biomphalaria glabrata
  ORGANISM  Biomphalaria glabrata
            Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata;
            Basommatophora; Lymnaeoidea; Planorbidae; Biomphalaria.
REFERENCE   1  (bases 1 to 454)
  AUTHORS   Caldeira,R.L., Carvalho,O.S., Lage,R.C.G., Cardoso,P.C.M. and
            Oliveira,G.C.
  TITLE     Sequence Characterization of Biomphalaria glabrata Simple Sequence
            Repeat Anchored Polymerase Chain Reaction Amplification Products
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Oliveira GC
            Laboratorio de Parasitologia Celular e Molecular
            Centro de Pesquisas Rene Rachou - FIOCRUZ
            Av. Augusto de Lima 1715, Barro Preto, Belo Horizonte, MG,
            30190-002, Brazil
            Tel: 55 31 32953566
            Fax: 55 31 32953115
            Email: oliveira@cpqrr.fiocruz.br
            PCR fragment amplified with CAA(CT)6.
            Seq primer: M13-Forward Universal
            Class: Random amplified microsatellites.
FEATURES             Location/Qualifiers
     source          1. .454
                     /organism="Biomphalaria glabrata"
                     /mol_type="genomic DNA"
                     /strain="Rene Rachou"
                     /db_xref="taxon:6526"
                     /clone="4-CTF"
                     /sex="hermaphrodite"
                     /dev_stage="Adult"
                     /clone_lib="CTSSR-PCRlibrary"
                     /note="The sequence was obtained by SSR-PCR amplification
                     using primer CAA(CT)6 for CT named clones or (CA)8RY for
                     CA named clones. The PCR products were cloned into the pCR
                     II vector (Invitrogen), selected on LB/amp plates and
                     sequenced in an ALF automated sequencer using the Thermo
                     Sequenase Kit (Amersham) using the universal reverse
                     primer."
ORIGIN

  Query Match             2.0%;  Score 20;  DB 11;  Length 454;
  Best Local Similarity   100.0%;  Pred. No. 94;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        848 ACAGAGAAAAGAAAGACAGA 867
              ||||||||||||||||||||
Db        404 ACAGAGAAAAGAAAGACAGA 423


RESULT 68
BM849607
LOCUS       BM849607                460 bp    mRNA    linear   EST 06-MAR-2002
DEFINITION  K-EST0129703 S21SNU520 Homo sapiens cDNA clone S21SNU520-38-F05 5',
            mRNA sequence.
ACCESSION   BM849607
VERSION     BM849607.1  GI:19206006
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 460)
  AUTHORS   Oh,J.H., Yang,J.O., Hahn,Y., Kim,M.R., Byun,S.S., Jeon,Y.J.,
            Kim,J.M., Song,K.S., Noh,S.M., Kim,S., Yoo,H.S., Kim,Y.S. and
            Kim,N.S.
  TITLE     Transcriptome analysis of human gastric cancer
  JOURNAL   Mamm. Genome 16 (12), 942-954 (2005)
   PUBMED   16341674
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 38  row: F  column: 05
            High quality sequence stop: 460.
FEATURES             Location/Qualifiers
     source          1. .460
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="S21SNU520-38-F05"
                     /sex="F"
                     /tissue_type="Stomach"
                     /cell_type="Floating aggregates"
                     /cell_line="SNU-520"
                     /lab_host="Top10F'"
                     /clone_lib="S21SNU520"
                     /note="Organ: Stomach; Vector: pTZ18RP1; Site_1: EcoRI;
                     Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
```

bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 2.0%; Score 20; DB 3; Length 460;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        842 AGAACAACAGAGAAAAGAAA 861
              ||||||||||||||||||||
Db         65 AGAACAACAGAGAAAAGAAA 84
```

RESULT 69
DN504486/c
LOCUS DN504486 467 bp mRNA linear EST 10-MAR-2005
DEFINITION HL010009000_F09_70_075 Equine lymphocyte cDNA Library Equus caballus cDNA clone HL010009000_F09_70_075, mRNA sequence.
ACCESSION DN504486
VERSION DN504486.1 GI:60714676
KEYWORDS EST.
SOURCE Equus caballus (horse)
ORGANISM Equus caballus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
REFERENCE 1 (bases 1 to 467)
AUTHORS Antczak,D.F.
TITLE Expressed sequence tags from a normalized equine lymphocyte cDNA library
JOURNAL Unpublished (2005)
COMMENT Contact: Antczak DF
Baker Institute for Animal Health, College of Veterinary Medicine
Cornell University
Hungerford Hill Rd., Ithaca, NY 14853, USA
Tel: 607.256.5633
Fax: 607.256.5608
Email: dfa1@cornell.edu
High quality sequence stop: 467.
FEATURES Location/Qualifiers
source 1. .467
/organism="Equus caballus"
/mol_type="mRNA"
/strain="Thoroughbred & Standardbred breeds"
/db_xref="taxon:9796"
/clone="HL010009000_F09_70_075"
/tissue_type="Lymphocytes"
/dev_stage="Unstimulated [Tag-(polyA)TCGGA] & stimulated in vitro with PWM [Tag-(polyA)TGCGA]"
/lab_host="DH12S E. coli cells (Invitrogen)"
/clone_lib="Equine lymphocyte cDNA Library"
/note="Vector: pGEM11Zf(+) (Promega); Site_1: EcoR1; Site_2: Not1"

ORIGIN

Query Match 2.0%; Score 20; DB 9; Length 467;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        356 AACAGAAAGAATCCAAAAAT 375
              ||||||||||||||||||||
Db         79 AACAGAAAGAATCCAAAAAT 60
```

RESULT 70
BI983815
LOCUS BI983815 479 bp mRNA linear EST 24-OCT-2001
DEFINITION fu08a02.x3 Campbell zebrafish ovary Danio rerio cDNA clone IMAGE:5304482 3', mRNA sequence.
ACCESSION BI983815
VERSION BI983815.1 GI:16374696
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 479)
AUTHORS Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
TITLE WashU Zebrafish EST Project 1998
JOURNAL Unpublished (1998)
COMMENT Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
cDNA Library constructed by Library constructed by Invitrogen and donated by R. Campbell (Marine Biology Laboratory, Woods Hole, MA).
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
Seq primer: T7 from Gibco
High quality sequence stop: 417.
FEATURES Location/Qualifiers
source 1. .479
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:5304482"
/sex="female"
/dev_stage="4-5 months, 1 year and 2 years"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Campbell zebrafish ovary"
/note="Organ: ovary(pooled); Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Whole ovaries collected from zebrafish aged 4-5 months, 1 year and 2 years. Oligo-dT primed, directionally cloned. Average insert size 2 kb. Library constructed by Invitrogen and donated by R. Campbell (Marine Biology Laboratory, Woods Hole, MA)."

ORIGIN

Query Match 2.0%; Score 20; DB 2; Length 479;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        842 AGAACAACAGAGAAAAGAAA 861
              ||||||||||||||||||||
Db        188 AGAACAACAGAGAAAAGAAA 207
```

RESULT 71
BH772785/c
LOCUS BH772785 486 bp DNA linear GSS 01-AUG-2002
DEFINITION 4CTr CTSSR-PCRlibrary Biomphalaria glabrata genomic clone 4-CTr, genomic survey sequence.
ACCESSION BH772785
VERSION BH772785.1 GI:22038715
KEYWORDS GSS.
SOURCE Biomphalaria glabrata

```
  ORGANISM  Biomphalaria glabrata
            Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata;
            Basommatophora; Lymnaeoidea; Planorbidae; Biomphalaria.
REFERENCE   1  (bases 1 to 486)
  AUTHORS   Caldeira,R.L., Carvalho,O.S., Lage,R.C.G., Cardoso,P.C.M. and
            Oliveira,G.C.
  TITLE     Sequence Characterization of Biomphalaria glabrata Simple Sequence
            Repeat Anchored Polymerase Chain Reaction Amplification Products
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Oliveira GC
            Laboratorio de Parasitologia Celular e Molecular
            Centro de Pesquisas Rene Rachou - FIOCRUZ
            Av. Augusto de Lima 1715, Barro Preto, Belo Horizonte, MG,
            30190-002, Brazil
            Tel: 55 31 32953566
            Fax: 55 31 32953115
            Email: oliveira@cpqrr.fiocruz.br
            PCR fragment amplified with CAA(CT)6.
            Seq primer: M13-Forward Universal
            Class: Random amplified microsatellites.
FEATURES             Location/Qualifiers
     source          1. .486
                     /organism="Biomphalaria glabrata"
                     /mol_type="genomic DNA"
                     /strain="Rene Rachou"
                     /db_xref="taxon:6526"
                     /clone="4-CTr"
                     /sex="hermaphrodite"
                     /dev_stage="Adult"
                     /clone_lib="CTSSR-PCRlibrary"
                     /note="The sequence was obtained by SSR-PCR amplification
                     using primer CAA(CT)6 for CT named clones or (CA)8RY for
                     CA named clones. The PCR products were cloned into the pCR
                     II vector (Invitrogen), selected on LB/amp plates and
                     sequenced in an ALF automated sequencer using the Thermo
                     Sequenase Kit (Amersham) using the universal reverse
                     primer."
ORIGIN

  Query Match             2.0%;  Score 20;  DB 11;  Length 486;
  Best Local Similarity   100.0%;  Pred. No. 95;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        848 ACAGAGAAAAGAAAGACAGA 867
              ||||||||||||||||||||
Db        201 ACAGAGAAAAGAAAGACAGA 182


RESULT 72
AI292392
LOCUS       AI292392                488 bp    mRNA    linear   EST 01-DEC-1998
DEFINITION  NYZ036 Appel-Eisen zebrafish embryo 15-19 hr Danio rerio cDNA clone
            ZAE24 3', mRNA sequence.
ACCESSION   AI292392
VERSION     AI292392.1  GI:3941779
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 488)
  AUTHORS   Gates,M.A., Cardozo,T., Tobin,T., Egan,E., Sirotkin,H., Schier,A.F.
            and Talbot,W.S.
  TITLE     NYU zebrafish embryo EST project
  JOURNAL   Unpublished (1998)
COMMENT     Contact: William S. Talbot
            Skirball Institute, New York University School of Medicine
            540 First Avenue, New York, NY 10016, USA
            Fax: 212 263 7760
            Email: talbot@saturn.med.nyu.edu
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .488
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="ZAE24"
                     /sex="mixed"
                     /tissue_type="pooled 15-19 hr zebrafish embryos"
                     /clone_lib="Appel-Eisen zebrafish embryo 15-19 hr"
                     /note="Vector: pBluescript SK (-); Site_1: EcoRI; Site_2:
                     XhoI; Library was constructed by Bruce Appel and Judith
                     Eisen in Stratagene Uni-Zap XR lambda vector with Zap-cDNA
                     synthesis kit: EcoRI linkers were added to 5' ends and
                     XhoI linkers were added to 3' ends and resulting cDNAs
                     were ligated into Uni-Zap XR lambda vector. In vivo mass
                     excision was used to generate cDNAs in pBluescript SK."
ORIGIN

  Query Match             2.0%;  Score 20;  DB 1;  Length 488;
  Best Local Similarity   100.0%;  Pred. No. 95;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        842 AGAACAACAGAGAAAAGAAA 861
              ||||||||||||||||||||
Db        149 AGAACAACAGAGAAAAGAAA 168


RESULT 73
BI476340
LOCUS       BI476340                496 bp    mRNA    linear   EST 26-JUL-2002
DEFINITION  fq26h04.x3 zebrafish adult brain Danio rerio cDNA clone
            IMAGE:4832862 3', mRNA sequence.
ACCESSION   BI476340
VERSION     BI476340.1  GI:15309207
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 496)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
            Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library Preparation: John Ngai. cDNA Library Arrayed by:
            Matthew Clark. DNA Sequencing by: Washington University Genome
            Sequencing Center Clone distribution: Genome Systems, St. Louis,
            Missouri (web address: www.genomesystems.com) (email contact:
            info@genomesystems.com) and Research Genetics, Huntsville, Alabama
            (web address: www.resgen.com) (email contact: info@resgen.com) and
            RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
            www.rzpd.de)
            Seq primer: -40UP
            High quality sequence stop: 447.
FEATURES             Location/Qualifiers
     source          1. .496
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:4832862"
                     /sex="mixed male and female"
                     /tissue_type="brain"
                     /dev_stage="adult"
```

```
                     /lab_host="E. coli DH10B"
                     /clone_lib="zebrafish adult brain"
                     /note="Vector: pZIPLOX; Site_1: NotI; Site_2: SalI;
                     Original library was constructed in lambdaZIPLOX.  Mass
                     excision of the cDNA library was performed to yield
                     pZIPLOX plasmids. Insert check was done in original
                     library."
ORIGIN

  Query Match             2.0%;  Score 20;  DB 2;  Length 496;
  Best Local Similarity   100.0%;  Pred. No. 95;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        842 AGAACAACAGAGAAAAGAAA 861
              ||||||||||||||||||||
Db         84 AGAACAACAGAGAAAAGAAA 103


RESULT 74
BI981239
LOCUS       BI981239                504 bp    mRNA    linear   EST 26-JUL-2002
DEFINITION  fu41h06.x1 zebrafish adult brain Danio rerio cDNA clone
            IMAGE:5332091 3', mRNA sequence.
ACCESSION   BI981239
VERSION     BI981239.1  GI:16369655
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 504)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
            Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library Preparation: John Ngai. cDNA Library Arrayed by:
            Matthew Clark. DNA Sequencing by: Washington University Genome
            Sequencing Center Clone distribution: Genome Systems, St. Louis,
            Missouri (web address: www.genomesystems.com) (email contact:
            info@genomesystems.com) and Research Genetics, Huntsville, Alabama
            (web address: www.resgen.com) (email contact: info@resgen.com) and
            RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
            www.rzpd.de)
            Seq primer: -40UP
            High quality sequence stop: 444.
FEATURES             Location/Qualifiers
     source          1. .504
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:5332091"
                     /sex="mixed male and female"
                     /tissue_type="brain"
                     /dev_stage="adult"
                     /lab_host="E. coli DH10B"
                     /clone_lib="zebrafish adult brain"
                     /note="Vector: pZIPLOX; Site_1: NotI; Site_2: SalI;
                     Original library was constructed in lambdaZIPLOX.  Mass
                     excision of the cDNA library was performed to yield
                     pZIPLOX plasmids. Insert check was done in original
                     library."
ORIGIN

  Query Match             2.0%;  Score 20;  DB 2;  Length 504;
  Best Local Similarity   100.0%;  Pred. No. 95;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        842 AGAACAACAGAGAAAAGAAA 861
              ||||||||||||||||||||
Db         83 AGAACAACAGAGAAAAGAAA 102


RESULT 75
CB179502
LOCUS       CB179502                515 bp    mRNA    linear   EST 31-JAN-2003
DEFINITION  EST0595 Zea mays sperm cell cDNA library Zea mays cDNA clone
            Zmsp3098 5' similar to putative polyprotein, mRNA sequence.
ACCESSION   CB179502
VERSION     CB179502.1  GI:28187892
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 515)
  AUTHORS   Engel,M.L., Chaboud,A., Dumas,C. and McCormick,S.
  TITLE     Sperm cells of Zea mays have a complex complement of mRNAs
  JOURNAL   Plant J. 34 (5), 697-707 (2003)
   PUBMED   12787250
COMMENT     Contact: McCormick, S.
            Plant Gene Expression Center
            USDA/ARS
            800 Buchanan St. Albany, CA 94710, USA
            Tel: 510 559 5906
            Fax: 510 559 5678
            Email: sheilamc@nature.berkeley.edu.
FEATURES             Location/Qualifiers
     source          1. .515
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="A188"
                     /db_xref="taxon:4577"
                     /clone="Zmsp3098"
                     /cell_type="sperm"
                     /clone_lib="Zea mays sperm cell cDNA library"
                     /note="Vector: Clontech Triplex2; RNA was isolated from
                     fluorescent-activated cell sorted sperm cells. A cDNA
                     library was constructed by oligo dT priming using the
                     Clontech SMART cDNA synthesis kit. The cDNAs were
                     directionally cloned."
ORIGIN

  Query Match             2.0%;  Score 20;  DB 4;  Length 515;
  Best Local Similarity   100.0%;  Pred. No. 95;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        375 TAAGATCTTTCTAAAATGTG 394
              ||||||||||||||||||||
Db        182 TAAGATCTTTCTAAAATGTG 201


RESULT 76
BM270069
LOCUS       BM270069                520 bp    mRNA    linear   EST 08-JUL-2004
DEFINITION  sak24b12.y1 Gm-c1075 Glycine max cDNA clone SOYBEAN CLONE ID:
            Gm-c1075-3912 5' similar to TR:O22892 O22892 T2P4.22 PROTEIN. ;,
            mRNA sequence.
ACCESSION   BM270069
VERSION     BM270069.1  GI:17963327
KEYWORDS    EST.
SOURCE      Glycine max (soybean)
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
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            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 520)
  AUTHORS   Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
            Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
            Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
            Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
            Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
            McCann,R., Waterston,R. and Wilson,R.
  TITLE     Public Soybean EST Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            When it has been determined, an EST from the other end of this
            clone is listed in the 'Other ESTs on clone' field. This clone is
            available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
            57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
            Seq primer: -40RP from Gibco
            High quality sequence stop: 435.
FEATURES             Location/Qualifiers
     source          1. .520
                     /organism="Glycine max"
                     /mol_type="mRNA"
                     /cultivar="Jack"
                     /db_xref="taxon:3847"
                     /clone="SOYBEAN CLONE ID: Gm-c1075-3912"
                     /tissue_type="differentiating somatic embryos cultered on
                     MSM6AC"
                     /lab_host="DH10B"
                     /clone_lib="Gm-c1075"
                     /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
                     XhoI; The cDNA library was constructed from mRNA isolated
                     from differentiating  somatic embryos cultered on MSM6AC.
                     The library was prepared using the  Stratagene pBluescript
                     II SK(+) library construction kit. Complementary  DNA was
                     synthesized from mRNA using a primer consisting of a
                     poly(dT)  sequence with an XhoI restriction site. EcoRI
                     adaptors were ligated to the  blunt-ended cDNA fragments
                     followed by XhoI digestion. The cDNA fragments  were
                     directionally cloned into the EcoRI-XhoI restriction site
                     of the  pBluescript vector. The ligated cDNA fragments
                     were transformed into E.coli ElectroMax DH10B host cells.
                     Tissue culture and library construction were performed by
                     Franooise Thibaud-Nissen and Anu Khana (Lila Vodkin lab,
                     University of Illinois)."
ORIGIN

  Query Match             2.0%;  Score 20;  DB 2;  Length 520;
  Best Local Similarity   100.0%;  Pred. No. 95;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        841 AAGAACAACAGAGAAAAGAA 860
              ||||||||||||||||||||
Db         35 AAGAACAACAGAGAAAAGAA 54


RESULT 77
BQ777940
LOCUS       BQ777940                526 bp    mRNA    linear   EST 26-JUL-2002
DEFINITION  il39a02.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6032162 5',
            mRNA sequence.
ACCESSION   BQ777940
VERSION     BQ777940.1  GI:21986412
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 526)
  AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
            Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
            Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
            Williams,T., Jackson,Y. and Bowers,Y.
  TITLE     Endocrine Pancreas Consortium
  JOURNAL   Unpublished (2000)
COMMENT     Other_ESTs: il39a02.x1
            Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
            Washington University Genome Sequencing Center For information on
            obtaining a clone please contact: Dr. Hiroshi Inoue
            (hinoue@im.wustl.edu)
            Seq primer: -40RP from Gibco
            High quality sequence stop: 412.
FEATURES             Location/Qualifiers
     source          1. .526
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6032162"
                     /tissue_type="Purified pancreatic islet"
                     /lab_host="DH10B"
                     /clone_lib="HR85 islet"
                     /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
                     NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
                     Size-selected on agarose gel. Average insert size ~1kb. 5'
                     XhoI site was destroyed after directional cloning.
                     Amplified once. Contact information: Hiroshi Inoue, MD,
                     Metabolism Div. (Alan Permutt Lab), Washington University
                     School of Medicine, Box 8127, 660 South Euclid Ave., St.
                     Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
                     314-362-1916, Fax: 314-747-2692."
ORIGIN

  Query Match             2.0%;  Score 20;  DB 3;  Length 526;
  Best Local Similarity   100.0%;  Pred. No. 95;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        842 AGAACAACAGAGAAAAGAAA 861
              ||||||||||||||||||||
Db        109 AGAACAACAGAGAAAAGAAA 128


RESULT 78
CW070565/c
LOCUS       CW070565                528 bp    DNA     linear   GSS 28-OCT-2004
DEFINITION  104_321_10526839_5_30098 Sorghum methylation filtered library
            (LibID: 104) Sorghum bicolor genomic clone 10526839, genomic survey
            sequence.
ACCESSION   CW070565
VERSION     CW070565.1  GI:54747295
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 528)
  AUTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
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            Martienssen,R.A.
  TITLE     Sorghum genome sequencing by methylation filtration
  JOURNAL   PLoS Biol. 3 (1), e13 (2005)
   PUBMED   15660154
COMMENT     Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: 321  row: n  column: 05
            Seq primer: SKPrimer Reverse
            Class: methylation filtered
            High quality sequence stop: 528.
FEATURES             Location/Qualifiers
     source          1. .528
                     /organism="Sorghum bicolor"
                     /mol_type="genomic DNA"
                     /cultivar="ATx623"
                     /db_xref="taxon:4558"
                     /clone="10526839"
                     /clone_lib="Sorghum methylation filtered library (LibID:
                     104)"
                     /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                     prepared from purified nuclei was randomly sheared,
                     end-repaired, size fractionated to enrich for the 0.5 to 5
                     kb fraction, ligated into HincII-digested pBCSK(-) vector
                     and electroporated into E. coli cells. This is a
                     methylation filtered library."
ORIGIN

  Query Match             2.0%;  Score 20;  DB 13;  Length 528;
  Best Local Similarity   100.0%;  Pred. No. 95;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        305 TCCTGATACACAAAAAGGAA 324
              ||||||||||||||||||||
Db        388 TCCTGATACACAAAAAGGAA 369


RESULT 79
CK902268
LOCUS       CK902268                535 bp    mRNA    linear   EST 11-MAR-2004
DEFINITION  il39a02.x5 HR85 islet Homo sapiens cDNA clone IMAGE:6032162 3',
            mRNA sequence.
ACCESSION   CK902268
VERSION     CK902268.1  GI:45363799
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 535)
  AUTHORS   Melton,D., Meadows,A., Clifton,S., Hillier,L., Marra,M., Pape,D.,
            Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B.,
            Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M.,
            McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and
            Bowers,Y.
  TITLE     WashU-Harvard Pancreas EST Project
  JOURNAL   Unpublished (2000)
COMMENT     Other_ESTs: il39a02.y1
            Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            This read is a 3' RESEQUENCE of a previously sequenced pancreas
            clone
            Good hit to opposite strand read. . .wrong orientation BUT PASSED FOR
            MOUSE-PANCREAS VERIFICATION
            Seq primer: -40RP from Gibco
            High quality sequence stop: 535.
FEATURES             Location/Qualifiers
     source          1. .535
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6032162"
                     /tissue_type="Purified pancreatic islet"
                     /lab_host="DH10B"
                     /clone_lib="HR85 islet"
                     /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
                     NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
                     Size-selected on agarose gel. Average insert size ~1kb. 5'
                     XhoI site was destroyed after directional cloning.
                     Amplified once. Contact information: Hiroshi Inoue, MD,
                     Metabolism Div. (Alan Permutt Lab), Washington University
                     School of Medicine, Box 8127, 660 South Euclid Ave., St.
                     Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
                     314-362-1916, Fax: 314-747-2692."
ORIGIN

  Query Match             2.0%;  Score 20;  DB 5;  Length 535;
  Best Local Similarity   100.0%;  Pred. No. 96;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        842 AGAACAACAGAGAAAAGAAA 861
              ||||||||||||||||||||
Db        108 AGAACAACAGAGAAAAGAAA 127


RESULT 80
CO854235/c
LOCUS       CO854235                555 bp    mRNA    linear   EST 21-NOV-2004
DEFINITION  LM_SH5_004998 Locusta migratoria solitarious phase's head cDNA
            library Locusta migratoria cDNA, mRNA sequence.
ACCESSION   CO854235
VERSION     CO854235.1  GI:55914042
KEYWORDS    EST.
SOURCE      Locusta migratoria (migratory locust)
  ORGANISM  Locusta migratoria
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
            Acridoidea; Acrididae; Oedipodinae; Locusta.
REFERENCE   1  (bases 1 to 555)
  AUTHORS   Kang,L., Chen,X., Zhou,Y., Liu,B., Zheng,W., Li,R., Wang,J. and
            Yu,J.
  TITLE     The analysis of large-scale gene expression correlated to the phase
            changes of the migratory locust
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 101 (51), 17611-17615 (2004)
   PUBMED   15591108
COMMENT     Contact: Le Kang
            National Laboratory of Integrated Management of Insect Pests and
            Rodents
            Institute of zoology, Chinese Academy of Sciences
            25 Beisihuanxi Road, Haidian, Beijing, 100080, China
            Tel: 86-10-68597439
            Fax: 86-10-68597486
            Email: lkang@panda.ioz.ac.cn
            High quality sequence stop: 555.
FEATURES             Location/Qualifiers
     source          1. .555
                     /organism="Locusta migratoria"
                     /mol_type="mRNA"
                     /db_xref="taxon:7004"
                     /tissue_type="head"
                     /dev_stage="fifth-instar"
                     /clone_lib="Locusta migratoria solitarious phase's head
                     cDNA library"
ORIGIN

  Query Match             2.0%;  Score 20;  DB 8;  Length 555;
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  Best Local Similarity   100.0%;  Pred. No. 96;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        674 CCAGCAGCTTCTTCATCAGG 693
              ||||||||||||||||||||
Db        362 CCAGCAGCTTCTTCATCAGG 343


RESULT 81
BI785024
LOCUS       BI785024                556 bp    mRNA    linear   EST 21-JUL-2004
DEFINITION  saf96h10.y3 Gm-c1079 Glycine max cDNA clone GENOME SYSTEMS CLONE
            ID: Gm-c1079-1915 5' similar to TR:O22892 O22892 T2P4.22 PROTEIN.
            ;, mRNA sequence.
ACCESSION   BI785024
VERSION     BI785024.1  GI:15812749
KEYWORDS    EST.
SOURCE      Glycine max (soybean)
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 556)
  AUTHORS   Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
            Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
            Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
            Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
            Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
            McCann,R., Waterston,R. and Wilson,R.
  TITLE     Public Soybean EST Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            When it has been determined, an EST from the other end of this
            clone is listed in the 'Other ESTs on clone' field. This clone is
            available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
            57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
            Seq primer: -40RP from Gibco
            High quality sequence stop: 421.
FEATURES             Location/Qualifiers
     source          1. .556
                     /organism="Glycine max"
                     /mol_type="mRNA"
                     /cultivar="Bragg"
                     /db_xref="taxon:3847"
                     /clone="GENOME SYSTEMS CLONE ID: Gm-c1079-1915"
                     /tissue_type="Roots of 8 day old 'Bragg' seedlings"
                     /dev_stage="8 days old"
                     /lab_host="DH10B"
                     /clone_lib="Gm-c1079"
                     /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
                     XhoI; The mRNA was isolated from roots of 8 day old
                     'Bragg' seedlings that were mock-infected 72 hours prior
                     to harvest. Dr. Gary Stacey generously  donated the
                     tissue. The roots were flash-frozen in liquid nitrogen.
                     Stratagene's cDNA Synthesis Kit (catalog number 200401)
                     was used  to synthesize the cDNA. First-strand synthesis
                     was performed with  5-methyl dCTP, hence the ligated cDNA
                     was hemimethylated. A modification  of Stratagene's
                     first-strand synthesis primer was used. An 'anchor'
                     nucleotide (V=A, C, or G) was added to the 3' end of the
                     primer [GAGAGAGAGAGAGAGAGAGAACTAGTCTCGAG(T)18V] to anchor
                     the primer at the 5' end of the poly(A) tract. After
                     second-strand synthesis, the cDNA ends were filled in with
                     cloned Pfu DNA, ligated to EcoRI adapters and subsequently
                     phosphorylated. The cDNA was then precipitated and
                     redissolved in sterile, RNase-, DNase-free water. The XhoI
                     site within the first- strand synthesis primer was then
                     restricted by digestion with XhoI from Promega (40U/ul);
                     all XhoI sites in the cDNA would be protected by their
                     hemimethylated status. The cDNA constructs were
                     size-fractionated with  a 500bp cutoff, using Sephacryl
                     S-500 High Resolution (Pharmacia Biotech) in a 2-mm
                     diameter column and a bed volume of approximately 1ml. The
                     column eluent was precipitated, redissolved, and ligated
                     into Stratagene's pBluescript II XR Predigested vector
                     (pBluescript II SK(+) vector that has been digested with
                     EcoRI and XhoI, and phosphorylated by Stratagene). This
                     library was constucted in the laboratory of Dr. Paul Keim
                     and Dr. Virginia H. Coryell at Northern Arizona
                     University."
ORIGIN

  Query Match             2.0%;  Score 20;  DB 2;  Length 556;
  Best Local Similarity   100.0%;  Pred. No. 96;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        841 AAGAACAACAGAGAAAAGAA 860
              ||||||||||||||||||||
Db        160 AAGAACAACAGAGAAAAGAA 179


RESULT 82
AL956562
LOCUS       AL956562                563 bp    mRNA    linear   EST 04-DEC-2003
DEFINITION  AL956562 XGC-gastrula Xenopus tropicalis cDNA clone TGas105e12 5',
            mRNA sequence.
ACCESSION   AL956562
VERSION     AL956562.2  GI:38706017
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 563)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     On Nov 27, 2002 this sequence version replaced gi:25780157.
            Contact: Taylor R
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TGas105e12.p1kSP6
            Sequencing primer: SP6
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from stages 10-13
            gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with
            EcoRI at the 5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli XL1- blue.
FEATURES             Location/Qualifiers
     source          1. .563
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TGas105e12"
                     /dev_stage="gastrula (stages 10.5-12 mixed)"
                     /lab_host="Escherichia coli XL1-blue"
                     /clone_lib="XGC-gastrula"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from stages
                     10-13 gastrulae.  EcoRI-NotI cut cDNA was then ligated
                     into pCS107 with EcoRI at the 5' end and NotI at the 3'
                     end."
ORIGIN
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  Query Match             2.0%;  Score 20;  DB 1;  Length 563;
  Best Local Similarity   100.0%;  Pred. No. 96;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        250 GATGCTGGCCAGTATACCTG 269
              ||||||||||||||||||||
Db        246 GATGCTGGCCAGTATACCTG 265


RESULT 83
BJ030774
LOCUS       BJ030774                564 bp    mRNA    linear   EST 26-SEP-2003
DEFINITION  BJ030774 NIBB Mochii normalized Xenopus neurula library Xenopus
            laevis cDNA clone XL005c01 5', mRNA sequence.
ACCESSION   BJ030774
VERSION     BJ030774.1  GI:17377868
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Xenopus.
REFERENCE   1  (bases 1 to 564)
  AUTHORS   Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
            Kohara,Y.
  TITLE     Expressed genes in X. laevis embryo
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp
            The information of this clone is available through the following
            URL.
            http://xenopus.nibb.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .564
                     /organism="Xenopus laevis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8355"
                     /clone="XL005c01"
                     /tissue_type="whole embryo"
                     /dev_stage="stage 15"
                     /clone_lib="NIBB Mochii normalized Xenopus neurula
                     library"
ORIGIN

  Query Match             2.0%;  Score 20;  DB 2;  Length 564;
  Best Local Similarity   100.0%;  Pred. No. 96;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        250 GATGCTGGCCAGTATACCTG 269
              ||||||||||||||||||||
Db        178 GATGCTGGCCAGTATACCTG 197


RESULT 84
AI666909
LOCUS       AI666909                570 bp    mRNA    linear   EST 08-JUN-1999
DEFINITION  fd16d08.x1 Sugano Kawakami zebrafish DRA Danio rerio cDNA clone
            IMAGE:2351727 3', mRNA sequence.
ACCESSION   AI666909
VERSION     AI666909.1  GI:4805265
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 570)
  AUTHORS   Sugano,S., Kawakami,K., Johnson,S., Li,F., Marra,M., Eddy,S.,
            Hillier,L., Clifton,S., Allen,M., Gibbons,M., Jost,S., Kucaba,T.,
            Martin,J., Pape,D., Steptoe,M., Underwood,K., Theising,B.,
            Ritter,E., Bowers,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1999
  JOURNAL   Unpublished (1999)
COMMENT     Contact: S.L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Library constructed by Dr. Sumio Sugano and D. Koichi Kawakami DNA
            Sequencing by: Washington University Genome Sequencing Center
            Seq primer: T7 ET from Amersham
            High quality sequence stop: 499.
FEATURES             Location/Qualifiers
     source          1. .570
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /strain="AB"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:2351727"
                     /sex="mixed (one male and one female, including
                     unfertilized eggs)"
                     /dev_stage="adult"
                     /lab_host="DH10B (phage resistant)"
                     /clone_lib="Sugano Kawakami zebrafish DRA"
                     /note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
                     Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
                     with an oligo(dT) primer  [ATGTGGCCTTTTTTTTTTTTTTTT];
                     double-stranded cDNA was ligated to a  DraIII adaptor
                     [TGTTGGCCTACTGG], digested and cloned into distinct DraIII
                     sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
                     CACCATGTG). XhoI should be used to isolate the cDNA
                     insert.  Size selection was performed to exclude fragments
                     <1.5kb.  Library constructed by Dr. Sumio Sugano
                     (University of Tokyo Institute of Medical Science) and
                     kindly donated by Dr. Koichi Kawakami.  Custom primers for
                     sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
                     primer CGACCTGCAGCTCGAGCACA.  "
ORIGIN

  Query Match             2.0%;  Score 20;  DB 1;  Length 570;
  Best Local Similarity   100.0%;  Pred. No. 96;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        842 AGAACAACAGAGAAAAGAAA 861
              ||||||||||||||||||||
Db         83 AGAACAACAGAGAAAAGAAA 102


RESULT 85
BJ032049
LOCUS       BJ032049                571 bp    mRNA    linear   EST 26-SEP-2003
DEFINITION  BJ032049 NIBB Mochii normalized Xenopus neurula library Xenopus
            laevis cDNA clone XL015h03 5', mRNA sequence.
ACCESSION   BJ032049
VERSION     BJ032049.1  GI:17375617
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Xenopus.
REFERENCE   1  (bases 1 to 571)
  AUTHORS   Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
            Kohara,Y.
  TITLE     Expressed genes in X. laevis embryo
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
```

```
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp
            The information of this clone is available through the following
            URL.
            http://xenopus.nibb.ac.jp.
FEATURES              Location/Qualifiers
     source           1. .571
                      /organism="Xenopus laevis"
                      /mol_type="mRNA"
                      /db_xref="taxon:8355"
                      /clone="XL015h03"
                      /tissue_type="whole embryo"
                      /dev_stage="stage 15"
                      /clone_lib="NIBB Mochii normalized Xenopus neurula
                      library"
ORIGIN

  Query Match             2.0%;  Score 20;  DB 2;  Length 571;
  Best Local Similarity   100.0%;  Pred. No. 96;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        250 GATGCTGGCCAGTATACCTG 269
              ||||||||||||||||||||
Db        140 GATGCTGGCCAGTATACCTG 159


RESULT 86
BJ627752
LOCUS       BJ627752                 578 bp    mRNA    linear   EST 01-OCT-2003
DEFINITION  BJ627752 NIBB Mochii normalized Xenopus early gastrula library
            Xenopus laevis cDNA clone XL219d21 5', mRNA sequence.
ACCESSION   BJ627752
VERSION     BJ627752.1  GI:37274652
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Xenopus.
REFERENCE   1  (bases 1 to 578)
  AUTHORS   Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
            Kohara,Y.
  TITLE     Expressed genes in X. laevis embryo
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp
            The information of this clone is available through the following
            URL.
            http://xenopus.nibb.ac.jp.
FEATURES              Location/Qualifiers
     source           1. .578
                      /organism="Xenopus laevis"
                      /mol_type="mRNA"
                      /db_xref="taxon:8355"
                      /clone="XL219d21"
                      /tissue_type="whole embryo"
                      /dev_stage="stage 10.5"
                      /clone_lib="NIBB Mochii normalized Xenopus early gastrula
                      library"
ORIGIN

  Query Match             2.0%;  Score 20;  DB 2;  Length 578;
  Best Local Similarity   100.0%;  Pred. No. 96;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        250 GATGCTGGCCAGTATACCTG 269
              ||||||||||||||||||||
Db        417 GATGCTGGCCAGTATACCTG 436


RESULT 87
CX600301/c
LOCUS       CX600301                 621 bp    mRNA    linear   EST 13-JAN-2005
DEFINITION  CT020026A20C01 Equine Articular Cartilage cDNA Library Equus
            caballus cDNA clone CT020026A20C01, mRNA sequence.
ACCESSION   CX600301
VERSION     CX600301.1  GI:57713619
KEYWORDS    EST.
SOURCE      Equus caballus (horse)
  ORGANISM  Equus caballus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
REFERENCE   1  (bases 1 to 621)
  AUTHORS   MacLeod,J.N.
  TITLE     Expressed sequence tags from a normalized equine articular
            cartilage cDNA library
  JOURNAL   Unpublished (2005)
COMMENT     Contact: MacLeod JN
            Department of Veterinary Science
            University of Kentucky
            Gluck Equine Research Center, Lexington, KY 40546-0099, USA
            Tel: 859.257.4757
            Fax: 859.257.8542
            Email: jnmacleod@uky.edu
            High quality sequence stop: 621.
FEATURES              Location/Qualifiers
     source           1. .621
                      /organism="Equus caballus"
                      /mol_type="mRNA"
                      /strain="Thoroughbred"
                      /db_xref="taxon:9796"
                      /clone="CT020026A20C01"
                      /sex="male"
                      /tissue_type="articular cartilage"
                      /dev_stage="1.5 year old"
                      /lab_host="DH12S E. Coli cells (Invitrogen)"
                      /clone_lib="Equine Articular Cartilage cDNA Library"
                      /note="Vector: pGEM11Zf(+) (Promega); Site_1: EcoR1;
                      Site_2: Not1"
ORIGIN

  Query Match             2.0%;  Score 20;  DB 9;  Length 621;
  Best Local Similarity   100.0%;  Pred. No. 97;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        356 AACAGAAAGAATCCAAAAAT 375
              ||||||||||||||||||||
Db        569 AACAGAAAGAATCCAAAAAT 550


RESULT 88
AL900775
LOCUS       AL900775                 633 bp    mRNA    linear   EST 04-DEC-2003
DEFINITION  AL900775 XGC-egg Xenopus tropicalis cDNA clone TEgg018m09 5', mRNA
            sequence.
ACCESSION   AL900775
VERSION     AL900775.2  GI:38699538
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 633)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     On Sep 16, 2002 this sequence version replaced gi:22953010.
            Contact: Taylor R
            Sanger Institute
```

```
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TEgg018m09.p1kSP6
            Sequencing primer: SP6
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from egg.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
            5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli XL1-blue.
FEATURES              Location/Qualifiers
     source           1. .633
                      /organism="Xenopus tropicalis"
                      /mol_type="mRNA"
                      /db_xref="taxon:8364"
                      /clone="TEgg018m09"
                      /dev_stage="egg"
                      /lab_host="Escherichia coli XL1-blue"
                      /clone_lib="XGC-egg"
                      /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                      was oligo dT primed from 5ug of poly A+ RNA from egg.
                      EcoRI-NotI cut cDNA was then ligated into pCS107 with
                      EcoRI at the 5' end and NotI at the 3' end"
ORIGIN

  Query Match             2.0%;  Score 20;  DB 1;  Length 633;
  Best Local Similarity   100.0%;  Pred. No. 97;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        250 GATGCTGGCCAGTATACCTG 269
              ||||||||||||||||||||
Db        183 GATGCTGGCCAGTATACCTG 202


RESULT 89
CE454520/c
LOCUS       CE454520                646 bp    DNA     linear   GSS 27-SEP-2003
DEFINITION  tigr-gss-dog-17000319465791 Dog Library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION   CE454520
VERSION     CE454520.1  GI:36748105
KEYWORDS    GSS.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 646)
  AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
            Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
            Venter,J.C.
  TITLE     The dog genome: survey sequencing and comparative analysis
  JOURNAL   Science 301 (5641), 1898-1903 (2003)
   PUBMED   14512627
COMMENT     Contact: Kirkness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirknes@tigr.org
            Class: shotgun.
FEATURES              Location/Qualifiers
     source           1. .646
                      /organism="Canis familiaris"
                      /mol_type="genomic DNA"
                      /strain="Standard Poodle"
                      /db_xref="taxon:9615"
                      /clone_lib="Dog Library"
                      /note="Site_1: BstXI; Libraries were prepared from
                      peripheral blood"
ORIGIN

  Query Match             2.0%;  Score 20;  DB 12;  Length 646;
  Best Local Similarity   100.0%;  Pred. No. 97;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        307 CTGATACACAAAAAGGAAGA 326
              ||||||||||||||||||||
Db        140 CTGATACACAAAAAGGAAGA 121


RESULT 90
CZ709509
LOCUS       CZ709509                649 bp    DNA     linear   GSS 25-JUL-2005
DEFINITION  OC__Ba0030E21.r OC__Ba Oryza coarctata genomic clone OC__Ba0030E21
            3', genomic survey sequence.
ACCESSION   CZ709509
VERSION     CZ709509.1  GI:71114283
KEYWORDS    GSS.
SOURCE      Oryza coarctata (Porteresia coarctata)
  ORGANISM  Oryza coarctata
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 649)
  AUTHORS   Kim,H., Collura,K., Wissotski,M., Byrne,M., Stum,D., Smart,D.,
            Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and
            Wing,R.
  TITLE     OMAP (Oryza Map Alignment Project)- Arizona Genomics Institute
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Rod A. Wing
            Arizona Genomics Institute
            University of Arizona
            Forbes Building Room 303, Tucson, AZ 85721-0036, USA
            Tel: 520 626 9595
            Fax: 520 621 1259
            Email: rwing@genome.arizona.edu
            PCR PRimers
            FORWARD: TAA TAC GAC TCA CTA TAG GG
            BACKWARD: CAC TCA TTA GGC ACC CCA
            Plate: 0030  row: E  column: 21
            Seq primer: CAC TCA TTA GGC ACC CCA
            Class: BAC ends.
FEATURES              Location/Qualifiers
     source           1. .649
                      /organism="Oryza coarctata"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:77588"
                      /clone="OC__Ba0030E21"
                      /tissue_type="leaves"
                      /dev_stage="mature"
                      /lab_host="DH10B"
                      /clone_lib="OC__Ba"
                      /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
ORIGIN

  Query Match             2.0%;  Score 20;  DB 13;  Length 649;
  Best Local Similarity   100.0%;  Pred. No. 98;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        310 ATACACAAAAAGGAAGATGG 329
              ||||||||||||||||||||
Db         27 ATACACAAAAAGGAAGATGG 46


RESULT 91
BM096034
LOCUS       BM096034                654 bp    mRNA    linear   EST 20-NOV-2001
DEFINITION  fv29g12.x1 Sugano SJD adult male Danio rerio cDNA clone
            IMAGE:5410006 3', mRNA sequence.
ACCESSION   BM096034
VERSION     BM096034.1  GI:17025000
KEYWORDS    EST.
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```
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 654)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
            Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution information can be found through the I.M.A.G.E.
            Consortium/LLNL, send email to: info@image.llnl.gov
            High quality sequence stop: 525.
FEATURES             Location/Qualifiers
     source          1. .654
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:5410006"
                     /sex="male"
                     /tissue_type="whole body"
                     /dev_stage="adult"
                     /lab_host="DH10B (phage resistant)"
                     /clone_lib="Sugano SJD adult male"
                     /note="Vector: pME18S-FL3; Site_1: DraIII (CACCATGTG);
                     Site_2: DraIII (CACTGTGTG); 1st strand cDNA was primed
                     with an oligo(dT) primer  [ATGTGGCCTTTTTTTTTTTTTTTT];
                     double-stranded cDNA was ligated to a  DraIII adaptor
                     [TGTTGGCCTACTGG], digested and cloned into distinct DraIII
                     sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
                     CACCATGTG). XhoI should be used to isolate the cDNA
                     insert. Size selection was performed to exclude fragments
                     <1.5kb. Library constructed and donated by Dr. Sumio
                     Sugano (University of Tokyo Institute of Medical Science).
                     Custom primers for sequencing: 5' end primer
                     CTTCTGCTCTAAAAGCTGCG and 3' end primer
                     CGACCTGCAGCTCGAGCACA. "
ORIGIN

  Query Match             2.0%;  Score 20;  DB 2;  Length 654;
  Best Local Similarity   100.0%;  Pred. No. 98;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        842 AGAACAACAGAGAAAAGAAA 861
              ||||||||||||||||||||
Db         95 AGAACAACAGAGAAAAGAAA 114


RESULT 92
BJ042592
LOCUS       BJ042592                667 bp    mRNA    linear   EST 29-SEP-2003
DEFINITION  BJ042592 NIBB Mochii normalized Xenopus neurula library Xenopus
            laevis cDNA clone XL032c23 5', mRNA sequence.
ACCESSION   BJ042592
VERSION     BJ042592.1  GI:17392768
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Xenopus.
REFERENCE   1  (bases 1 to 667)
  AUTHORS   Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
            Kohara,Y.
  TITLE     Expressed genes in X. laevis embryo
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp
            The information of this clone is available through the following
            URL.
            http://xenopus.nibb.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .667
                     /organism="Xenopus laevis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8355"
                     /clone="XL032c23"
                     /tissue_type="whole embryo"
                     /dev_stage="stage 15"
                     /clone_lib="NIBB Mochii normalized Xenopus neurula
                     library"
ORIGIN

  Query Match             2.0%;  Score 20;  DB 2;  Length 667;
  Best Local Similarity   100.0%;  Pred. No. 98;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        250 GATGCTGGCCAGTATACCTG 269
              ||||||||||||||||||||
Db        281 GATGCTGGCCAGTATACCTG 300


RESULT 93
CT167835
LOCUS       CT167835                667 bp    DNA     linear   GSS 02-NOV-2005
DEFINITION  Sus scrofa genomic clone CH242-122N13, genomic survey sequence.
ACCESSION   CT167835
VERSION     CT167835.1  GI:79683824
KEYWORDS    GSS.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 667)
  AUTHORS   Humphray,S.J., Plumb,R.W. and Durham,J.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Unpublished
COMMENT     This sequence was generated from the SP6 end of BAC 122N13. 122N13
            is part of the CHORI-242 BAC Library created by P. de Jong. Further
            details: http://www.sanger.ac.uk/Projects/S_scrofa/.
FEATURES             Location/Qualifiers
     source          1. .667
                     /organism="Sus scrofa"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9823"
                     /clone="CH242-122N13"
                     /tissue_type="White blood cells"
                     /note="vector pTARBAC1.3_BamHI
                     sex female"
ORIGIN

  Query Match             2.0%;  Score 20;  DB 14;  Length 667;
  Best Local Similarity   100.0%;  Pred. No. 98;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        842 AGAACAACAGAGAAAAGAAA 861
```

```
                    ||||||||||||||||||||
Db        164 AGAACAACAGAGAAAAGAAA 183


RESULT 94
CC008436/c
LOCUS       CC008436                681 bp    DNA     linear   GSS 31-MAR-2003
DEFINITION  PUDHR12TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa213B24,
            genomic survey sequence.
ACCESSION   CC008436
VERSION     CC008436.1  GI:29387056
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 681)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
  TITLE     Maize Genomics Consortium
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .681
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBTa213B24"
                     /clone_lib="ZM_0.6_1.0_KB"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
                     CoT selected genomic DNA library"
ORIGIN

  Query Match             2.0%;  Score 20;  DB 12;  Length 681;
  Best Local Similarity   100.0%;  Pred. No. 98;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        375 TAAGATCTTTCTAAAATGTG 394
              ||||||||||||||||||||
Db        677 TAAGATCTTTCTAAAATGTG 658


RESULT 95
AZ424475/c
LOCUS       AZ424475                690 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0204A12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0204A12 F, genomic survey sequence.
ACCESSION   AZ424475
VERSION     AZ424475.1  GI:10548488
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 690)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0204  row: A  column: 12
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 690.
FEATURES             Location/Qualifiers
     source          1. .690
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0204A12"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             2.0%;  Score 20;  DB 11;  Length 690;
  Best Local Similarity   100.0%;  Pred. No. 98;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        551 ACAGGGATTATAAGAAGTAC 570
              ||||||||||||||||||||
Db        250 ACAGGGATTATAAGAAGTAC 231


RESULT 96
BZ240832/c
LOCUS       BZ240832                696 bp    DNA     linear   GSS 12-OCT-2002
DEFINITION  CH230-272O10.TJB CHORI-230 Segment 2 Rattus norvegicus genomic
            clone CH230-272O10, genomic survey sequence.
ACCESSION   BZ240832
VERSION     BZ240832.1  GI:23901096
KEYWORDS    GSS.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 696)
  AUTHORS   Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
            Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D.,
            Riggs,F., de Jong,P. and Fraser,C.M.
  TITLE     Rat BAC End Sequences from Library CHORI-230 MboI segment
  JOURNAL   Unpublished (1999)
COMMENT     Other_GSSs: CH230-272O10.TV
```

```
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the rat BAC library CHORI-230
            (http://www.chori.org/bacpac/rat230.htm). For BAC library
            availability, please contact Pieter de Jong (pdejong@mail.cho.org).
            Clones may be purchased from BACPAC Resources
            (http://www.chori.org/bacpac/or ering_information.htm). BAC end
            page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
            Plate: 272  row: O  column: 10
            Seq primer: SP6
            Class: BAC ends.
FEATURES              Location/Qualifiers
     source           1. .696
                      /organism="Rattus norvegicus"
                      /mol_type="genomic DNA"
                      /strain="BN/SsNHsd/MCW"
                      /db_xref="taxon:10116"
                      /clone="CH230-272O10"
                      /sex="Female"
                      /cell_type="Brain"
                      /clone_lib="CHORI-230 Segment 2"
                      /note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
                      CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
                      Pieter de Jong"
ORIGIN

  Query Match             2.0%;  Score 20;  DB 11;  Length 696;
  Best Local Similarity   100.0%;  Pred. No. 98;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        155 CTCCTGAAGAAGATGACATC 174
              ||||||||||||||||||||
Db        105 CTCCTGAAGAAGATGACATC 86


RESULT 97
BG740695
LOCUS       BG740695                698 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602631544F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4776634 5',
            mRNA sequence.
ACCESSION   BG740695
VERSION     BG740695.1  GI:14051348
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 698)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
            Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10629  row: h  column: 11
            High quality sequence stop: 694.
FEATURES              Location/Qualifiers
     source           1. .698
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:4776634"
                      /lab_host="DH10B (T1 phage-resistant)"
                      /clone_lib="NCI_CGAP_Skn3"
                      /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                      Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                      Average insert size 1.5kb.  Library constructed by Life
                      Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match             2.0%;  Score 20;  DB 2;  Length 698;
  Best Local Similarity   100.0%;  Pred. No. 98;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        842 AGAACAACAGAGAAAAGAAA 861
              ||||||||||||||||||||
Db        281 AGAACAACAGAGAAAAGAAA 300


RESULT 98
DT267303/c
LOCUS       DT267303                701 bp    mRNA    linear   EST 18-AUG-2005
DEFINITION  JGI_CAAV1671.rev CAAV Pimephales promelas testis 7-8 month adults,
            males and females pooled (H) Pimephales promelas cDNA clone
            CAAV1671 3', mRNA sequence.
ACCESSION   DT267303
VERSION     DT267303.1  GI:73569252
KEYWORDS    EST.
SOURCE      Pimephales promelas
  ORGANISM  Pimephales promelas
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Pimephales.
REFERENCE   1  (bases 1 to 701)
  AUTHORS   Richardson,P., Lucas,S., Rokhsar,D., Detter,J.C., Ng,D.C.,
            Brokstein,P. and Lindquist,E.A.
  TITLE     DOE Joint Genome Institute Pimephales promelas EST project
  JOURNAL   Unpublished (2005)
COMMENT     Other_ESTs: JGI_CAAV1671.fwd
            Contact: Lindquist,E.A., Richardson,P.
            DOE Joint Genome Institute
            2800 Mitchell Drive, Walnut Creek, CA 94598, USA
            Tel: 925 296 5600
            Fax: 925 296 5710
            Email: cdna@jgi-psf.org
            cDNA Library Preparation: DOE Joint Genome Institute:
            http://www.jgi.doe.gov
            DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
            Naming Conventions: EST name is generated by the concatenation of
            the JGI Clone Id and the direction of sequencing. The suffix '.rev'
            indicates a reverse sequencing read of the insert. It does not
            necessarily reflect the orientation of the insert.
            Small Insert: Based upon one or more sequencing reads of this clone
            where vector sequence was present at both ends, this clone has been
            determined to contain a cDNA insert on the order of 600-1000 bases.
            Plate: CAAV 0017  row: n  column: 9
            High quality sequence stop: 701.
FEATURES              Location/Qualifiers
     source           1. .701
                      /organism="Pimephales promelas"
                      /mol_type="mRNA"
                      /db_xref="taxon:90988"
                      /clone="CAAV1671"
                      /tissue_type="testis"
                      /clone_lib="CAAV Pimephales promelas testis 7-8 month
                      adults, males and females pooled (H)"
                      /note="Vector: pCMVsport6; The library was made from dT
                      primed cDNA and cloned into Invitrogen vector pCMVsport6.
                      Poly A RNA were primed with an oligo dT primer (5'-
                      GACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTT -3') ligated
                      to a SalI adapter (5'- TCGACCCACGCGTCCG and 5'-
                      CGGACGCGTGGG) and digested with NotI. cDNA was size
                      selected using 1.1% agarose gel electrophoresis (L
                      ~0.5-1.2k, M ~1.2-2.5k, H ~>2.5k) then ligated into NotI
```

and SalI digested pCMVsport6 vector. The work was done at DOE Joint Genome Institute."

ORIGIN

Query Match 2.0%; Score 20; DB 10; Length 701;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 684 CTTCATCAGGGACATCATCA 703
||||||||||||||||||||
Db 660 CTTCATCAGGGACATCATCA 641

RESULT 99
DT267304
LOCUS DT267304 701 bp mRNA linear EST 18-AUG-2005
DEFINITION JGI_CAAV1671.fwd CAAV Pimephales promelas testis 7-8 month adults, males and females pooled (H) Pimephales promelas cDNA clone CAAV1671 5', mRNA sequence.
ACCESSION DT267304
VERSION DT267304.1 GI:73569253
KEYWORDS EST.
SOURCE Pimephales promelas
ORGANISM Pimephales promelas
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Pimephales.
REFERENCE 1 (bases 1 to 701)
AUTHORS Richardson,P., Lucas,S., Rokhsar,D., Detter,J.C., Ng,D.C., Brokstein,P. and Lindquist,E.A.
TITLE DOE Joint Genome Institute Pimephales promelas EST project
JOURNAL Unpublished (2005)
COMMENT Other_ESTs: JGI_CAAV1671.rev
Contact: Lindquist,E.A., Richardson,P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org
cDNA Library Preparation: DOE Joint Genome Institute: http://www.jgi.doe.gov
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Naming Conventions: EST name is generated by the concatenation of the JGI Clone Id and the direction of sequencing. The suffix '.fwd' indicates a forward sequencing read of the insert. It does not necessarily reflect the orientation of the insert.
Small Insert: Based upon one or more sequencing reads of this clone where vector sequence was present at both ends, this clone has been determined to contain a cDNA insert on the order of 600-1000 bases.
Plate: CAAV 0017 row: n column: 9
High quality sequence stop: 701.
FEATURES Location/Qualifiers
source 1. .701
/organism="Pimephales promelas"
/mol_type="mRNA"
/db_xref="taxon:90988"
/clone="CAAV1671"
/tissue_type="testis"
/clone_lib="CAAV Pimephales promelas testis 7-8 month adults, males and females pooled (H)"
/note="Vector: pCMVsport6; The library was made from dT primed cDNA and cloned into Invitrogen vector pCMVsport6. Poly A RNA were primed with an oligo dT primer (5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTT -3') ligated to a SalI adapter (5'- TCGACCCACGCGTCCG and 5'-CGGACGCGTGGG) and digested with NotI. cDNA was size selected using 1.1% agarose gel electrophoresis (L ~0.5-1.2k, M ~1.2-2.5k, H ~>2.5k) then ligated into NotI and SalI digested pCMVsport6 vector. The work was done at DOE Joint Genome Institute."

ORIGIN

Query Match 2.0%; Score 20; DB 10; Length 701;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 684 CTTCATCAGGGACATCATCA 703
||||||||||||||||||||
Db 42 CTTCATCAGGGACATCATCA 61

RESULT 100
DT283860/c
LOCUS DT283860 719 bp mRNA linear EST 18-AUG-2005
DEFINITION JGI_CAAV11218.rev CAAV Pimephales promelas testis 7-8 month adults, males and females pooled (H) Pimephales promelas cDNA clone CAAV11218 3', mRNA sequence.
ACCESSION DT283860
VERSION DT283860.1 GI:73585809
KEYWORDS EST.
SOURCE Pimephales promelas
ORGANISM Pimephales promelas
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Pimephales.
REFERENCE 1 (bases 1 to 719)
AUTHORS Richardson,P., Lucas,S., Rokhsar,D., Detter,J.C., Ng,D.C., Brokstein,P. and Lindquist,E.A.
TITLE DOE Joint Genome Institute Pimephales promelas EST project
JOURNAL Unpublished (2005)
COMMENT Other_ESTs: JGI_CAAV11218.fwd
Contact: Lindquist,E.A., Richardson,P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org
cDNA Library Preparation: DOE Joint Genome Institute: http://www.jgi.doe.gov
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Naming Conventions: EST name is generated by the concatenation of the JGI Clone Id and the direction of sequencing. The suffix '.rev' indicates a reverse sequencing read of the insert. It does not necessarily reflect the orientation of the insert.
Poly-A: Based upon the presence of a run of 14 or more T residues at the beginning of the sequence, this clone was polyadenylated. The resulting Poly-T sequence has been removed.
Plate: CAAV 0117 row: c column: 21
High quality sequence stop: 643
POLYA=Yes.
FEATURES Location/Qualifiers
source 1. .719
/organism="Pimephales promelas"
/mol_type="mRNA"
/db_xref="taxon:90988"
/clone="CAAV11218"
/tissue_type="testis"
/clone_lib="CAAV Pimephales promelas testis 7-8 month adults, males and females pooled (H)"
/note="Vector: pCMVsport6; The library was made from dT primed cDNA and cloned into Invitrogen vector pCMVsport6. Poly A RNA were primed with an oligo dT primer (5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTT -3') ligated to a SalI adapter (5'- TCGACCCACGCGTCCG and 5'-CGGACGCGTGGG) and digested with NotI. cDNA was size selected using 1.1% agarose gel electrophoresis (L ~0.5-1.2k, M ~1.2-2.5k, H ~>2.5k) then ligated into NotI and SalI digested pCMVsport6 vector. The work was done at DOE Joint Genome Institute."

ORIGIN

Query Match 2.0%; Score 20; DB 10; Length 719;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 684 CTTCATCAGGGACATCATCA 703

```
                    ||||||||||||||||||||
Db        641 CTTCATCAGGGACATCATCA 622
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Search completed: June 10, 2006, 14:53:48
Job time : 6062.24 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 9, 2006, 22:44:33 ; Search time 224.385 Seconds
(without alignments)
8230.433 Million cell updates/sec

Title: US-10-821-670A-29
Perfect score: 987
Sequence: 1 atgcatcctcagcagttggt.....gggcatccgtgtcctgcagt 987

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1403666 seqs, 935554401 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2806514

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 200 summaries

Database : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	987	100.0	987	3	US-09-917-265A-29	Sequence 29, Appl
c	2	987	100.0	987	3	US-09-917-265A-31	Sequence 31, Appl
	3	985	99.8	985	3	US-09-917-265A-55	Sequence 55, Appl
c	4	985	99.8	985	3	US-09-917-265A-57	Sequence 57, Appl
	5	930	94.2	2193	3	US-09-011-143-5	Sequence 5, Appli
	6	930	94.2	2193	3	US-09-302-495-5	Sequence 5, Appli
	7	930	94.2	2193	3	US-10-079-616-5	Sequence 5, Appli
	8	921	93.3	921	3	US-09-011-143-6	Sequence 6, Appli
	9	921	93.3	921	3	US-09-302-495-6	Sequence 6, Appli
	10	921	93.3	921	3	US-10-079-616-6	Sequence 6, Appli
	11	905	91.7	1599	3	US-09-917-265A-38	Sequence 38, Appl
c	12	905	91.7	1599	3	US-09-917-265A-40	Sequence 40, Appl
	13	870	88.1	921	3	US-09-011-143-7	Sequence 7, Appli
	14	870	88.1	921	3	US-09-302-495-7	Sequence 7, Appli
	15	870	88.1	921	3	US-10-079-616-7	Sequence 7, Appli
	16	870	88.1	921	3	US-09-917-265A-26	Sequence 26, Appl
c	17	870	88.1	921	3	US-09-917-265A-28	Sequence 28, Appl
	18	870	88.1	1533	3	US-09-917-265A-43	Sequence 43, Appl
c	19	870	88.1	1533	3	US-09-917-265A-45	Sequence 45, Appl
	20	66	6.7	921	3	US-09-917-265A-52	Sequence 52, Appl
c	21	66	6.7	921	3	US-09-917-265A-54	Sequence 54, Appl
	22	66	6.7	987	3	US-09-917-265A-58	Sequence 58, Appl
c	23	66	6.7	987	3	US-09-917-265A-60	Sequence 60, Appl
	24	66	6.7	990	3	US-09-079-984A-1	Sequence 1, Appli
	25	66	6.7	990	3	US-09-079-984A-11	Sequence 11, Appl
	26	66	6.7	990	3	US-09-390-729-1	Sequence 1, Appli
	27	66	6.7	990	3	US-09-390-729-11	Sequence 11, Appl
	28	66	6.7	1533	3	US-09-917-265A-66	Sequence 66, Appl
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128	18	1.8	6348	3	US-09-919-039-366	Sequence 366, App
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156	17	1.7	301	3	US-09-023-655-249	Sequence 249, App
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188	17	1.7	821	3	US-09-533-559-7444	Sequence 7444, Ap
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ALIGNMENTS

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RESULT 1
US-09-917-265A-29
; Sequence 29, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
US-09-917-265A-29

  Query Match           100.0%;  Score 987;  DB 3;  Length 987;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  987;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 2
US-09-917-265A-31/c
; Sequence 31, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-31

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Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88
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Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGCAGT 1


RESULT 3
US-09-917-265A-55
; Sequence 55, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(984)
US-09-917-265A-55

  Query Match             99.8%;  Score 985;  DB 3;  Length 985;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 4
US-09-917-265A-57/c
; Sequence 57, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-57

  Query Match             99.8%;  Score 985;  DB 3;  Length 985;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806
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Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGCA 1
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RESULT 5
US-09-011-143-5
; Sequence 5, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2193 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-5

  Query Match             94.2%;  Score 930;  DB 3;  Length 2193;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  930;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         58 CTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCT 117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCT 180

Qy        118 GATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACC 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACC 240

Qy        178 TGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTC 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTC 300

Qy        238 AAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCAT 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCAT 360

Qy        298 TCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAA 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAA 420

Qy        358 CAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGT 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGT 480

Qy        418 TTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGC 477
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGC 540

Qy        478 AGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAG 537
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAG 600

Qy        538 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 597
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 660
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Qy        598 TGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTC 657
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTC 720

Qy        658 AAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCC 717
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCC 780

Qy        718 AAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATAC 777
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATAC 840

Qy        778 CCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAG 837
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAG 900

Qy        838 GGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTC 897
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTC 960

Qy        898 GTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCC 957
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCC 1020

Qy        958 TGGAGCAACTGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||||||||||
Db       1021 TGGAGCAACTGGGCATCCGTGTCCTGCAGT 1050


RESULT 6
US-09-302-495-5
; Sequence 5, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;    INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2193 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-302-495-5

  Query Match            94.2%;  Score 930;  DB 3;  Length 2193;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  930;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         58 CTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCT 117
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Db        121 CTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCT 180

Qy        118 GATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACC 177
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Db        181 GATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACC 240

Qy        178 TGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTC 237
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Qy        238 AAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCAT 297
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Db        301 AAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCAT 360

Qy        298 TCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAA 357
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Db        361 TCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAA 420

Qy        358 CAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGT 417
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Qy        418 TTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGC 477
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Db        481 TTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGC 540

Qy        478 AGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAG 537
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Db        541 AGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAG 600

Qy        538 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 597
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Db        601 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 660

Qy        598 TGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTC 657
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Db        661 TGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTC 720

Qy        658 AAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCC 717
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Db        721 AAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCC 780

Qy        718 AAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATAC 777
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Db        781 AAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATAC 840

Qy        778 CCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAG 837
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Db        841 CCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAG 900

Qy        838 GGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTC 897
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Db        901 GGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTC 960

Qy        898 GTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCC 957
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Db        961 GTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCC 1020
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Qy        958 TGGAGCAACTGGGCATCCGTGTCCTGCAGT 987
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Db       1021 TGGAGCAACTGGGCATCCGTGTCCTGCAGT 1050


RESULT 7
US-10-079-616-5
; Sequence 5, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2193 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-079-616-5

  Query Match             94.2%;  Score 930;  DB 3;  Length 2193;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  930;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         58 CTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCT 117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCT 180

Qy        118 GATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACC 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACC 240

Qy        178 TGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTC 237
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Qy        238 AAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCAT 297
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Db        301 AAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCAT 360

Qy        298 TCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAA 357
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Qy        358 CAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAAATTATTCTGGACGT 417
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Db        421 CAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAAATTATTCTGGACGT 480

Qy        418 TTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGC 477
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Db        481 TTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGC 540

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Db        541 AGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAG 600

Qy        538 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 597
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Db        601 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 660

Qy        598 TGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTC 657
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Db        661 TGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTC 720

Qy        658 AAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCC 717
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Db        721 AAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCC 780

Qy        718 AAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATAC 777
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATAC 840

Qy        778 CCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAG 837
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAG 900

Qy        838 GGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTC 897
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Db        901 GGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTC 960

Qy        898 GTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCC 957
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Qy        958 TGGAGCAACTGGGCATCCGTGTCCTGCAGT 987
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Db       1021 TGGAGCAACTGGGCATCCGTGTCCTGCAGT 1050


RESULT 8
US-09-011-143-6
; Sequence 6, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  BROWDY AND NEIMARK
;     STREET:  419 Seventh Street, N.W., Suite 300
;     CITY:  Washington
;     STATE:  D.C.
;     COUNTRY:  USA
;     ZIP:  20004
;    COMPUTER READABLE FORM:
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;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/011,143
;       FILING DATE:  04-FEB-1998
;       CLASSIFICATION:  536
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/JP97/01824
;       FILING DATE:  29-MAY-1997
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 165249/1996
;       FILING DATE:  04-JUN-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  BROWDY, Roger L.
;       REGISTRATION NUMBER:  25,618
;       REFERENCE/DOCKET NUMBER:  IMAMURA=1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-628-5197
;       TELEFAX:  202-737-3528
;   INFORMATION FOR SEQ ID NO:  6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  921 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-09-011-143-6

  Query Match             93.3%;  Score 921;  DB 3;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
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Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
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Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
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Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

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Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

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Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
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Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

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Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

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Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
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Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

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Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
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Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

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Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
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Qy        967 TGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 9
US-09-302-495-6
; Sequence 6, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/302,495
;            FILING DATE: 30-Apr-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 6:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 921 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
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;           TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-302-495-6

  Query Match            93.3%;  Score 921;  DB 3;  Length 921;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
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Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
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Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
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Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
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Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
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Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
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Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
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Db        901 TGGGCATCCGTGTCCTGCAGT 921
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RESULT 10
US-10-079-616-6
; Sequence 6, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 6:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 921 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-079-616-6

  Query Match            93.3%;  Score 921;  DB 3;  Length 921;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240
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Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921
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RESULT 11
US-09-917-265A-38
; Sequence 38, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1599)
US-09-917-265A-38

Query Match 91.7%; Score 905; DB 3; Length 1599;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 955; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy         32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91

Qy         92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151

Qy        152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211

Qy        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271

Qy        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331

Qy        332 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 391

Qy        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451

Qy        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTG 511
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTG 511

Qy        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571

Qy        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631

Qy        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691

Qy        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751

Qy        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811

Qy        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGAACAGACTCT 871
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGAACAGACTCT 871

Qy        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931

Qy        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987
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RESULT 12
US-09-917-265A-40/c
; Sequence 40, Application US/09917265A

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; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-40

  Query Match             91.7%;  Score 905;  DB 3;  Length 1599;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  955;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91
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Db       1568 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 1509

Qy         92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1508 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 1449

Qy        152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211
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Db       1448 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 1389

Qy        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1388 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 1329

Qy        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1328 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 1269

Qy        332 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 391
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Db       1268 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 1209

Qy        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1208 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 1149

Qy        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTG 511
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1148 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTG 1089

Qy        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1088 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 1029

Qy        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1028 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 969

Qy        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        968 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 909

Qy        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        908 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 849

Qy        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 789

Qy        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 871
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        788 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 729

Qy        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 669

Qy        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 613


RESULT 13
US-09-011-143-7
; Sequence 7, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  921 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-7

  Query Match             88.1%;  Score 870;  DB 3;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60
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Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 14
US-09-302-495-7
; Sequence 7, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 7:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-302-495-7

  Query Match            88.1%;  Score 870;  DB 3;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
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Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
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Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
                |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 15
US-10-079-616-7
; Sequence 7, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 7:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-079-616-7

  Query Match           88.1%;  Score 870;  DB 3;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
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Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
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Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 16
US-09-917-265A-26
; Sequence 26, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(921)
US-09-917-265A-26

  Query Match            88.1%;  Score 870;  DB 3;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
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Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
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Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 17
US-09-917-265A-28/c
; Sequence 28, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-28

  Query Match            88.1%;  Score 870;  DB 3;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682
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Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCAGT 1
```

RESULT 18
US-09-917-265A-43
; Sequence 43, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)

US-09-917-265A-43

Query Match 88.1%; Score 870; DB 3; Length 1533;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 920; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921
```

RESULT 19
US-09-917-265A-45/c

```
; Sequence 45, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265A-45

  Query Match             88.1%;  Score 870;  DB 3;  Length 1533;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613


RESULT 20
US-09-917-265A-52
; Sequence 52, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(921)
US-09-917-265A-52

  Query Match              6.7%;  Score 66;  DB 3;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy        597 CTGCCC 602
              ||||||
Db        531 CTGCCC 536


RESULT 21
US-09-917-265A-54/c
; Sequence 54, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
;   LENGTH: 921
;   TYPE: DNA
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;   ORGANISM: Canis familiaris
US-09-917-265A-54

  Query Match             6.7%;  Score 66;  DB 3;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy        597 CTGCCC 602
              ||||||
Db        391 CTGCCC 386


RESULT 22
US-09-917-265A-58
; Sequence 58, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
US-09-917-265A-58

  Query Match             6.7%;  Score 66;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 23
US-09-917-265A-60/c
; Sequence 60, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-60

  Query Match             6.7%;  Score 66;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy        597 CTGCCC 602
              ||||||
Db        391 CTGCCC 386


RESULT 24
US-09-079-984A-1
; Sequence 1, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,984A
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  990 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 987
;      IDENTIFICATION METHOD:  Similarity
US-09-079-984A-1

  Query Match             6.7%;  Score 66;  DB 3;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
```

```
Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 25
US-09-079-984A-11
; Sequence 11, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,984A
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  990 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 987
;      IDENTIFICATION METHOD:  Similarity
US-09-079-984A-11

  Query Match             6.7%;  Score 66;  DB 3;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 26
US-09-390-729-1
; Sequence 1, Application US/09390729
; Patent No. 6562334
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/390,729
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/079,984
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  990 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 987
;      IDENTIFICATION METHOD:  Similarity
US-09-390-729-1

  Query Match             6.7%;  Score 66;  DB 3;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 27
US-09-390-729-11
; Sequence 11, Application US/09390729
; Patent No. 6562334
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
```

```
;       STREET:  1600 Market Street, 39th Floor
;       CITY:  Philadelphia
;       STATE:  PA
;       COUNTRY:  USA
;       ZIP:  19103
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy Disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  WordPerfect 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/390,729
;       FILING DATE:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  09/079,984
;       FILING DATE:  15-MAY-1998
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Austin R. Miller
;       REGISTRATION NUMBER:  16,602
;       REFERENCE/DOCKET NUMBER:  1051-98
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (215) 563-1810
;       TELEFAX:  (215) 568-6946
;   INFORMATION FOR SEQ ID NO:  11:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  990 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA to mRNA
;     ORIGINAL SOURCE:
;       ORGANISM:  Canis familiaris
;     FEATURE:
;       NAME/KEY:  Canine IL12
;       LOCATION:  1 to 987
;       IDENTIFICATION METHOD:  Similarity
US-09-390-729-11

  Query Match             6.7%;  Score 66;  DB 3;  Length 990;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 28
US-09-917-265A-66
; Sequence 66, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-09-917-265A-66

  Query Match             6.7%;  Score 66;  DB 3;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy        597 CTGCCC 602
              ||||||
Db        531 CTGCCC 536


RESULT 29
US-09-917-265A-68/c
; Sequence 68, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-68

  Query Match             6.7%;  Score 66;  DB 3;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy        597 CTGCCC 602
              ||||||
Db       1003 CTGCCC 998


RESULT 30
US-09-917-265A-61
; Sequence 61, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
```

```
;   LOCATION: (1)..(1599)
US-09-917-265A-61

  Query Match             6.7%;  Score 66;  DB 3;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 31
US-09-917-265A-63/c
; Sequence 63, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-63

  Query Match             6.7%;  Score 66;  DB 3;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy        597 CTGCCC 602
              ||||||
Db       1003 CTGCCC 998


RESULT 32
US-09-917-265A-107
; Sequence 107, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 107
;   LENGTH: 2267
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (154)..(1140)
US-09-917-265A-107

  Query Match             6.7%;  Score 66;  DB 3;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 749

Qy        597 CTGCCC 602
              ||||||
Db        750 CTGCCC 755


RESULT 33
US-09-917-265A-109/c
; Sequence 109, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 109
;   LENGTH: 2267
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265A-109

  Query Match             6.7%;  Score 66;  DB 3;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1578 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1519

Qy        597 CTGCCC 602
              ||||||
Db       1518 CTGCCC 1513


RESULT 34
US-08-186-529-1
; Sequence 1, Application US/08186529
; Patent No. 5573764
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
```

```
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/186,529
;       FILING DATE:
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  McDaniels, Patricia A.
;       REGISTRATION NUMBER:  33,194
;       REFERENCE/DOCKET NUMBER:  GI 5225
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-498-8401
;       TELEFAX:  617-876-5851
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  987 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     ORIGINAL SOURCE:
;       ORGANISM:  Homo sapiens
;       CELL TYPE:  Lymphoblast
;       CELL LINE:  RPMI 8866
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..987
US-08-186-529-1

  Query Match             4.5%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 35
US-08-640-386A-1
; Sequence 1, Application US/08640386A
; Patent No. 5756085
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/640,386A
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;      REFERENCE/DOCKET NUMBER:  GI 5225A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8224
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  987 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Lymphoblast
;      CELL LINE:  RPMI 8866
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..987
US-08-640-386A-1

  Query Match             4.5%;  Score 44;  DB 2;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 36
US-08-848-760B-24
; Sequence 24, Application US/08848760B
; Patent No. 6248721
;   GENERAL INFORMATION:
;       APPLICANT: Chang, Lung-Ji
;       TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
;       NUMBER OF SEQUENCES: 33
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
;            STREET: 2421 N.W. 41st Street, Suite A-1
;            CITY: Gainesville
;            STATE: Florida
;            COUNTRY: United States of America
;            ZIP: 32606
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/848,760B
;            FILING DATE: 25-Jan-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/838,702
;            FILING DATE: 09-APR-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: PACE, DORAN R.
;            REGISTRATION NUMBER: 38,261
;            REFERENCE/DOCKET NUMBER: CNG-100C1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (352) 375-8100
;            TELEFAX: (352) 372-5800
;   INFORMATION FOR SEQ ID NO: 24:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 987 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: other nucleic acid
;            DESCRIPTION: /desc = "DNA"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-08-848-760B-24

  Query Match             4.5%;  Score 44;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704
```

```
RESULT 37
US-09-826-025-24
; Sequence 24, Application US/09826025
; Patent No. 6730512
;  GENERAL INFORMATION:
;       APPLICANT: Chang, Lung-Ji
;       TITLE OF INVENTION: Combination Immunogene Therapy
;       NUMBER OF SEQUENCES: 25
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Medlen & Carroll, LLP
;            STREET: 220 Montgomery Street, Suite 2200
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: United States of America
;            ZIP: 94104
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/826,025
;            FILING DATE: 04-Apr-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/838,702
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Ingolia, Diane E.
;            REGISTRATION NUMBER: 40,027
;            REFERENCE/DOCKET NUMBER: CHANG-02687
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 705-8410
;            TELEFAX: (415) 397-8338
;  INFORMATION FOR SEQ ID NO: 24:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 987 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: other nucleic acid
;            DESCRIPTION: /desc = "DNA"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-826-025-24

  Query Match             4.5%;  Score 44;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 38
US-08-184-009-194
; Sequence 194, Application US/08184009
; Patent No. 5833975
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/184,009
;      FILING DATE:  19-JAN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  194:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1018 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-184-009-194

  Query Match             4.5%;  Score 44;  DB 2;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 39
US-08-458-356-194
; Sequence 194, Application US/08458356
; Patent No. 5942235
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,356
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  194:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1018 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-458-356-194

  Query Match             4.5%;  Score 44;  DB 2;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 40
US-08-460-736-194
; Sequence 194, Application US/08460736
; Patent No. 6265189
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,736
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  194:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1018 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-460-736-194

  Query Match             4.5%;  Score 44;  DB 3;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 41
US-09-535-370-194
; Sequence 194, Application US/09535370
; Patent No. 6537594
;  GENERAL INFORMATION:
;       APPLICANT: Paoletti, Enzo
;                  Tartaglia, James
;                  Cox, William I.
;       TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
;       NUMBER OF SEQUENCES: 217
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Curtis, Morris & Safford
;            STREET: 530 Fifth Avenue
;            CITY: New York
;            STATE: NY
;            COUNTRY: USA
;            ZIP: 10036
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/535,370
;            FILING DATE: 24-Mar-2000
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/460,736
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Frommer, William S.
;            REGISTRATION NUMBER: 25,506
;            REFERENCE/DOCKET NUMBER: 454310-2530
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 840-3333
;            TELEFAX: (212) 840-0712
;            TELEX: 425066CURTMS
;  INFORMATION FOR SEQ ID NO: 194:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1018 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-09-535-370-194

  Query Match             4.5%;  Score 44;  DB 3;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 42
US-09-663-667-194
; Sequence 194, Application US/09663667
; Patent No. 6780407
;  GENERAL INFORMATION:
;       APPLICANT: Paoletti, Enzo
;                  Tartaglia, James
;                  Cox, William I.
;       TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
;       NUMBER OF SEQUENCES: 217
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Curtis, Morris & Safford
;            STREET: 530 Fifth Avenue
;            CITY: New York
;            STATE: NY
;            COUNTRY: USA
;            ZIP: 10036
;       COMPUTER READABLE FORM:
```

```
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/663,667
;             FILING DATE: 15-Sep-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/184,009
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Frommer, William S.
;             REGISTRATION NUMBER: 25,506
;             REFERENCE/DOCKET NUMBER: 454310-2530
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 840-3333
;             TELEFAX: (212) 840-0712
;             TELEX: 425066CURTMS
;    INFORMATION FOR SEQ ID NO: 194:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1018 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-09-663-667-194

  Query Match             4.5%;  Score 44;  DB 3;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 43
US-09-634-368-4
; Sequence 4, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 1389
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: human
;   OTHER INFORMATION: p40-IL-2 fusion protein coding sequence
US-09-634-368-4

  Query Match             4.5%;  Score 44;  DB 3;  Length 1389;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 44
US-08-751-767A-3
; Sequence 3, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1399 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  43..1026
US-08-751-767A-3

  Query Match             4.5%;  Score 44;  DB 2;  Length 1399;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        703 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 746


RESULT 45
US-08-751-767A-11
; Sequence 11, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/751,767A
;       FILING DATE:  08-NOV-1996
;       CLASSIFICATION:  536
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  SADOFF, B.J.
;       REGISTRATION NUMBER:  36,663
;       REFERENCE/DOCKET NUMBER:  117-221
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  7038164091
;       TELEFAX:  7038164100
;   INFORMATION FOR SEQ ID NO:  11:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1560 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..1557
US-08-751-767A-11

  Query Match             4.5%;  Score 44;  DB 2;  Length 1560;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 641


RESULT 46
US-08-751-767A-9
; Sequence 9, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;     APPLICANT:  ANDERSON, ROBERT J.
;     APPLICANT:  GRANT, HUGH
;     APPLICANT:  MACDONALD, IAN D.
;     TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;     NUMBER OF SEQUENCES:  80
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  NIXON & VANDERHYE P.C.
;       STREET:  1100 NORTH GLEBE ROAD
;       CITY:  ARLINGTON
;       STATE:  VA
;       COUNTRY:  USA
;       ZIP:  22201
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/751,767A
;       FILING DATE:  08-NOV-1996
;       CLASSIFICATION:  536
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  SADOFF, B.J.
;       REGISTRATION NUMBER:  36,663
;       REFERENCE/DOCKET NUMBER:  117-221
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  7038164091
;       TELEFAX:  7038164100
;   INFORMATION FOR SEQ ID NO:  9:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1623 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..1620
US-08-751-767A-9

  Query Match             4.5%;  Score 44;  DB 2;  Length 1623;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 47
US-09-310-842-4
; Sequence 4, Application US/09310842A
; Patent No. 6451593
; GENERAL INFORMATION:
;  APPLICANT: Wittig, Prof. Burghardt
;  APPLICANT: Junghans, Claas
;  TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
;  TITLE OF INVENTION: Therapy
;  FILE REFERENCE: XI 597/99
;  CURRENT APPLICATION NUMBER: US/09/310,842A
;  CURRENT FILING DATE: 1999-05-12
;  EARLIER APPLICATION NUMBER: DE 196 48 625.4
;  EARLIER FILING DATE: 1996-11-13
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 1870
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (1)..(1870)
;   OTHER INFORMATION: Interleukin-12 (IL-12, p40-subunit); Oligo DNA Dumbbell
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1)..(2)
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to
;   OTHER INFORMATION: 2  can be modified with amino or caroxy features
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1869)..(1870)
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1869
;   OTHER INFORMATION: to 1870  can be modified with amino or caroxy features
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Strandness: both;  nucleic
;   OTHER INFORMATION: acid (linear),  hypothetical: No. 6451593 anti-sense: No
US-09-310-842-4

  Query Match             4.5%;  Score 44;  DB 3;  Length 1870;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db       1293 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 1336


RESULT 48
US-09-949-016-5452
; Sequence 5452, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
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;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5452
;   LENGTH: 2307
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-5452

  Query Match             4.5%;  Score 44;  DB 3;  Length 2307;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        663 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 706


RESULT 49
US-09-851-062-3
; Sequence 3, Application US/09851062
; Patent No. 6448081
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0247
;  CURRENT APPLICATION NUMBER: US/09/851,062
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 3
;   LENGTH: 2318
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (14)...(1000)
US-09-851-062-3

  Query Match             4.5%;  Score 44;  DB 3;  Length 2318;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        674 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 717


RESULT 50
US-09-949-016-315
; Sequence 315, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 315
;   LENGTH: 2318
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-315

  Query Match             4.5%;  Score 44;  DB 3;  Length 2318;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        674 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 717


RESULT 51
US-08-265-087-1
; Sequence 1, Application US/08265087
; Patent No. 5571515
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/265,087
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2362 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  33..1016
US-08-265-087-1

  Query Match             4.5%;  Score 44;  DB 2;  Length 2362;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        693 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 736


RESULT 52
US-08-621-493-1
```

```
; Sequence 1, Application US/08621493
; Patent No. 5723127
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/621,493
;      FILING DATE:  25-MAR-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2362 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  33..1016
US-08-621-493-1

  Query Match             4.5%;  Score 44;  DB 2;  Length 2362;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        693 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 736


RESULT 53
US-08-965-688-1
; Sequence 1, Application US/08965688
; Patent No. 5976539
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/965,688
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/621,493
;      FILING DATE:  25-MAR-1996
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2362 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  33..1016
US-08-965-688-1

  Query Match             4.5%;  Score 44;  DB 2;  Length 2362;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        693 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 736


RESULT 54
US-09-260-173-1
; Sequence 1, Application US/09260173
; Patent No. 6168923
;   GENERAL INFORMATION:
;        APPLICANT: Scott, Phillip
;                   Trinchieri, Giorgio
;        TITLE OF INVENTION: Compositions and Methods for Use of
;                            IL-12 as an Adjuvant
;        NUMBER OF SEQUENCES: 4
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Howson and Howson
;             STREET: Spring House Corporate Center, PO Box 457
;             CITY: Spring House
;             STATE: Pennsylvania
;             COUNTRY: USA
;             ZIP: 19477
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/260,173
;             FILING DATE: 01-Mar-1999
;             CLASSIFICATION: <Unknown>
;                             17-JUN-1994
;                             18-APR-1994
```

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;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/965,688
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: 08/265,087
;            FILING DATE: 17-JUN-1994
;            APPLICATION NUMBER: US 08/229,282
;            FILING DATE: 18-APR-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Bak, Mary E.
;            REGISTRATION NUMBER: 31,215
;            REFERENCE/DOCKET NUMBER: WST51AUSA
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 215-540-9206
;            TELEFAX: 215-540-5818
;   INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 2362 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: unknown
;       MOLECULE TYPE: cDNA
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  33..1016
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-260-173-1

  Query Match             4.5%;  Score 44;  DB 3;  Length 2362;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        693 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 736


RESULT 55
US-09-924-703-3
; Sequence 3, Application US/09924703
; Patent No. 6555658
; GENERAL INFORMATION:
;  APPLICANT: TRINCHIERI, GIORGIO
;  APPLICANT:  PERUSSIA, BICE
;  APPLICANT:  CLARK, STEVEN C.
;  APPLICANT:  WONG, GORDON G.
;  APPLICANT:  HEWICK, RODNEY
;  APPLICANT:  KOBAYASHI, MICHIKO
;  TITLE OF INVENTION: ANTIBODIES TO NATURAL KILLER STIMULATORY FACTOR
;  FILE REFERENCE: 01142.0142.0100
;  CURRENT APPLICATION NUMBER: US/09/924,703
;  CURRENT FILING DATE:  2001-08-09
;  PRIOR APPLICATION NUMBER: 09/325,958
;  PRIOR FILING DATE: 1999-06-04
;  PRIOR APPLICATION NUMBER: 08/858,000
;  PRIOR FILING DATE: 1997-05-16
;  PRIOR APPLICATION NUMBER: 08/403,013
;  PRIOR FILING DATE: 1995-03-13
;  PRIOR APPLICATION NUMBER: 07/584,941
;  PRIOR FILING DATE: 1990-09-18
;  PRIOR APPLICATION NUMBER: 07/307,817
;  PRIOR FILING DATE: 1989-02-07
;  PRIOR APPLICATION NUMBER: 07/269,945
;  PRIOR FILING DATE: 1988-11-10
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 2362
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
;   OTHER INFORMATION: sequence of the 40 kD subunit of NKSF
;   NAME/KEY: CDS
;   LOCATION: (33)..(1016)
US-09-924-703-3

  Query Match             4.5%;  Score 44;  DB 3;  Length 2362;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        693 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 736


RESULT 56
US-08-751-767A-7
; Sequence 7, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6139 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3222..4841
US-08-751-767A-7

  Query Match             4.5%;  Score 44;  DB 2;  Length 6139;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db       3882 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 3925


RESULT 57
US-09-949-016-12057
; Sequence 12057, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
```

```
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12057
;   LENGTH: 16002
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-12057

  Query Match             4.0%;  Score 39;  DB 3;  Length 16002;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-09;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        400 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 438
              |||||||||||||||||||||||||||||||||||||||
Db       6309 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 6347


RESULT 58
US-09-949-016-17194
; Sequence 17194, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17194
;   LENGTH: 16003
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-17194

  Query Match             4.0%;  Score 39;  DB 3;  Length 16003;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-09;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        400 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 438
              |||||||||||||||||||||||||||||||||||||||
Db       6309 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 6347


RESULT 59
US-09-949-016-24253/c
; Sequence 24253, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24253
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-24253

  Query Match             3.7%;  Score 37;  DB 3;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-08;
  Matches   37;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCA 700
              |||||||||||||||||||||||||||||||||||||
Db         87 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCA 51


RESULT 60
US-09-949-016-190686/c
; Sequence 190686, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 190686
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-190686

  Query Match             3.7%;  Score 37;  DB 3;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-08;
  Matches   37;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCA 700
              |||||||||||||||||||||||||||||||||||||
Db         87 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCA 51


RESULT 61
US-09-823-549-77
; Sequence 77, Application US/09823549
; Patent No. 6664442
; GENERAL INFORMATION:
;  APPLICANT: McConlogue, Lisa  C
;  APPLICANT:  Games, Kate D.
;  APPLICANT:  Yednock, Theodore A.
;  APPLICANT:  Hua, Tan
;  APPLICANT:  Messersmith, Elizabeth
;  APPLICANT:  Bard, Frederique
;  TITLE OF INVENTION: SCREENING MARKERS AND METHODS FOR NEURODEGENERATIVE DISORDERS
;  FILE REFERENCE: 015270-009110US
;  CURRENT APPLICATION NUMBER: US/09/823,549
;  CURRENT FILING DATE:  2001-03-30
;  PRIOR APPLICATION NUMBER: US 60/193,847
;  PRIOR FILING DATE: 2000-03-30
```

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;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
;   LENGTH: 73
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: IL-12 p40, #1 marker
US-09-823-549-77

  Query Match             3.0%;  Score 30;  DB 3;  Length 73;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-05;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||
Db          8 CAGCTTCTTCATCAGGGACATCATCAAACC 37


RESULT 62
US-08-385-335A-13
; Sequence 13, Application US/08385335A
; Patent No. 5891680
;  GENERAL INFORMATION:
;    APPLICANT:  Lieschke, Graham J.
;    APPLICANT:  Mulligan, Richard C.
;    TITLE OF INVENTION:  Bioactive Fusion Proteins
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/385,335A
;      FILING DATE:  08-FEB-1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  WHI95-01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-861-6240
;      TELEFAX:  617-861-9540
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1061 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-08-385-335A-13

  Query Match             3.0%;  Score 30;  DB 2;  Length 1061;
  Best Local Similarity   100.0%;  Pred. No. 6e-05;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||
Db        715 CAGCTTCTTCATCAGGGACATCATCAAACC 744


RESULT 63
US-09-634-368-3
; Sequence 3, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1409
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p40-GM-CSF fusion protein coding sequence
US-09-634-368-3

  Query Match             3.0%;  Score 30;  DB 3;  Length 1409;
  Best Local Similarity   100.0%;  Pred. No. 6.1e-05;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||
Db        689 CAGCTTCTTCATCAGGGACATCATCAAACC 718


RESULT 64
US-09-634-368-2
; Sequence 2, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 1472
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p40-IL-2 fusion protein coding sequence
US-09-634-368-2

  Query Match             3.0%;  Score 30;  DB 3;  Length 1472;
  Best Local Similarity   100.0%;  Pred. No. 6.1e-05;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||
Db        689 CAGCTTCTTCATCAGGGACATCATCAAACC 718


RESULT 65
US-09-634-368-12
; Sequence 12, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
```

```
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 1569
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p35-linker-p40 fusion protein coding sequence
US-09-634-368-12

  Query Match             3.0%;  Score 30;  DB 3;  Length 1569;
  Best Local Similarity   100.0%;  Pred. No. 6.1e-05;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||
Db       1230 CAGCTTCTTCATCAGGGACATCATCAAACC 1259


RESULT 66
US-09-634-368-11
; Sequence 11, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 2013
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p35-linker-p40-IL-2 fusion protein coding sequence
US-09-634-368-11

  Query Match             3.0%;  Score 30;  DB 3;  Length 2013;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-05;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||
Db       1230 CAGCTTCTTCATCAGGGACATCATCAAACC 1259


RESULT 67
US-09-634-368-13
; Sequence 13, Application US/09634368
; Patent No. 6617135
; GENERAL INFORMATION:
;  APPLICANT:  Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION:  Multiple Cytokine Protein Complexes
;  FILE REFERENCE:  LEX-010
;  CURRENT APPLICATION NUMBER: US/09/634,368
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/147,924
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 13
;   LENGTH: 2709
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: Fc-p35-linker-p40-IL-2 fusion protein coding
;   OTHER INFORMATION: sequence
US-09-634-368-13

  Query Match             3.0%;  Score 30;  DB 3;  Length 2709;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-05;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||
Db       1926 CAGCTTCTTCATCAGGGACATCATCAAACC 1955


RESULT 68
US-08-659-206A-4
; Sequence 4, Application US/08659206A
; Patent No. 5922685
;  GENERAL INFORMATION:
;    APPLICANT:  Rakhmilevich, Alexander
;    TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/659,206A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  110229.91144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6295 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "plasmid pWRG3196"
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(955..1260, 1334..1675)
;      OTHER INFORMATION:  /product= "p35 gene product"
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2377..3384
;      OTHER INFORMATION:  /product= "p40 gene product"
US-08-659-206A-4

  Query Match             3.0%;  Score 30;  DB 2;  Length 6295;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-05;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||
Db       3045 CAGCTTCTTCATCAGGGACATCATCAAACC 3074
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RESULT 69
US-08-659-206A-1
; Sequence 1, Application US/08659206A
; Patent No. 5922685
;  GENERAL INFORMATION:
;    APPLICANT:  Rakhmilevich, Alexander
;    TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/659,206A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  110229.91144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7287 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Plasmid DNA"
;    IMMEDIATE SOURCE:
;      CLONE:  pWRG3169
;    FEATURE:
;      NAME/KEY:  promoter
;      LOCATION:  1..628
;    FEATURE:
;      NAME/KEY:  iDNA
;      LOCATION:  629..810
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(953..1258, 1332..1673)
;      OTHER INFORMATION:  /product= "p35 gene product"
;    FEATURE:
;      NAME/KEY:  polyA_site
;      LOCATION:  1797..2024
;    FEATURE:
;      NAME/KEY:  promoter
;      LOCATION:  2110..2737
;    FEATURE:
;      NAME/KEY:  iDNA
;      LOCATION:  2738..2919
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2983..3990
;      OTHER INFORMATION:  /product= "p40 gene product"
;    FEATURE:
;      NAME/KEY:  polyA_site
;      LOCATION:  4075..4306
US-08-659-206A-1

  Query Match             3.0%;  Score 30;  DB 2;  Length 7287;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-05;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||
Db       3651 CAGCTTCTTCATCAGGGACATCATCAAACC 3680


RESULT 70
US-09-917-265A-85
; Sequence 85, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 85
;   LENGTH: 28
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-917-265A-85

  Query Match             2.8%;  Score 28;  DB 3;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00055;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCT 28
              ||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCT 28


RESULT 71
US-09-917-265A-87
; Sequence 87, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 87
;   LENGTH: 37
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-917-265A-87

  Query Match             2.8%;  Score 28;  DB 3;  Length 37;
  Best Local Similarity   100.0%;  Pred. No. 0.00055;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCT 28
              ||||||||||||||||||||||||||||
Db         10 ATGCATCCTCAGCAGTTGGTCATCGCCT 37


RESULT 72
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US-09-917-265A-86/c
; Sequence 86, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 86
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-917-265A-86

  Query Match             2.5%;  Score 25;  DB 3;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 0.019;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGCA 1


RESULT 73
US-09-079-984A-13
; Sequence 13, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,984A
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  39 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other DNA; synthetic DNA
US-09-079-984A-13

  Query Match             2.4%;  Score 24;  DB 3;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 0.061;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATC 24
              ||||||||||||||||||||||||
Db         10 ATGCATCCTCAGCAGTTGGTCATC 33


RESULT 74
US-09-390-729-13
; Sequence 13, Application US/09390729
; Patent No. 6562334
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/390,729
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/079,984
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  39 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other DNA; synthetic DNA
US-09-390-729-13

  Query Match             2.4%;  Score 24;  DB 3;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 0.061;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATC 24
              ||||||||||||||||||||||||
Db         10 ATGCATCCTCAGCAGTTGGTCATC 33


RESULT 75
US-09-445-724B-13
; Sequence 13, Application US/09445724B
; Patent No. 6600020
; GENERAL INFORMATION:
;  APPLICANT: OKANO, FUMIYOSHI
;  TITLE OF INVENTION: CANINE INTERLEUKIN 18, CANINE INTERLEUKIN 1 CONVERTING
```

```
;  TITLE OF INVENTION:  ENZYME, DNA SEQUENCES ENCODING THESE, INTERLEUKIN 18
;  TITLE OF INVENTION:  PRODUCTION METHOD AND CANINE IMMUNE DISEASE REMEDY
;  FILE REFERENCE: 2109-15
;  CURRENT APPLICATION NUMBER: US/09/445,724B
;  CURRENT FILING DATE:  1999-12-13
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
;   LENGTH: 540
;   TYPE: DNA
;   ORGANISM: Caninus sp.
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(537)
US-09-445-724B-13

  Query Match             2.4%;  Score 24;  DB 3;  Length 540;
  Best Local Similarity   100.0%;  Pred. No. 0.068;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATC 24
              ||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATC 24


RESULT 76
US-09-949-016-24250/c
; Sequence 24250, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24250
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-24250

  Query Match             2.3%;  Score 23;  DB 3;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 0.22;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        127 GGAGAAATGGTGGTCCTCACCTG 149
              |||||||||||||||||||||||
Db         69 GGAGAAATGGTGGTCCTCACCTG 47


RESULT 77
US-09-949-016-24251/c
; Sequence 24251, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24251
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-24251

  Query Match             2.3%;  Score 23;  DB 3;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 0.22;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        127 GGAGAAATGGTGGTCCTCACCTG 149
              |||||||||||||||||||||||
Db         88 GGAGAAATGGTGGTCCTCACCTG 66


RESULT 78
US-09-949-016-190683/c
; Sequence 190683, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 190683
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-190683

  Query Match             2.3%;  Score 23;  DB 3;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 0.22;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        127 GGAGAAATGGTGGTCCTCACCTG 149
              |||||||||||||||||||||||
Db         69 GGAGAAATGGTGGTCCTCACCTG 47


RESULT 79
US-09-949-016-190684/c
; Sequence 190684, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
```

```
; SEQ ID NO 190684
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-190684

  Query Match             2.3%;  Score 23;  DB 3;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 0.22;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        127 GGAGAAATGGTGGTCCTCACCTG 149
              |||||||||||||||||||||||
Db         88 GGAGAAATGGTGGTCCTCACCTG 66


RESULT 80
US-09-917-265A-88/c
; Sequence 88, Application US/09917265A
; Patent No. 6818444
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265A
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 88
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-917-265A-88

  Query Match             2.2%;  Score 22;  DB 3;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 0.63;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        966 CTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||
Db         25 CTGGGCATCCGTGTCCTGCAGT 4


RESULT 81
US-08-781-891-79/c
; Sequence 79, Application US/08781891
; Patent No. 6090620
;  GENERAL INFORMATION:
;    APPLICANT:  Fu, Ying-Hui
;    APPLICANT:  Yu, Chang-En
;    APPLICANT:  Oshima, Junko
;    APPLICANT:  Mulligan, John T.
;    APPLICANT:  Schellenberg, Gerald D.
;    TITLE OF INVENTION:  GENE AND GENE PRODUCTS RELATED TO
;    TITLE OF INVENTION:  WERNER'S SYNDROME
;    NUMBER OF SEQUENCES:  209
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/781,891
;      FILING DATE:  27-DEC-1996
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 6090620tenburg Ph.D., Carol
;      REGISTRATION NUMBER:  39,317
;      REFERENCE/DOCKET NUMBER:  240052.419
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  79:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  87350 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-781-891-79

  Query Match             2.2%;  Score 22;  DB 3;  Length 87350;
  Best Local Similarity   100.0%;  Pred. No. 0.86;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        843 GAACAACAGAGAAAAGAAAGAC 864
              ||||||||||||||||||||||
Db      80388 GAACAACAGAGAAAAGAAAGAC 80367


RESULT 82
US-09-618-166-79/c
; Sequence 79, Application US/09618166
; Patent No. 6583112
;  GENERAL INFORMATION:
;       APPLICANT: Fu, Ying-Hui
;                  Yu, Chang-En
;                  Oshima, Junko
;                  Mulligan, John T.
;                  Schellenberg, Gerald D.
;       TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
;                           WERNER'S SYNDROME
;       NUMBER OF SEQUENCES: 209
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Seed Intellectual Property Law Group
;            STREET: 701 Fifth Avenue, Suite 6300
;            CITY: Seattle
;            STATE: Washington
;            COUNTRY: USA
;            ZIP: 98104-7092
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/618,166
;            FILING DATE: 17-Jul-2000
;            CLASSIFICATION: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: McMasters, David D.
;            REGISTRATION NUMBER: 33,963
;            REFERENCE/DOCKET NUMBER: 240052.419C1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (206) 622-4900
;            TELEFAX: (206) 682-6031
;  INFORMATION FOR SEQ ID NO: 79:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 87350 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-09-618-166-79
```

```
  Query Match             2.2%;  Score 22;  DB 3;  Length 87350;
  Best Local Similarity   100.0%;  Pred. No. 0.86;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        843 GAACAACAGAGAAAAGAAAGAC 864
              ||||||||||||||||||||||
Db      80388 GAACAACAGAGAAAAGAAAGAC 80367


RESULT 83
US-09-791-211-3/c
; Sequence 3, Application US/09791211
; Patent No. 6448080
; GENERAL INFORMATION:
;  APPLICANT:  Donna T. Ward
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION:  ANTISENSE MODULATION OF WRN EXPRESSION
;  FILE REFERENCE:  RTS-0205
;  CURRENT APPLICATION NUMBER: US/09/791,211
;  CURRENT FILING DATE:  2001-02-23
;  NUMBER OF SEQ ID NOS:  90
; SEQ ID NO 3
;   LENGTH: 87543
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 7421
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 7427
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 11609
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 12605
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 12742
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 29370
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 29422
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 29979
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 29980
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 29981
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 30136
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 30140
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 31205
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 31206
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 31592
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 33095
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 33160
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 34066
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 34072
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 36816
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 39020
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 42164
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 42459
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 46808
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 46823
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 46826
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 47291
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 52786
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 52787
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 53384
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 54684
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 59215
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 59235
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 59242
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 63290
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 66614
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 68660
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 68697
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 68718
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 68733
;   OTHER INFORMATION: unknown
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;   NAME/KEY: unsure
;   LOCATION: 68739
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 69785
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 79134
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 79198
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 86336
;   OTHER INFORMATION: unknown
;   OTHER INFORMATION:
US-09-791-211-3

  Query Match             2.2%;  Score 22;  DB 3;  Length 87543;
  Best Local Similarity   100.0%;  Pred. No. 0.86;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        843 GAACAACAGAGAAAAGAAAGAC 864
              ||||||||||||||||||||||
Db      80581 GAACAACAGAGAAAAGAAAGAC 80560


RESULT 84
US-09-011-143-14
; Sequence 14, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  44 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-14

  Query Match             2.1%;  Score 21;  DB 3;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 2.1;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        547 GACAACAGGGATTATAAGAAG 567
              |||||||||||||||||||||
Db         24 GACAACAGGGATTATAAGAAG 44


RESULT 85
US-09-302-495-14
; Sequence 14, Application US/09302495
; Patent No. 6518045
;  GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/302,495
;            FILING DATE: 30-Apr-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;  INFORMATION FOR SEQ ID NO: 14:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 44 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-302-495-14

  Query Match             2.1%;  Score 21;  DB 3;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 2.1;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        547 GACAACAGGGATTATAAGAAG 567
              |||||||||||||||||||||
Db         24 GACAACAGGGATTATAAGAAG 44
```

```
RESULT 86
US-10-079-616-14
; Sequence 14, Application US/10079616
; Patent No. 6566097
;  GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 14:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 44 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-079-616-14

  Query Match             2.1%;  Score 21;  DB 3;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 2.1;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        547 GACAACAGGGATTATAAGAAG 567
              |||||||||||||||||||||
Db         24 GACAACAGGGATTATAAGAAG 44


RESULT 87
US-09-851-062-17/c
; Sequence 17, Application US/09851062
; Patent No. 6448081
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0247
;  CURRENT APPLICATION NUMBER: US/09/851,062
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 17
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-062-17

  Query Match             2.0%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        223 CTGACCATCCAAGTCAAAGA 242
              ||||||||||||||||||||
Db         20 CTGACCATCCAAGTCAAAGA 1


RESULT 88
US-09-851-062-22/c
; Sequence 22, Application US/09851062
; Patent No. 6448081
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0247
;  CURRENT APPLICATION NUMBER: US/09/851,062
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 22
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-062-22

  Query Match             2.0%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        320 AGGAAGATGGAATTTGGTCC 339
              ||||||||||||||||||||
Db         20 AGGAAGATGGAATTTGGTCC 1


RESULT 89
US-09-851-062-23/c
; Sequence 23, Application US/09851062
; Patent No. 6448081
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0247
;  CURRENT APPLICATION NUMBER: US/09/851,062
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 23
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-062-23

  Query Match             2.0%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        326 ATGGAATTTGGTCCACTGAT 345
              ||||||||||||||||||||
```

```
Db         20 ATGGAATTTGGTCCACTGAT 1


RESULT 90
US-09-851-062-26/c
; Sequence 26, Application US/09851062
; Patent No. 6448081
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0247
;  CURRENT APPLICATION NUMBER: US/09/851,062
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 26
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-062-26

  Query Match             2.0%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        418 TTCACCTGCTGGTGGCTGAC 437
              ||||||||||||||||||||
Db         20 TTCACCTGCTGGTGGCTGAC 1


RESULT 91
US-09-851-062-34/c
; Sequence 34, Application US/09851062
; Patent No. 6448081
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0247
;  CURRENT APPLICATION NUMBER: US/09/851,062
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 34
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-062-34

  Query Match             2.0%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACA 697
              ||||||||||||||||||||
Db         20 CAGCTTCTTCATCAGGGACA 1


RESULT 92
US-09-851-062-35/c
; Sequence 35, Application US/09851062
; Patent No. 6448081
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0247
;  CURRENT APPLICATION NUMBER: US/09/851,062
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 35
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-062-35

  Query Match             2.0%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        683 TCTTCATCAGGGACATCATC 702
              ||||||||||||||||||||
Db         20 TCTTCATCAGGGACATCATC 1


RESULT 93
US-09-851-062-36/c
; Sequence 36, Application US/09851062
; Patent No. 6448081
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0247
;  CURRENT APPLICATION NUMBER: US/09/851,062
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 36
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-062-36

  Query Match             2.0%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        688 ATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||
Db         20 ATCAGGGACATCATCAAACC 1


RESULT 94
US-09-011-143-13/c
; Sequence 13, Application US/09011143
; Patent No. 6472509
;  GENERAL INFORMATION:
;    APPLICANT:  IMAMURA, Takayuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  FUJIYASU, Takeshi
;    APPLICANT:  IMAGAWA, Yoshitaka
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  NOVEL FELINE CYTOKINE PROTEIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,143
;      FILING DATE:  04-FEB-1998
```

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;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP97/01824
;      FILING DATE:  29-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 165249/1996
;      FILING DATE:  04-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  IMAMURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-011-143-13

  Query Match             2.0%;  Score 20;  DB 3;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 6.7;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        526 TCAGCAGAGAAGGTCAGAGT 545
              ||||||||||||||||||||
Db         32 TCAGCAGAGAAGGTCAGAGT 13


RESULT 95
US-09-302-495-13/c
; Sequence 13, Application US/09302495
; Patent No. 6518045
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/302,495
;             FILING DATE: 30-Apr-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 13:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 32 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-302-495-13

  Query Match             2.0%;  Score 20;  DB 3;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 6.7;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        526 TCAGCAGAGAAGGTCAGAGT 545
              ||||||||||||||||||||
Db         32 TCAGCAGAGAAGGTCAGAGT 13


RESULT 96
US-10-079-616-13/c
; Sequence 13, Application US/10079616
; Patent No. 6566097
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 13:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 32 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-079-616-13

  Query Match             2.0%;  Score 20;  DB 3;  Length 32;
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Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        526 TCAGCAGAGAAGGTCAGAGT 545
              ||||||||||||||||||||
Db         32 TCAGCAGAGAAGGTCAGAGT 13
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RESULT 97
US-09-949-016-11844
; Sequence 11844, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11844
; LENGTH: 119981
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11844

Query Match 2.0%; Score 20; DB 3; Length 119981;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        371 AAAATAAGATCTTTCTAAAA 390
              ||||||||||||||||||||
Db      89012 AAAATAAGATCTTTCTAAAA 89031
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RESULT 98
US-09-949-016-13606
; Sequence 13606, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13606
; LENGTH: 119982
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13606

Query Match 2.0%; Score 20; DB 3; Length 119982;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        371 AAAATAAGATCTTTCTAAAA 390
              ||||||||||||||||||||
Db      89012 AAAATAAGATCTTTCTAAAA 89031
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RESULT 99
US-09-949-016-15787
; Sequence 15787, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15787
; LENGTH: 120727
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(120727)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15787

Query Match 2.0%; Score 20; DB 3; Length 120727;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        485 CCTCTGACCCCCAAGGGGTG 504
              ||||||||||||||||||||
Db      80796 CCTCTGACCCCCAAGGGGTG 80815
```

RESULT 100
US-09-949-016-15788
; Sequence 15788, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15788
; LENGTH: 120727
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(120727)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15788

Query Match 2.0%; Score 20; DB 3; Length 120727;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        485 CCTCTGACCCCCAAGGGGTG 504
              ||||||||||||||||||||
Db      80796 CCTCTGACCCCCAAGGGGTG 80815
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Job time : 230.385 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2006, 23:31:05 ; Search time 1659.11 Seconds
(without alignments)
7309.894 Million cell updates/sec

Title: US-10-821-670A-29
Perfect score: 987
Sequence: 1 atgcatcctcagcagttggt.....gggcatccgtgtcctgcagt 987

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 18892170 seqs, 6143817638 residues

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Minimum DB seq length: 0
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3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
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9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
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11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	987	100.0	987	3	US-09-917-265-29	Sequence 29, Appl
c	2	987	100.0	987	3	US-09-917-265-31	Sequence 31, Appl
	3	987	100.0	987	9	US-10-821-670-29	Sequence 29, Appl
c	4	987	100.0	987	9	US-10-821-670-31	Sequence 31, Appl
	5	985	99.8	985	3	US-09-917-265-55	Sequence 55, Appl
c	6	985	99.8	985	3	US-09-917-265-57	Sequence 57, Appl
	7	985	99.8	985	9	US-10-821-670-55	Sequence 55, Appl
c	8	985	99.8	985	9	US-10-821-670-57	Sequence 57, Appl
	9	930	94.2	2193	6	US-10-079-616-5	Sequence 5, Appli
	10	921	93.3	921	6	US-10-079-616-6	Sequence 6, Appli
	11	905	91.7	1599	3	US-09-917-265-38	Sequence 38, Appl
c	12	905	91.7	1599	3	US-09-917-265-40	Sequence 40, Appl
	13	905	91.7	1599	9	US-10-821-670-38	Sequence 38, Appl
c	14	905	91.7	1599	9	US-10-821-670-40	Sequence 40, Appl
	15	885	89.7	990	7	US-10-041-672C-1	Sequence 1, Appli
	16	885	89.7	4522	7	US-10-041-672C-10	Sequence 10, Appl
	17	870	88.1	921	3	US-09-917-265-26	Sequence 26, Appl
c	18	870	88.1	921	3	US-09-917-265-28	Sequence 28, Appl
	19	870	88.1	921	6	US-10-079-616-7	Sequence 7, Appli
	20	870	88.1	921	9	US-10-821-670-26	Sequence 26, Appl
c	21	870	88.1	921	9	US-10-821-670-28	Sequence 28, Appl
	22	870	88.1	1533	3	US-09-917-265-43	Sequence 43, Appl
c	23	870	88.1	1533	3	US-09-917-265-45	Sequence 45, Appl
	24	870	88.1	1533	9	US-10-821-670-43	Sequence 43, Appl
c	25	870	88.1	1533	9	US-10-821-670-45	Sequence 45, Appl
	26	66	6.7	921	3	US-09-917-265-52	Sequence 52, Appl
c	27	66	6.7	921	3	US-09-917-265-54	Sequence 54, Appl
	28	66	6.7	921	9	US-10-821-670-52	Sequence 52, Appl
c	29	66	6.7	921	9	US-10-821-670-54	Sequence 54, Appl
	30	66	6.7	987	3	US-09-917-265-58	Sequence 58, Appl
c	31	66	6.7	987	3	US-09-917-265-60	Sequence 60, Appl
	32	66	6.7	987	9	US-10-821-670-58	Sequence 58, Appl
c	33	66	6.7	987	9	US-10-821-670-60	Sequence 60, Appl
	34	66	6.7	1533	3	US-09-917-265-66	Sequence 66, Appl
c	35	66	6.7	1533	3	US-09-917-265-68	Sequence 68, Appl
	36	66	6.7	1533	9	US-10-821-670-66	Sequence 66, Appl
c	37	66	6.7	1533	9	US-10-821-670-68	Sequence 68, Appl
	38	66	6.7	1599	3	US-09-917-265-61	Sequence 61, Appl
c	39	66	6.7	1599	3	US-09-917-265-63	Sequence 63, Appl
	40	66	6.7	1599	9	US-10-821-670-61	Sequence 61, Appl
c	41	66	6.7	1599	9	US-10-821-670-63	Sequence 63, Appl
	42	66	6.7	2267	3	US-09-917-265-107	Sequence 107, App
c	43	66	6.7	2267	3	US-09-917-265-109	Sequence 109, App
	44	66	6.7	2267	9	US-10-821-670-107	Sequence 107, App
c	45	66	6.7	2267	9	US-10-821-670-109	Sequence 109, App
	46	51	5.2	600	16	US-11-136-527-4408	Sequence 4408, Ap
	47	51	5.2	1024	16	US-11-136-527-312	Sequence 312, App
	48	44	4.5	987	3	US-09-754-014-2	Sequence 2, Appli
	49	44	4.5	987	3	US-09-836-866-2	Sequence 2, Appli
	50	44	4.5	987	3	US-09-826-025-24	Sequence 24, Appl
	51	44	4.5	987	9	US-10-785-577-24	Sequence 24, Appl
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ALIGNMENTS

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RESULT 1
US-09-917-265-29
; Sequence 29, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
;   OTHER INFORMATION:
US-09-917-265-29

  Query Match           100.0%;  Score 987;  DB 3;  Length 987;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  987;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 2
US-09-917-265-31/c
; Sequence 31, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-31

  Query Match            100.0%;  Score 987;  DB 3;  Length 987;
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Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGCAGT 1


RESULT 3
US-10-821-670-29
; Sequence 29, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
US-10-821-670-29

  Query Match             100.0%;  Score 987;  DB 9;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  987;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987


RESULT 4
US-10-821-670-31/c
; Sequence 31, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-31

  Query Match             100.0%;  Score 987;  DB 9;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  987;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868
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Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGCAGT 1


RESULT 5
US-09-917-265-55
; Sequence 55, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(984)
;   OTHER INFORMATION:
US-09-917-265-55

  Query Match             99.8%;  Score 985;  DB 3;  Length 985;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
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Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 6
US-09-917-265-57/c
; Sequence 57, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-57

  Query Match             99.8%;  Score 985;  DB 3;  Length 985;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGCA 1


RESULT 7
US-10-821-670-55
; Sequence 55, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(984)
US-10-821-670-55

  Query Match             99.8%;  Score 985;  DB 9;  Length 985;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
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Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
              |||||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGCA 1


RESULT 9
US-10-079-616-5
; Sequence 5, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2193 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-079-616-5

  Query Match             94.2%;  Score 930;  DB 6;  Length 2193;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  930;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         58 CTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCT 117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCT 180

Qy        118 GATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACC 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACC 240

Qy        178 TGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTC 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTC 300

Qy        238 AAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCAT 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAAGAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCAT 360

Qy        298 TCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAA 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCGTTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAA 420

Qy        358 CAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGT 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGAAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGT 480

Qy        418 TTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGC 477
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTCACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGC 540

Qy        478 AGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAG 537
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAG 600

Qy        538 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 597
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 660

Qy        598 TGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTC 657
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTC 720

Qy        658 AAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCC 717
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGTACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCC 780

Qy        718 AAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATAC 777
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGAACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATAC 840

Qy        778 CCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAG 837
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCTGACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAG 900

Qy        838 GGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTC 897
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCAAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTC 960

Qy        898 GTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCC 957
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCC 1020

Qy        958 TGGAGCAACTGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||||||||||
Db       1021 TGGAGCAACTGGGCATCCGTGTCCTGCAGT 1050


RESULT 10
US-10-079-616-6
; Sequence 6, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
```

```
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;       COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 6:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-079-616-6

  Query Match             93.3%;  Score 921;  DB 6;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy         367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy         427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy         487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy         547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy         607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy         667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy         727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy         787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy         847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy         907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy         967 TGGGCATCCGTGTCCTGCAGT 987
               |||||||||||||||||||||
Db         901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 11
US-09-917-265-38
; Sequence 38, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE(
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
US-09-917-265-38

  Query Match             91.7%;  Score 905;  DB 3;  Length 1599;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  955;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91

Qy          92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151

Qy         152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211
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Qy        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271

Qy        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331

Qy        332 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 391

Qy        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451

Qy        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTG 511
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTG 511

Qy        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571

Qy        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631

Qy        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691

Qy        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751

Qy        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811

Qy        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 871
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 871

Qy        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931

Qy        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987
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RESULT 12
US-09-917-265-40/c
; Sequence 40, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265-40

Query Match 91.7%; Score 905; DB 3; Length 1599;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 955; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy         32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1568 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 1509

Qy         92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1508 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 1449

Qy        152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1448 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 1389

Qy        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1388 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 1329

Qy        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1328 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 1269

Qy        332 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1268 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 1209

Qy        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1208 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 1149

Qy        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTG 511
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       1148 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTG 1089

Qy        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1088 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 1029

Qy        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1028 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 969

Qy        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        968 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 909

Qy        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        908 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 849

Qy        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811
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Db        848 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 789

Qy        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 871
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        788 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 729

Qy        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 669

Qy        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 613
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RESULT 13
US-10-821-670-38
; Sequence 38, Application US/10821670

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; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-10-821-670-38

  Query Match            91.7%;  Score 905;  DB 9;  Length 1599;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches  955;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91
Db         32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91

Qy         92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151
Db         92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151

Qy        152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211
Db        152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211

Qy        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271
Db        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271

Qy        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331
Db        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331

Qy        332 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 391
Db        332 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 391

Qy        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451
Db        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451

Qy        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTG 511
Db        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTG 511

Qy        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571
Db        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571

Qy        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631
Db        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631

Qy        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691
Db        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691

Qy        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751
Db        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751

Qy        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811
Db        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811

Qy        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 871
Db        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 871

Qy        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931
Db        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931

Qy        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987
Db        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987


RESULT 14
US-10-821-670-40/c
; Sequence 40, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-40

  Query Match            91.7%;  Score 905;  DB 9;  Length 1599;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches  955;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         32 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 91
Db       1568 TTTCCCTGGTTTTGCTGGCACCTCCCCTCATGGCCATATGGGAACTGGAGAAAAACGTTT 1509

Qy         92 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 151
Db       1508 ATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACCTGCA 1449

Qy        152 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 211
Db       1448 ATACTCCTGAAGAAGATGACATCACCTGGACCTCTGACCAGAGCAGTGAAGTCCTAGGCT 1389

Qy        212 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 271
Db       1388 CTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGCAGATGCTGGCCAGTATACCTGTC 1329

Qy        272 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 331
Db       1328 ATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTCCTGATACACAAAAAGGAAGATGGAA 1269

Qy        332 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 391
Db       1268 TTTGGTCCACTGATATCTTAAGGGAACAGAAAGAATCCAAAAATAAGATCTTTCTAAAAT 1209

Qy        392 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 451
Db       1208 GTGAGGCAAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGGCAATCAGTACCG 1149

Qy        452 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGGGGTGACTTGTG 511
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                ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       1148 ATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCCTCTGACCCCCAAGAGGTGACTTGTG 1089

Qy        512 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 571
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1088 GAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTGGACAACAGGGATTATAAGAAGTACA 1029

Qy        572 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 631
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1028 CAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCTGCCGAGGAGAGCCTACCCATTGAAG 969

Qy        632 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 691
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        968 TCGTGGTGGACGCTATTCACAAGCTCAAGTACGAAAACTACACCAGCAGCTTCTTCATCA 909

Qy        692 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 751
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        908 GGGACATCATCAAACCGGACCCACCCAAGAACCTGCAACTGAAGCCATTAAAAAATTCTC 849

Qy        752 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 811
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 GGCATGTGGAAGTGAGCTGGGAATACCCTGACACCTGGAGCACCCCACATTCCTACTTCT 789

Qy        812 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 871
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        788 CCTTAACATTTGGCGTACAGGTCCAGGGCAAGAACAACAGAGAAAAGAAAGACAGACTCT 729

Qy        872 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 931
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 CCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCACAAGGATGCCAAGATCCGCGTGCAAG 669

Qy        932 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 987
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 CCAGAGACCGCTACTATAGCTCATCCTGGAGCAACTGGGCATCCGTGTCCTGCAGT 613


RESULT 15
US-10-041-672C-1
; Sequence 1, Application US/10041672C
; Publication No. US20030157059A1
; GENERAL INFORMATION:
;  APPLICANT: Mologen Forschungs-, Entwicklungs- und Vetriebs GmbH
;  APPLICANT:  Universitat Zurich
;  TITLE OF INVENTION: FELINE INTERLEUKIN-12 AS IMMUNOSTIMULANT
;  FILE REFERENCE: NHL-NP-36
;  CURRENT APPLICATION NUMBER: US/10/041,672C
;  CURRENT FILING DATE:  2002-01-08
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 990
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: feline IL-12 p40
US-10-041-672C-1

  Query Match             89.7%;  Score 885;  DB 7;  Length 990;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987


RESULT 16
US-10-041-672C-10
; Sequence 10, Application US/10041672C
; Publication No. US20030157059A1
; GENERAL INFORMATION:
;  APPLICANT: Mologen Forschungs-, Entwicklungs- und Vetriebs GmbH
;  APPLICANT:  Universitat Zurich
;  TITLE OF INVENTION: FELINE INTERLEUKIN-12 AS IMMUNOSTIMULANT
;  FILE REFERENCE: NHL-NP-36
;  CURRENT APPLICATION NUMBER: US/10/041,672C
;  CURRENT FILING DATE:  2002-01-08
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 4522
;   TYPE: DNA
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;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pMol-fill2p40
US-10-041-672C-10

  Query Match            89.7%;  Score 885;  DB 7;  Length 4522;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
              ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db       3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

Qy        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
              ||||||||||||||||||||||||||||
Db       4007 AGCAACTGGGCATCCGTGTCCTGCAGT 4033


RESULT 17
US-09-917-265-26
; Sequence 26, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(921)
;   OTHER INFORMATION:
US-09-917-265-26

  Query Match            88.1%;  Score 870;  DB 3;  Length 921;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600
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Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 18
US-09-917-265-28/c
; Sequence 28, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-28

  Query Match             88.1%;  Score 870;  DB 3;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCAGT 1


RESULT 19
US-10-079-616-7
; Sequence 7, Application US/10079616
; Publication No. US20020107366A1
;  GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
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;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 7:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-079-616-7

  Query Match             88.1%;  Score 870;  DB 6;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy         367 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy         427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy         487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTC 480

Qy         547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy         607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy         667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy         727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy         787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy         847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy         907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy         967 TGGGCATCCGTGTCCTGCAGT 987
               |||||||||||||||||||||
Db         901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 20
US-10-821-670-26
; Sequence 26, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(921)
US-10-821-670-26

  Query Match             88.1%;  Score 870;  DB 9;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy         367 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy         427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 21
US-10-821-670-28/c
; Sequence 28, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-28

  Query Match             88.1%;  Score 870;  DB 9;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 802

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 682

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 622

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 562

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 502

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 442

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 382

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 322

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 262

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 202

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 142

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 22

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||
Db         21 TGGGCATCCGTGTCCTGCAGT 1


RESULT 22
US-09-917-265-43
; Sequence 43, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
```

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;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
;   OTHER INFORMATION:
US-09-917-265-43

  Query Match            88.1%;  Score 870;  DB 3;  Length 1533;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 23
US-09-917-265-45/c
; Sequence 45, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-45

  Query Match            88.1%;  Score 870;  DB 3;  Length 1533;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874
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Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613


RESULT 24
US-10-821-670-43
; Sequence 43, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-10-821-670-43

  Query Match             88.1%;  Score 870;  DB 9;  Length 1533;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||
Db        901 TGGGCATCCGTGTCCTGCAGT 921


RESULT 25
US-10-821-670-45/c
; Sequence 45, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-821-670-45

  Query Match             88.1%;  Score 870;  DB 9;  Length 1533;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474
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Qy        127 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy        187 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        247 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy        307 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy        367 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy        427 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy        487 TCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 546
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy        607 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy        667 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy        727 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy        847 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy        967 TGGGCATCCGTGTCCTGCAGT 987
              |||||||||||||||||||||
Db        633 TGGGCATCCGTGTCCTGCAGT 613


RESULT 26
US-09-917-265-52
; Sequence 52, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(921)
;   OTHER INFORMATION:
US-09-917-265-52

  Query Match             6.7%;  Score 66;  DB 3;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy        597 CTGCCC 602
              ||||||
Db        531 CTGCCC 536


RESULT 27
US-09-917-265-54/c
; Sequence 54, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-54

  Query Match             6.7%;  Score 66;  DB 3;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy        597 CTGCCC 602
              ||||||
Db        391 CTGCCC 386


RESULT 28
US-10-821-670-52
; Sequence 52, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
```

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;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(921)
US-10-821-670-52

  Query Match             6.7%;  Score 66;  DB 9;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy        597 CTGCCC 602
              ||||||
Db        531 CTGCCC 536


RESULT 29
US-10-821-670-54/c
; Sequence 54, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-54

  Query Match             6.7%;  Score 66;  DB 9;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy        597 CTGCCC 602
              ||||||
Db        391 CTGCCC 386


RESULT 30
US-09-917-265-58
; Sequence 58, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
;   OTHER INFORMATION:
US-09-917-265-58

  Query Match             6.7%;  Score 66;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 31
US-09-917-265-60/c
; Sequence 60, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-60

  Query Match             6.7%;  Score 66;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy        597 CTGCCC 602
              ||||||
Db        391 CTGCCC 386


RESULT 32
US-10-821-670-58
; Sequence 58, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
```

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;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
US-10-821-670-58

  Query Match             6.7%;  Score 66;  DB 9;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 33
US-10-821-670-60/c
; Sequence 60, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-60

  Query Match             6.7%;  Score 66;  DB 9;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 392

Qy        597 CTGCCC 602
              ||||||
Db        391 CTGCCC 386


RESULT 34
US-09-917-265-66
; Sequence 66, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
;   OTHER INFORMATION:
US-09-917-265-66

  Query Match             6.7%;  Score 66;  DB 3;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy        597 CTGCCC 602
              ||||||
Db        531 CTGCCC 536


RESULT 35
US-09-917-265-68/c
; Sequence 68, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-68

  Query Match             6.7%;  Score 66;  DB 3;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy        597 CTGCCC 602
              ||||||
Db       1003 CTGCCC 998


RESULT 36
US-10-821-670-66
; Sequence 66, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
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;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
US-10-821-670-66

  Query Match             6.7%;  Score 66;  DB 9;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 530

Qy        597 CTGCCC 602
              ||||||
Db        531 CTGCCC 536


RESULT 37
US-10-821-670-68/c
; Sequence 68, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-68

  Query Match             6.7%;  Score 66;  DB 9;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy        597 CTGCCC 602
              ||||||
Db       1003 CTGCCC 998


RESULT 38
US-09-917-265-61
; Sequence 61, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
US-09-917-265-61

  Query Match             6.7%;  Score 66;  DB 3;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 39
US-09-917-265-63/c
; Sequence 63, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-63

  Query Match             6.7%;  Score 66;  DB 3;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy        597 CTGCCC 602
              ||||||
Db       1003 CTGCCC 998


RESULT 40
US-10-821-670-61
; Sequence 61, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
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; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
US-10-821-670-61

  Query Match             6.7%;  Score 66;  DB 9;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596

Qy        597 CTGCCC 602
              ||||||
Db        597 CTGCCC 602


RESULT 41
US-10-821-670-63/c
; Sequence 63, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-63

  Query Match             6.7%;  Score 66;  DB 9;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1004

Qy        597 CTGCCC 602
              ||||||
Db       1003 CTGCCC 998


RESULT 42
US-09-917-265-107
; Sequence 107, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 107
;   LENGTH: 2267
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (154)..(1140)
;   OTHER INFORMATION:
US-09-917-265-107

  Query Match             6.7%;  Score 66;  DB 3;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 749

Qy        597 CTGCCC 602
              ||||||
Db        750 CTGCCC 755


RESULT 43
US-09-917-265-109/c
; Sequence 109, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 109
;   LENGTH: 2267
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-109

  Query Match             6.7%;  Score 66;  DB 3;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1578 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1519

Qy        597 CTGCCC 602
              ||||||
Db       1518 CTGCCC 1513


RESULT 44
US-10-821-670-107
; Sequence 107, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 107
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;   LENGTH: 2267
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (154)..(1140)
US-10-821-670-107

  Query Match             6.7%;  Score 66;  DB 9;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 749

Qy        597 CTGCCC 602
              ||||||
Db        750 CTGCCC 755


RESULT 45
US-10-821-670-109/c
; Sequence 109, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 109
;   LENGTH: 2267
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-821-670-109

  Query Match             6.7%;  Score 66;  DB 9;  Length 2267;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1578 GGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGC 1519

Qy        597 CTGCCC 602
              ||||||
Db       1518 CTGCCC 1513


RESULT 46
US-11-136-527-4408
; Sequence 4408, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William M
;  TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
;  FILE REFERENCE: 031896-041000 (AM101086)
;  CURRENT APPLICATION NUMBER: US/11/136,527
;  CURRENT FILING DATE:  2005-05-25
;  PRIOR APPLICATION NUMBER: US 60/574,294
;  PRIOR FILING DATE: 2005-05-26
;  NUMBER OF SEQ ID NOS: 362830
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4408
;   LENGTH: 600
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-11-136-527-4408

  Query Match             5.2%;  Score 51;  DB 16;  Length 600;
  Best Local Similarity   100.0%;  Pred. No. 5.9e-16;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCA 728
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCA 311


RESULT 47
US-11-136-527-312
; Sequence 312, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William M
;  TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
;  FILE REFERENCE: 031896-041000 (AM101086)
;  CURRENT APPLICATION NUMBER: US/11/136,527
;  CURRENT FILING DATE:  2005-05-25
;  PRIOR APPLICATION NUMBER: US 60/574,294
;  PRIOR FILING DATE: 2005-05-26
;  NUMBER OF SEQ ID NOS: 362830
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 312
;   LENGTH: 1024
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-11-136-527-312

  Query Match             5.2%;  Score 51;  DB 16;  Length 1024;
  Best Local Similarity   100.0%;  Pred. No. 5.9e-16;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCA 728
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 CAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTGCA 735


RESULT 48
US-09-754-014-2
; Sequence 2, Application US/09754014
; Patent No. US20020119940A1
;   GENERAL INFORMATION:
;        APPLICANT: Jeff No. US20020119940A1dstrom
;                   Bruce Freimark
;                   Deepa Deshpande
;        TITLE OF INVENTION: GENE EXPRESSION AND DELIVERY SYTEMS
;                            AND USES
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                     Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 90071-2066
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                          storage
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: IBM P.C. DOS 5.0
;             SOFTWARE: FastSEQ for Windows 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/754,014
;             FILING DATE: 03-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
```

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;             APPLICATION NUMBER: 08/948,958
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Berkman, Charles S.
;             REGISTRATION NUMBER: 38,077
;             REFERENCE/DOCKET NUMBER: 226/284
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 987 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-754-014-2

  Query Match             4.5%;  Score 44;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 49
US-09-836-866-2
; Sequence 2, Application US/09836866
; Patent No. US20020123473A1
;   GENERAL INFORMATION:
;        APPLICANT: No. US20020123473A1dstrom, Jeff
;                   Freimark, Bruce
;                   Deshpande, Deepa
;        TITLE OF INVENTION: IL-12 GENE EXPRESSION AND
;                            DELIVERY SYTEMS AND USES
;        NUMBER OF SEQUENCES: 8
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                     Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 90071-2066
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                          storage
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: IBM P.C. DOS 5.0
;             SOFTWARE: FastSEQ for Windows 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/836,866
;             FILING DATE: 16-Apr-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/949,160
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Warburg, Richard J.
;             REGISTRATION NUMBER: 32,327
;             REFERENCE/DOCKET NUMBER: 226/285
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 987 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-836-866-2

  Query Match             4.5%;  Score 44;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 50
US-09-826-025-24
; Sequence 24, Application US/09826025
; Patent No. US20020162123A1
;   GENERAL INFORMATION:
;        APPLICANT: Chang, Lung-Ji
;        TITLE OF INVENTION: Combination Immunogene Therapy
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Medlen & Carroll, LLP
;             STREET: 220 Montgomery Street, Suite 2200
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: United States of America
;             ZIP: 94104
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/826,025
;             FILING DATE: 04-Apr-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/838,702
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ingolia, Diane E.
;             REGISTRATION NUMBER: 40,027
;             REFERENCE/DOCKET NUMBER: CHANG-02687
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 705-8410
;             TELEFAX: (415) 397-8338
;   INFORMATION FOR SEQ ID NO: 24:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 987 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: other nucleic acid
;             DESCRIPTION: /desc = "DNA"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-826-025-24

  Query Match             4.5%;  Score 44;  DB 3;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 51
US-10-785-577-24
; Sequence 24, Application US/10785577
; Publication No. US20040237129A1
;   GENERAL INFORMATION:
;        APPLICANT: Chang, Lung-Ji
```

```
;       TITLE OF INVENTION: Combination Immunogene Therapy
;       NUMBER OF SEQUENCES: 25
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Medlen & Carroll, LLP
;            STREET: 220 Montgomery Street, Suite 2200
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: United States of America
;            ZIP: 94104
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/785,577
;            FILING DATE: 23-Feb-2004
;            CLASSIFICATION: 424
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/838,702
;            FILING DATE: 9-Apr-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Ingolia, Diane E.
;            REGISTRATION NUMBER: 40,027
;            REFERENCE/DOCKET NUMBER: CHANG-02687
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 705-8410
;            TELEFAX: (415) 397-8338
;   INFORMATION FOR SEQ ID NO: 24:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 987 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: other nucleic acid
;            DESCRIPTION: /desc = "DNA"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-785-577-24

  Query Match             4.5%;  Score 44;  DB 9;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 52
US-10-373-456-18
; Sequence 18, Application US/10373456
; Publication No. US20040009146A1
; GENERAL INFORMATION:
;  APPLICANT: Podhajcer, Osvaldo
;  TITLE OF INVENTION: Anti-Tumor Vaccine and Method
;  FILE REFERENCE: 1423P-US/101141-14
;  CURRENT APPLICATION NUMBER: US/10/373,456
;  CURRENT FILING DATE:  2003-02-25
;  PRIOR APPLICATION NUMBER: US 60/359,836
;  PRIOR FILING DATE: 2002-02-26
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 1005
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-373-456-18

  Query Match             4.5%;  Score 44;  DB 7;  Length 1005;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        669 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 712


RESULT 53
US-10-221-975A-1
; Sequence 1, Application US/10221975A
; Publication No. US20040023332A1
; GENERAL INFORMATION:
;  APPLICANT: Pohang University of Science and Technology
;  APPLICANT:  Progen Co., Ltd.
;  APPLICANT:  Sung, Young Chul
;  APPLICANT:  Lee, Sung Hee
;  APPLICANT:  Ha, Sang Jun
;  APPLICANT:  Song, Man Ki
;  APPLICANT:  Chang, Jun
;  TITLE OF INVENTION: Genes of IL-12p40 Subunit Mutated for Improving the Activity of
;  TITLE OF INVENTION:  IL-12 and Use Thereof for DNA Vaccine Adjuvant
;  FILE REFERENCE: 59520-00005
;  CURRENT APPLICATION NUMBER: US/10/221,975A
;  CURRENT FILING DATE:  2003-04-02
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 1007
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-221-975A-1

  Query Match             4.5%;  Score 44;  DB 8;  Length 1007;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        667 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 710


RESULT 54
US-10-373-456-20
; Sequence 20, Application US/10373456
; Publication No. US20040009146A1
; GENERAL INFORMATION:
;  APPLICANT: Podhajcer, Osvaldo
;  TITLE OF INVENTION: Anti-Tumor Vaccine and Method
;  FILE REFERENCE: 1423P-US/101141-14
;  CURRENT APPLICATION NUMBER: US/10/373,456
;  CURRENT FILING DATE:  2003-02-25
;  PRIOR APPLICATION NUMBER: US 60/359,836
;  PRIOR FILING DATE: 2002-02-26
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 1017
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-373-456-20

  Query Match             4.5%;  Score 44;  DB 7;  Length 1017;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        673 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 716


RESULT 55
US-10-267-384-194
; Sequence 194, Application US/10267384
; Publication No. US20030198623A1
;   GENERAL INFORMATION:
;        APPLICANT: Paoletti, Enzo
```

```
;                  Tartaglia, James
;                  Cox, William I.
;       TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
;       NUMBER OF SEQUENCES: 217
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Curtis, Morris & Safford
;            STREET: 530 Fifth Avenue
;            CITY: New York
;            STATE: NY
;            COUNTRY: USA
;            ZIP: 10036
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/267,384
;            FILING DATE: 09-Oct-2002
;            CLASSIFICATION: 435
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Frommer, William S.
;            REGISTRATION NUMBER: 25,506
;            REFERENCE/DOCKET NUMBER: 454310-2530
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 840-3333
;            TELEFAX: (212) 840-0712
;            TELEX: 425066CURTMS
;   INFORMATION FOR SEQ ID NO: 194:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1018 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-10-267-384-194

  Query Match             4.5%;  Score 44;  DB 7;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        692 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 735


RESULT 56
US-10-603-064-4
; Sequence 4, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
;  APPLICANT: Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION: Multiple Cytokine Protein Complexes
;  FILE REFERENCE: LEX-010
;  CURRENT APPLICATION NUMBER: US/10/603,064
;  CURRENT FILING DATE:  2003-06-24
;  PRIOR APPLICATION NUMBER: US/09/634,368
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: 60/147,924
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 1389
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: human
;   OTHER INFORMATION: p40-IL-2 fusion protein coding sequence
US-10-603-064-4

  Query Match             4.5%;  Score 44;  DB 8;  Length 1389;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 704


RESULT 57
US-10-349-507-2
; Sequence 2, Application US/10349507
; Publication No. US20030199002A1
; GENERAL INFORMATION:
;  APPLICANT: Hekimi , Siegfried
;  APPLICANT:  Jiang , Ning
;  APPLICANT:  Benard, Claire
;  APPLICANT:  Kebir , Hania
;  APPLICANT:  McCright, Brenton
;  APPLICANT:  Lakowski , Bernard
;  TITLE OF INVENTION: CLK-2 NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
;  FILE REFERENCE: 11202-006-999
;  CURRENT APPLICATION NUMBER: US/10/349,507
;  CURRENT FILING DATE:  2003-01-22
;  PRIOR APPLICATION NUMBER: 10/312,187
;  PRIOR FILING DATE: 2002-12-20
;  PRIOR APPLICATION NUMBER: PCT/CA01/00913
;  PRIOR FILING DATE: 2001-06-20
;  PRIOR APPLICATION NUMBER: 60/213,174
;  PRIOR FILING DATE: 2000-06-22
;  PRIOR APPLICATION NUMBER: 60/254,932
;  PRIOR FILING DATE: 2000-12-13
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 1397
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (41)...(1024)
US-10-349-507-2

  Query Match             4.5%;  Score 44;  DB 7;  Length 1397;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        701 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 744


RESULT 58
US-10-267-565-2
; Sequence 2, Application US/10267565
; Publication No. US20030204059A1
; GENERAL INFORMATION:
;  APPLICANT: Gately, Maurice
;  APPLICANT:  Gubler, Ulrich
;  APPLICANT:  Hulmes, Jeffery
;  APPLICANT:  Podlaski, Frank
;  APPLICANT:  Stern, Alvin
;  TITLE OF INVENTION: PURIFICATION AND CHARACTERIZATION OF CYTOTOXIC
;  TITLE OF INVENTION:  LYMPHOCYTE MATURATION FACTOR AND MONOCLONAL
;  TITLE OF INVENTION:  ANTIBODIES THERETO
;  FILE REFERENCE: 11126-005
;  CURRENT APPLICATION NUMBER: US/10/267,565
;  CURRENT FILING DATE:  2003-01-23
;  PRIOR APPLICATION NUMBER: 09/401,839
;  PRIOR FILING DATE: 1999-09-22
;  PRIOR APPLICATION NUMBER: 08/459,151
;  PRIOR FILING DATE: 1995-06-02
;  PRIOR APPLICATION NUMBER: 08/205,011
```

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;  PRIOR FILING DATE: 1994-03-02
;  PRIOR APPLICATION NUMBER: 07/857,023
;  PRIOR FILING DATE: 1992-03-24
;  PRIOR APPLICATION NUMBER: 07/572,284
;  PRIOR FILING DATE: 1990-08-27
;  PRIOR APPLICATION NUMBER: 07/520,935
;  PRIOR FILING DATE: 1990-05-09
;  PRIOR APPLICATION NUMBER: 07/455,708
;  PRIOR FILING DATE: 1989-12-22
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 1397
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (41)...(1024)
US-10-267-565-2

  Query Match             4.5%;  Score 44;  DB 7;  Length 1397;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        701 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 744


RESULT 59
US-10-929-182-22
; Sequence 22, Application US/10929182
; Publication No. US20050064483A1
; GENERAL INFORMATION:
;  APPLICANT: Zang, Jingwu
;  APPLICANT:  Hong, Jian
;  TITLE OF INVENTION: Gene Expression Profiling Technology for Treatment Evaluation of
;  TITLE OF INVENTION:  Multiple Sclerosis
;  FILE REFERENCE: HO-P02859US1
;  CURRENT APPLICATION NUMBER: US/10/929,182
;  CURRENT FILING DATE:  2004-08-30
;  PRIOR APPLICATION NUMBER: US 60/498,731
;  PRIOR FILING DATE: 2003-08-28
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
;   LENGTH: 1399
;   TYPE: DNA
;   ORGANISM: HUMAN
US-10-929-182-22

  Query Match             4.5%;  Score 44;  DB 10;  Length 1399;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        703 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 746


RESULT 60
US-10-742-405-7
; Sequence 7, Application US/10742405
; Publication No. US20040213761A1
; GENERAL INFORMATION:
;  APPLICANT: Bowman, Edward P.
;  APPLICANT:  Chan, Jason R.
;  APPLICANT:  Moore, Kevin
;  APPLICANT:  Nguyen, Nhung
;  APPLICANT:  Churakova, Tatyana
;  APPLICANT:  Chen, Shi-Juan
;  APPLICANT:  Cua, Daniel J.
;  TITLE OF INVENTION: Uses of mammalian cytokine; related reagents
;  FILE REFERENCE: DX01578K
;  CURRENT APPLICATION NUMBER: US/10/742,405
;  CURRENT FILING DATE:  2003-12-18
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
;   LENGTH: 1580
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (7)..(1569)
US-10-742-405-7

  Query Match             4.5%;  Score 44;  DB 9;  Length 1580;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        673 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 716


RESULT 61
US-10-373-456-2
; Sequence 2, Application US/10373456
; Publication No. US20040009146A1
; GENERAL INFORMATION:
;  APPLICANT: Podhajcer, Osvaldo
;  TITLE OF INVENTION: Anti-Tumor Vaccine and Method
;  FILE REFERENCE: 1423P-US/101141-14
;  CURRENT APPLICATION NUMBER: US/10/373,456
;  CURRENT FILING DATE:  2003-02-25
;  PRIOR APPLICATION NUMBER: US 60/359,836
;  PRIOR FILING DATE: 2002-02-26
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 1828
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: p40-linker-p35 fragment cloned into MVL-hIL12lig vector (Fig. 11)
US-10-373-456-2

  Query Match             4.5%;  Score 44;  DB 7;  Length 1828;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        673 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 716


RESULT 62
US-10-228-811-4
; Sequence 4, Application US/10228811
; Publication No. US20030054392A1
; GENERAL INFORMATION:
;  APPLICANT: Wittig, Prof. Burghardt
;  APPLICANT:  Junghans, Claas
;  TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
;  TITLE OF INVENTION:  Therapy
;  FILE REFERENCE: XI 597/99
;  CURRENT APPLICATION NUMBER: US/10/228,811
;  CURRENT FILING DATE:  2002-08-27
;  PRIOR APPLICATION NUMBER: DE 196 48 625.4
;  PRIOR FILING DATE: 1996-11-13
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 1870
;   TYPE: DNA
```

```
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (1)..(1870)
;   OTHER INFORMATION: Interleukin-12 (IL-12, p40-subunit); Oligo DNA Dumbbell
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1)..(2)
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to
;   OTHER INFORMATION: 2  can be modified with amino or caroxy features
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1869)..(1870)
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1869
;   OTHER INFORMATION: to 1870  can be modified with amino or caroxy features
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Strandness: both;  nucleic
;   OTHER INFORMATION: acid (linear),  hypothetical: No. US20030054392A1 anti-sense: No
US-10-228-811-4

  Query Match             4.5%;  Score 44;  DB 6;  Length 1870;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db       1293 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 1336


RESULT 63
US-10-172-399-7
; Sequence 7, Application US/10172399
; Publication No. US20030045495A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Chuan-Yuan
;  APPLICANT:  Dewhirst, Mark
;  APPLICANT:  Huang, Qian
;  TITLE OF INVENTION: A METHOD FOR SELECTIVE EXPRESSION OF THERAPEUTIC GENES BY HYPERTH
;  FILE REFERENCE: 180-129
;  CURRENT APPLICATION NUMBER: US/10/172,399
;  CURRENT FILING DATE:  2002-06-14
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
;   LENGTH: 2318
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (14)..(1000)
US-10-172-399-7

  Query Match             4.5%;  Score 44;  DB 6;  Length 2318;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        674 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 717


RESULT 64
US-10-476-961-3
; Sequence 3, Application US/10476961
; Publication No. US20040241843A1
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Isis Pharmaceuticals, Inc.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTSP-0393
;  CURRENT APPLICATION NUMBER: US/10/476,961
;  CURRENT FILING DATE:  2003-11-05
;  PRIOR APPLICATION NUMBER: 2001-05-07
;  PRIOR FILING DATE: 09/851,062
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 3
;   LENGTH: 2318
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (14)...(1000)
US-10-476-961-3

  Query Match             4.5%;  Score 44;  DB 9;  Length 2318;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        674 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 717


RESULT 65
US-10-429-802-44
; Sequence 44, Application US/10429802
; Publication No. US20030228285A1
; GENERAL INFORMATION:
;  APPLICANT: HUNG, MIEN-CHIE
;  APPLICANT:  WONG, KA YIN
;  APPLICANT:  ZOU, YIYU
;  TITLE OF INVENTION: BIPARTITE T-CELL FACTOR (TCF)-RESPONSIVE PROMOTER
;  FILE REFERENCE: UTSC:752US
;  CURRENT APPLICATION NUMBER: US/10/429,802
;  CURRENT FILING DATE:  2003-05-05
;  PRIOR APPLICATION NUMBER: 60/377,672
;  PRIOR FILING DATE: 2002-05-03
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
;   LENGTH: 2347
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-429-802-44

  Query Match             4.5%;  Score 44;  DB 7;  Length 2347;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db        703 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 746


RESULT 66
US-10-430-503-35
; Sequence 35, Application US/10430503
; Publication No. US20040005684A1
; GENERAL INFORMATION:
;  APPLICANT: HUNG, MIEN-CHIE
;  APPLICANT:  LAN, KENG-LI
;  APPLICANT:  OU-YANG, FU
;  APPLICANT:  LIU, JAW-CHING
;  APPLICANT:  LAN, KENG-HSIN
;  TITLE OF INVENTION: TARGETING PROTEINS TO DELIVER THERAPEUTIC OR DIAGNOSTIC
;  TITLE OF INVENTION:  REAGENTS
;  FILE REFERENCE: UTSC:797US
;  CURRENT APPLICATION NUMBER: US/10/430,503
;  CURRENT FILING DATE:  2003-05-06
;  PRIOR APPLICATION NUMBER: 60/383,063
;  PRIOR FILING DATE: 2002-05-06
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
;   LENGTH: 2347
```

```
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-430-503-35

  Query Match             4.5%;  Score 44;  DB 7;  Length 2347;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        703 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 746


RESULT 67
US-09-924-703-3
; Sequence 3, Application US/09924703
; Patent No. US20020137898A1
; GENERAL INFORMATION:
;  APPLICANT: TRINCHIERI, GIORGIO
;  APPLICANT:  PERUSSIA, BICE
;  APPLICANT:  CLARK, STEVEN C.
;  APPLICANT:  WONG, GORDON G.
;  APPLICANT:  HEWICK, RODNEY
;  APPLICANT:  KOBAYASHI, MICHIKO
;  TITLE OF INVENTION: ANTIBODIES TO NATURAL KILLER STIMULATORY FACTOR
;  FILE REFERENCE: 01142.0142.0100
;  CURRENT APPLICATION NUMBER: US/09/924,703
;  CURRENT FILING DATE:  2001-08-09
;  PRIOR APPLICATION NUMBER: 09/325,958
;  PRIOR FILING DATE: 1999-06-04
;  PRIOR APPLICATION NUMBER: 08/858,000
;  PRIOR FILING DATE: 1997-05-16
;  PRIOR APPLICATION NUMBER: 08/403,013
;  PRIOR FILING DATE: 1995-03-13
;  PRIOR APPLICATION NUMBER: 07/584,941
;  PRIOR FILING DATE: 1990-09-18
;  PRIOR APPLICATION NUMBER: 07/307,817
;  PRIOR FILING DATE: 1989-02-07
;  PRIOR APPLICATION NUMBER: 07/269,945
;  PRIOR FILING DATE: 1988-11-10
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 2362
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
;   OTHER INFORMATION: sequence of the 40 kD subunit of NKSF
;   NAME/KEY: CDS
;   LOCATION: (33)..(1016)
US-09-924-703-3

  Query Match             4.5%;  Score 44;  DB 3;  Length 2362;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        693 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 736


RESULT 68
US-10-358-395-3
; Sequence 3, Application US/10358395
; Publication No. US20040044186A1
; GENERAL INFORMATION:
;  APPLICANT: TRINCHIERI, GIORGIO
;  APPLICANT:  PERUSSIA, BICE
;  APPLICANT:  CLARK, STEVEN C.
;  APPLICANT:  WONG, GORDON G.
;  APPLICANT:  HEWICK, RODNEY
;  APPLICANT:  KOBAYASHI, MICHIKO
;  TITLE OF INVENTION: ANTIBODIES TO NATURAL KILLER STIMULATORY FACTOR
;  FILE REFERENCE: 01142.0142.0100
;  CURRENT APPLICATION NUMBER: US/10/358,395
;  CURRENT FILING DATE:  2003-02-05
;  PRIOR APPLICATION NUMBER: US/09/924,703
;  PRIOR FILING DATE: 2001-08-09
;  PRIOR APPLICATION NUMBER: 09/325,958
;  PRIOR FILING DATE: 1999-06-04
;  PRIOR APPLICATION NUMBER: 08/858,000
;  PRIOR FILING DATE: 1997-05-16
;  PRIOR APPLICATION NUMBER: 08/403,013
;  PRIOR FILING DATE: 1995-03-13
;  PRIOR APPLICATION NUMBER: 07/584,941
;  PRIOR FILING DATE: 1990-09-18
;  PRIOR APPLICATION NUMBER: 07/307,817
;  PRIOR FILING DATE: 1989-02-07
;  PRIOR APPLICATION NUMBER: 07/269,945
;  PRIOR FILING DATE: 1988-11-10
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 2362
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
;   OTHER INFORMATION: sequence of the 40 kD subunit of NKSF
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (33)..(1016)
US-10-358-395-3

  Query Match             4.5%;  Score 44;  DB 8;  Length 2362;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db        693 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 736


RESULT 69
US-10-373-456-1
; Sequence 1, Application US/10373456
; Publication No. US20040009146A1
; GENERAL INFORMATION:
;  APPLICANT: Podhajcer, Osvaldo
;  TITLE OF INVENTION: Anti-Tumor Vaccine and Method
;  FILE REFERENCE: 1423P-US/101141-14
;  CURRENT APPLICATION NUMBER: US/10/373,456
;  CURRENT FILING DATE:  2003-02-25
;  PRIOR APPLICATION NUMBER: US 60/359,836
;  PRIOR FILING DATE: 2002-02-26
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 2466
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: p35-IRES-p40 fragment cloned into MVL-hIL-12 and MVL-hIL-12-hIL-1
;   OTHER INFORMATION: 0 vectors (Fig 11)
US-10-373-456-1

  Query Match             4.5%;  Score 44;  DB 7;  Length 2466;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db       2130 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 2173
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RESULT 70
US-10-136-837-1
; Sequence 1, Application US/10136837
; Publication No. US20030181405A1
; GENERAL INFORMATION:
;  APPLICANT: NORDSTROM, Jeffrey L
;  APPLICANT:  PERICLE, Federica
;  APPLICANT:  ROLLAND, Alain
;  APPLICANT:  RALSTON, Robert
;  TITLE OF INVENTION: Interferon Alpha Plasmids and Delivery Systems, and Methods of Ma
;  TITLE OF INVENTION:  Using the Same
;  FILE REFERENCE: 273/082 (GM15-1USC1)
;  CURRENT APPLICATION NUMBER: US/10/136,837
;  CURRENT FILING DATE:  2002-04-29
;  PRIOR APPLICATION NUMBER: US 09/268,135
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 5686
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Human IL-12 Plasmid pIN1143
US-10-136-837-1

  Query Match             4.5%;  Score 44;  DB 7;  Length 5686;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db       3879 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 3922


RESULT 71
US-09-828-825-1
; Sequence 1, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 8578
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: enhancer
;   LOCATION: (1)..(659)
;   OTHER INFORMATION: CMV IE
;   NAME/KEY: promoter
;   LOCATION: (669)..(750)
;   OTHER INFORMATION: CMV  IE
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA Promoter
;   NAME/KEY: mRNA
;   LOCATION: (1090)..(1984)
;   OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
;   NAME/KEY: RBS
;   LOCATION: (2013)..(2593)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: mRNA
;   LOCATION: (2627)..(4263)
;   OTHER INFORMATION: Human IL12.0 (2640-4223 coding sequence, flexible
;   OTHER INFORMATION: linker at 3624-3629)
;   NAME/KEY: promoter
;   LOCATION: (4352)..(4431)
;   OTHER INFORMATION: T3 RNA polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4362)..(4583)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4678)..(5133)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5197)..(6564)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (6975)..(7835)
;   OTHER INFORMATION: Ampicillin resistance
;   OTHER INFORMATION: Description of Artificial Sequence: Plasmid
;   NAME/KEY: CDS
;   LOCATION: (2640)..(4223)
;   OTHER INFORMATION: IL 12.0 coding sequence - 2 amino acid linker at
;   OTHER INFORMATION: 3624
US-09-828-825-1

  Query Match             4.5%;  Score 44;  DB 3;  Length 8578;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db       3300 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 3343


RESULT 72
US-09-828-825-3
; Sequence 3, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 8578
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
;   NAME/KEY: enhancer
;   LOCATION: (1)..(659)
;   OTHER INFORMATION: CMV IE Enhancer
;   NAME/KEY: promoter
;   LOCATION: (669)..(750)
;   OTHER INFORMATION: CMV IE Promoter
;   NAME/KEY: misc_feature
;   LOCATION: (890)..(1002)
;   OTHER INFORMATION: InTervening Sequence
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(1984)
;   OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
;   NAME/KEY: RBS
;   LOCATION: (2013)..(2593)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (2627)..(4263)
```

```
;   OTHER INFORMATION: Human IL12.0 sequence (2640-4217 is coding
;   OTHER INFORMATION: sequence)
;   NAME/KEY: promoter
;   LOCATION: (4346)..(4425)
;   OTHER INFORMATION: T3 RNA polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4356)..(4577)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4672)..(5127)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5191)..(6558)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (6969)..(7829)
;   OTHER INFORMATION: Ampicillin resistance
;   NAME/KEY: CDS
;   LOCATION: (2640)..(4217)
;   OTHER INFORMATION: IL12.0 coding sequence - no linker
US-09-828-825-3

  Query Match             4.5%;  Score 44;  DB 3;  Length 8578;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db       3300 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 3343


RESULT 73
US-09-828-825-7
; Sequence 7, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 8608
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: misc_feature
;   LOCATION: (890)..(1002)
;   OTHER INFORMATION: Intervening sequence
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(1984)
;   OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
;   NAME/KEY: RBS
;   LOCATION: (2013)..(2593)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (2627)..(4263)
;   OTHER INFORMATION: Human IL12.2 sequence (2460-4253 is coding
;   OTHER INFORMATION: sequence, 13 amino acid flexible linker at
;   OTHER INFORMATION: 3606-3676)
;   NAME/KEY: CDS
;   LOCATION: (2640)..(4253)
;   OTHER INFORMATION: IL12.2 coding sequence (13 amino acid linker)
;   NAME/KEY: promoter
;   LOCATION: (4362)..(4383)
;   OTHER INFORMATION: T3 RNA Polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4393)..(4614)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4709)..(5164)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5228)..(6595)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (7006)..(7866)
;   OTHER INFORMATION: Ampicillin resistance
US-09-828-825-7

  Query Match             4.5%;  Score 44;  DB 3;  Length 8608;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              |||||||||||||||||||||||||||||||||||||||||||
Db       3300 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 3343


RESULT 74
US-09-828-825-5
; Sequence 5, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 8623
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: misc_feature
;   LOCATION: (890)..(1002)
;   OTHER INFORMATION: Intervening sequence
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(1984)
;   OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
;   NAME/KEY: RBS
;   LOCATION: (2013)..(2593)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (2627)..(4278)
;   OTHER INFORMATION: Human IL12.3 - 2640-4268 is coding sequence,
;   OTHER INFORMATION: flexible linker from 3606-3690
;   NAME/KEY: CDS
;   LOCATION: (2640)..(4268)
;   OTHER INFORMATION: IL 12.3 coding sequence - has 28 amino acid linker
;   OTHER INFORMATION: sequence
;   NAME/KEY: promoter
;   LOCATION: (4398)..(4407)
```

```
;   OTHER INFORMATION: T3 RNA polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4408)..(4629)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4724)..(5179)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5243)..(6610)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (7021)..(7881)
;   OTHER INFORMATION: Ampicillin resistance
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-828-825-5

  Query Match             4.5%;  Score 44;  DB 3;  Length 8623;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db       3300 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 3343


RESULT 75
US-09-828-825-15
; Sequence 15, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 8629
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(2726)
;   OTHER INFORMATION: Human IL12.2 (coding sequence is 1103-2716, 10
;   OTHER INFORMATION: amino acid linker at 2087-2116)
;   NAME/KEY: CDS
;   LOCATION: (1103)..(2716)
;   OTHER INFORMATION: Human IL12.2 (10 amino acid linker)
;   NAME/KEY: RBS
;   LOCATION: (2752)..(3332)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (3369)..(4263)
;   OTHER INFORMATION: Human B7.1 sequence
;   NAME/KEY: promoter
;   LOCATION: (4383)..(4404)
;   OTHER INFORMATION: T3 RNA Polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4414)..(4635)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4730)..(5185)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5249)..(6616)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (7027)..(7887)
;   OTHER INFORMATION: Ampicillin resistance gene
US-09-828-825-15

  Query Match             4.5%;  Score 44;  DB 3;  Length 8629;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db       1763 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 1806


RESULT 76
US-09-828-825-9
; Sequence 9, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 8638
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: misc_feature
;   LOCATION: (890)..(1002)
;   OTHER INFORMATION: Intervening sequence
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(1984)
;   OTHER INFORMATION: Human B7.1 (1090-1954 is coding sequence)
;   NAME/KEY: RBS
;   LOCATION: (2013)..(2593)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (2627)..(4293)
;   OTHER INFORMATION: Human IL12.4 (coding sequence is 2640-4283, 33
;   OTHER INFORMATION: amino acid linker at 3606-3706)
;   NAME/KEY: CDS
;   LOCATION: (2640)..(4283)
;   OTHER INFORMATION: IL12.4 coding sequence (33 amino acid linker)
;   NAME/KEY: promoter
;   LOCATION: (4392)..(4413)
;   OTHER INFORMATION: T3 RNA Polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4423)..(4644)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4739)..(5194)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5258)..(6625)
;   OTHER INFORMATION: Neo r expression cassette
```

```
;   NAME/KEY: misc_feature
;   LOCATION: (7036)..(7896)
;   OTHER INFORMATION: Ampicillin resistance
US-09-828-825-9

  Query Match             4.5%;  Score 44;  DB 3;  Length 8638;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db       3300 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 3343


RESULT 77
US-09-828-825-13
; Sequence 13, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
;   LENGTH: 8644
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(2731)
;   OTHER INFORMATION: Human IL12.3 (1103-2731 is coding sequence, 15
;   OTHER INFORMATION: amino acid linker at 2087-2131)
;   NAME/KEY: CDS
;   LOCATION: (1103)..(2731)
;   OTHER INFORMATION: IL12.3 (15 amino acid linker)
;   NAME/KEY: RBS
;   LOCATION: (2767)..(3347)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (3384)..(4278)
;   OTHER INFORMATION: Human B7.1 sequence
;   NAME/KEY: promoter
;   LOCATION: (4398)..(4419)
;   OTHER INFORMATION: T3 RNA polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4429)..(4650)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4745)..(5200)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5264)..(5681)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (7042)..(7902)
;   OTHER INFORMATION: Ampicillin resistance gene
US-09-828-825-13

  Query Match             4.5%;  Score 44;  DB 3;  Length 8644;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db       1763 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 1806


RESULT 78
US-09-828-825-11
; Sequence 11, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 8659
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(2756)
;   OTHER INFORMATION: Human IL12.4 (coding sequence 1103-2746, 19 amino
;   OTHER INFORMATION: acid linker at 2087-2146)
;   NAME/KEY: CDS
;   LOCATION: (1103)..(2746)
;   OTHER INFORMATION: Human IL12.4 (19 amino acid linker)
;   NAME/KEY: RBS
;   LOCATION: (2782)..(3362)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (3399)..(4293)
;   OTHER INFORMATION: Human B7.1 sequence
;   NAME/KEY: promoter
;   LOCATION: (4413)..(4434)
;   OTHER INFORMATION: T3 RNA polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4444)..(4665)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4760)..(5215)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5279)..(6646)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (7057)..(7917)
;   OTHER INFORMATION: Ampicillin resistance gene
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-828-825-11

  Query Match             4.5%;  Score 44;  DB 3;  Length 8659;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db       1763 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 1806
```

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RESULT 79
US-10-511-237-3
; Sequence 3, Application US/10511237
; Publication No. US20050233457A1
; GENERAL INFORMATION:
;  APPLICANT: Block, Andreas
;  TITLE OF INVENTION: Recombinant Viral Vectors for the Tetracycline-regulated Expressi
;  TITLE OF INVENTION:  Genes
;  FILE REFERENCE: 66741-043
;  CURRENT APPLICATION NUMBER: US/10/511,237
;  CURRENT FILING DATE:  2004-10-12
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 11453
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Adenoviral expression plasmid pShuttle.3r.hscIL-12 for regulated
;   OTHER INFORMATION: expression of human IL-12 following virus generation using AdEasy
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (327)..(713)
;   OTHER INFORMATION: VP16
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (714)..(1352)
;   OTHER INFORMATION: TetR
;   FEATURE:
;   NAME/KEY: Intron
;   LOCATION: (1353)..(1912)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: promoter
;   LOCATION: (1864)..(1902)
;   OTHER INFORMATION: TK-min
;   FEATURE:
;   NAME/KEY: protein_bind
;   LOCATION: (1913)..(2212)
;   OTHER INFORMATION: TetO7
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2213)..(2709)
;   OTHER INFORMATION: CMV-min + Intron
;   FEATURE:
;   NAME/KEY: promoter
;   LOCATION: (2226)..(2264)
;   OTHER INFORMATION: CMV-min
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (2710)..(4308)
;   OTHER INFORMATION: Human singe-chain IL-12
;   FEATURE:
;   NAME/KEY: mutation
;   LOCATION: (4020)..(4023)
;   OTHER INFORMATION: T/C, A/T, G/C, T/G
US-10-511-237-3

  Query Match             4.5%;  Score 44;  DB 10;  Length 11453;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db       3370 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 3413


RESULT 80
US-10-511-237-1
; Sequence 1, Application US/10511237
; Publication No. US20050233457A1
; GENERAL INFORMATION:
;  APPLICANT: Block, Andreas
;  TITLE OF INVENTION: Recombinant Viral Vectors for the Tetracycline-regulated Expressio
;  TITLE OF INVENTION:  Genes
;  FILE REFERENCE: 66741-043
;  CURRENT APPLICATION NUMBER: US/10/511,237
;  CURRENT FILING DATE:  2004-10-12
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 11569
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Adenoviral expression plasmid pAd.3r.hscIL-12 for regulated expres
;   OTHER INFORMATION: human IL-12
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (327)..(713)
;   OTHER INFORMATION: VP16
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (714)..(1352)
;   OTHER INFORMATION: TetR
;   FEATURE:
;   NAME/KEY: Intron
;   LOCATION: (1353)..(1912)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: promoter
;   LOCATION: (1864)..(1902)
;   OTHER INFORMATION: TK-min
;   FEATURE:
;   NAME/KEY: protein_bind
;   LOCATION: (1913)..(2212)
;   OTHER INFORMATION: TetO7
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2213)..(2709)
;   OTHER INFORMATION: CMV-min + Intron
;   FEATURE:
;   NAME/KEY: promoter
;   LOCATION: (2226)..(2264)
;   OTHER INFORMATION: CMV-min
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (2710)..(4308)
;   OTHER INFORMATION: Human single-chain IL-12
;   FEATURE:
;   NAME/KEY: mutation
;   LOCATION: (4020)..(4023)
;   OTHER INFORMATION: T/C, A/T, G/C, T/G
US-10-511-237-1

  Query Match             4.5%;  Score 44;  DB 10;  Length 11569;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-12;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||||||||||||||||
Db       3370 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACC 3413


RESULT 81
US-10-528-644A-53
; Sequence 53, Application US/10528644A
; Publication No. US20050287117A1
; GENERAL INFORMATION:
;  APPLICANT: SUNG, Young Chul
;  APPLICANT:  YOUN, Jin-Won
;  APPLICANT:  YANG, Se-Hwan
;  APPLICANT:  PARK, Su-Hwan
;  APPLICANT:  LEE, Chang Geun
;  TITLE OF INVENTION: A VACCINE ENHANCING THE PROTECTIVE IMMUNITY TO
;  TITLE OF INVENTION:  HEPATITIS C VIRUS USING PLASMID DNA AND RECOMBINANT ADENOVIRUS
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;  FILE REFERENCE: 428.1049
;  CURRENT APPLICATION NUMBER: US/10/528,644A
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: PCT/KR03/01951
;  PRIOR FILING DATE: 2003-11-19
;  PRIOR APPLICATION NUMBER: KR 2002-0058712
;  PRIOR FILING DATE: 2002-09-27
;  PRIOR APPLICATION NUMBER: KR 2002-68496
;  PRIOR FILING DATE: 2002-11-06
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: KopatentIn 1.71
; SEQ ID NO 53
;   LENGTH: 2390
;   TYPE: DNA
;   ORGANISM: Homo sapiens (hIL-12m)
US-10-528-644A-53

  Query Match             4.0%;  Score 39;  DB 10;  Length 2390;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-09;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        400 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 438
              |||||||||||||||||||||||||||||||||||||||
Db       1803 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 1841


RESULT 82
US-10-240-376A-130
; Sequence 130, Application US/10240376A
; Publication No. US20040161747A1
; GENERAL INFORMATION:
;  APPLICANT: Morahan, Grant
;  TITLE OF INVENTION: A METHOD FOR SCREENING FOR AUTOIMMUNE
;  TITLE OF INVENTION:  DISEASE BY IDENTIFYING POLYMORPHISMS IN IL-12 p40
;  FILE REFERENCE: DAVI186.001APC
;  CURRENT APPLICATION NUMBER: US/10/240,376A
;  CURRENT FILING DATE:  2002-09-27
;  PRIOR APPLICATION NUMBER: PCT/AU01/00340
;  PRIOR FILING DATE: 2001-03-27
;  PRIOR APPLICATION NUMBER: PQ 6466
;  PRIOR FILING DATE: 2000-03-27
;  PRIOR APPLICATION NUMBER: US 60/204,366
;  PRIOR FILING DATE: 2000-05-15
;  NUMBER OF SEQ ID NOS: 140
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 130
;   LENGTH: 18340
;   TYPE: DNA
;   ORGANISM: mammalian
US-10-240-376A-130

  Query Match             4.0%;  Score 39;  DB 8;  Length 18340;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-09;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        400 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 438
              |||||||||||||||||||||||||||||||||||||||
Db      10439 AAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACG 10477


RESULT 83
US-10-029-386-16833/c
; Sequence 16833, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
;  TITLE OF INVENTION:  EXPRESSION ANALYSIS TWO
;  FILE REFERENCE: AEOMICA-X-2
;  CURRENT APPLICATION NUMBER: US/10/029,386
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 34288
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 16833
;   LENGTH: 270
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO CHR5.1
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.84
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.72
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.93
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.79
;   OTHER INFORMATION: NT HIT: AY008847.1, EVALUE 0.00e+00
;   OTHER INFORMATION: EST_HUMAN HIT: BF204907.1, EVALUE 9.20e-02
;   OTHER INFORMATION: SWISSPROT HIT: P29460, EVALUE 4.00e-41
US-10-029-386-16833

  Query Match             3.5%;  Score 35;  DB 7;  Length 270;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-07;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        313 CACAAAAAGGAAGATGGAATTTGGTCCACTGATAT 347
              |||||||||||||||||||||||||||||||||||
Db         41 CACAAAAAGGAAGATGGAATTTGGTCCACTGATAT 7


RESULT 84
US-10-029-386-3133/c
; Sequence 3133, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GE
;  TITLE OF INVENTION:  EXPRESSION ANALYSIS TWO
;  FILE REFERENCE: AEOMICA-X-2
;  CURRENT APPLICATION NUMBER: US/10/029,386
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 34288
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 3133
;   LENGTH: 556
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO CHR5.1
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.84
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.72
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.93
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.79
;   OTHER INFORMATION: NT HIT: AY008847.1, EVALUE 0.00e+00
;   OTHER INFORMATION: SWISSPROT HIT: P29460, EVALUE 5.00e-43
;   OTHER INFORMATION: EST_HUMAN HIT: BG389008.1, EVALUE 2.00e-01
US-10-029-386-3133

  Query Match             3.5%;  Score 35;  DB 7;  Length 556;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        313 CACAAAAAGGAAGATGGAATTTGGTCCACTGATAT 347
              |||||||||||||||||||||||||||||||||||
Db        236 CACAAAAAGGAAGATGGAATTTGGTCCACTGATAT 202


RESULT 85
US-09-823-549-77
; Sequence 77, Application US/09823549
; Publication No. US20020147998A1
; GENERAL INFORMATION:
;  APPLICANT: McConlogue, Lisa  C
;  APPLICANT:  Games, Kate D.
;  APPLICANT:  Yednock, Theodore A.
```

```
;  APPLICANT:  Hua, Tan
;  APPLICANT:  Messersmith, Elizabeth
;  APPLICANT:  Bard, Frederique
;  TITLE OF INVENTION: SCREENING MARKERS AND METHODS FOR NEURODEGENERATIVE DISORDERS
;  FILE REFERENCE: 015270-009110US
;  CURRENT APPLICATION NUMBER: US/09/823,549
;  CURRENT FILING DATE:  2001-03-30
;  PRIOR APPLICATION NUMBER: US 60/193,847
;  PRIOR FILING DATE: 2000-03-30
;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
;   LENGTH: 73
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: IL-12 p40, #1 marker
US-09-823-549-77

  Query Match             3.0%;  Score 30;  DB 3;  Length 73;
  Best Local Similarity   100.0%;  Pred. No. 0.0001;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||
Db          8 CAGCTTCTTCATCAGGGACATCATCAAACC 37


RESULT 86
US-10-685-992-77
; Sequence 77, Application US/10685992
; Publication No. US20040213739A1
; GENERAL INFORMATION:
;  APPLICANT: McConlogue, Lisa  C
;  APPLICANT:  Games, Kate D.
;  APPLICANT:  Yednock, Theodore A.
;  APPLICANT:  Hua, Tan
;  APPLICANT:  Messersmith, Elizabeth
;  APPLICANT:  Bard, Frederique
;  TITLE OF INVENTION: SCREENING MARKERS AND METHODS FOR NEURODEGENERATIVE DISORDERS
;  FILE REFERENCE: 015270-009110US
;  CURRENT APPLICATION NUMBER: US/10/685,992
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US/09/823,549
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: US 60/193,847
;  PRIOR FILING DATE: 2000-03-30
;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
;   LENGTH: 73
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: IL-12 p40, #1 marker
US-10-685-992-77

  Query Match             3.0%;  Score 30;  DB 9;  Length 73;
  Best Local Similarity   100.0%;  Pred. No. 0.0001;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||
Db          8 CAGCTTCTTCATCAGGGACATCATCAAACC 37


RESULT 87
US-10-603-064-3
; Sequence 3, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
;  APPLICANT: Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION: Multiple Cytokine Protein Complexes
;  FILE REFERENCE: LEX-010
;  CURRENT APPLICATION NUMBER: US/10/603,064
;  CURRENT FILING DATE:  2003-06-24
;  PRIOR APPLICATION NUMBER: US/09/634,368
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: 60/147,924
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1409
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p40-GM-CSF fusion protein coding sequence
US-10-603-064-3

  Query Match             3.0%;  Score 30;  DB 8;  Length 1409;
  Best Local Similarity   100.0%;  Pred. No. 0.0001;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||
Db        689 CAGCTTCTTCATCAGGGACATCATCAAACC 718


RESULT 88
US-10-603-064-2
; Sequence 2, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
;  APPLICANT: Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION: Multiple Cytokine Protein Complexes
;  FILE REFERENCE: LEX-010
;  CURRENT APPLICATION NUMBER: US/10/603,064
;  CURRENT FILING DATE:  2003-06-24
;  PRIOR APPLICATION NUMBER: US/09/634,368
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: 60/147,924
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 1472
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p40-IL-2 fusion protein coding sequence
US-10-603-064-2

  Query Match             3.0%;  Score 30;  DB 8;  Length 1472;
  Best Local Similarity   100.0%;  Pred. No. 0.0001;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||
Db        689 CAGCTTCTTCATCAGGGACATCATCAAACC 718


RESULT 89
US-10-603-064-12
; Sequence 12, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
;  APPLICANT: Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION: Multiple Cytokine Protein Complexes
;  FILE REFERENCE: LEX-010
;  CURRENT APPLICATION NUMBER: US/10/603,064
```

```
;  CURRENT FILING DATE:  2003-06-24
;  PRIOR APPLICATION NUMBER: US/09/634,368
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: 60/147,924
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 1569
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p35-linker-p40 fusion protein coding sequence
US-10-603-064-12

  Query Match             3.0%;  Score 30;  DB 8;  Length 1569;
  Best Local Similarity   100.0%;  Pred. No. 0.0001;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||
Db       1230 CAGCTTCTTCATCAGGGACATCATCAAACC 1259


RESULT 90
US-10-742-405-5
; Sequence 5, Application US/10742405
; Publication No. US20040213761A1
; GENERAL INFORMATION:
;  APPLICANT: Bowman, Edward P.
;  APPLICANT:  Chan, Jason R.
;  APPLICANT:  Moore, Kevin
;  APPLICANT:  Nguyen, Nhung
;  APPLICANT:  Churakova, Tatyana
;  APPLICANT:  Chen, Shi-Juan
;  APPLICANT:  Cua, Daniel J.
;  TITLE OF INVENTION: Uses of mammalian cytokine; related reagents
;  FILE REFERENCE: DX01578K
;  CURRENT APPLICATION NUMBER: US/10/742,405
;  CURRENT FILING DATE:  2003-12-18
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 1610
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (7)..(1599)
US-10-742-405-5

  Query Match             3.0%;  Score 30;  DB 9;  Length 1610;
  Best Local Similarity   100.0%;  Pred. No. 0.0001;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
              ||||||||||||||||||||||||||||||
Db        681 CAGCTTCTTCATCAGGGACATCATCAAACC 710


RESULT 91
US-10-172-399-3
; Sequence 3, Application US/10172399
; Publication No. US20030045495A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Chuan-Yuan
;  APPLICANT:  Dewhirst, Mark
;  APPLICANT:  Huang, Qian
;  TITLE OF INVENTION: A METHOD FOR SELECTIVE EXPRESSION OF THERAPEUTIC GENES BY HYPERTH
;  FILE REFERENCE: 180-129
;  CURRENT APPLICATION NUMBER: US/10/172,399
;  CURRENT FILING DATE:  2002-06-14
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 1840
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (35)..(1042)
US-10-172-399-3

  Query Match             3.0%;  Score 30;  DB 6;  Length 1840;
  Best Local Similarity   100.0%;  Pred. No. 0.0001;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db        703 CAGCTTCTTCATCAGGGACATCATCAAACC 732


RESULT 92
US-10-603-064-11
; Sequence 11, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
;  APPLICANT: Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION: Multiple Cytokine Protein Complexes
;  FILE REFERENCE: LEX-010
;  CURRENT APPLICATION NUMBER: US/10/603,064
;  CURRENT FILING DATE:  2003-06-24
;  PRIOR APPLICATION NUMBER: US/09/634,368
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: 60/147,924
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 2013
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: p35-linker-p40-IL-2 fusion protein coding sequence
US-10-603-064-11

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Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db       1230 CAGCTTCTTCATCAGGGACATCATCAAACC 1259


RESULT 93
US-10-603-064-13
; Sequence 13, Application US/10603064
; Publication No. US20040072299A1
; GENERAL INFORMATION:
;  APPLICANT: Gillies, Stephen
;  APPLICANT:  Lo, Kin Ming
;  TITLE OF INVENTION: Multiple Cytokine Protein Complexes
;  FILE REFERENCE: LEX-010
;  CURRENT APPLICATION NUMBER: US/10/603,064
;  CURRENT FILING DATE:  2003-06-24
;  PRIOR APPLICATION NUMBER: US/09/634,368
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: 60/147,924
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
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;   LENGTH: 2709
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: murine
;   OTHER INFORMATION: Fc-p35-linker-p40-IL-2 fusion protein coding
;   OTHER INFORMATION: sequence
US-10-603-064-13

  Query Match             3.0%;  Score 30;  DB 8;  Length 2709;
  Best Local Similarity   100.0%;  Pred. No. 0.0001;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db       1926 CAGCTTCTTCATCAGGGACATCATCAAACC 1955


RESULT 94
US-10-136-837-3
; Sequence 3, Application US/10136837
; Publication No. US20030181405A1
; GENERAL INFORMATION:
;  APPLICANT: NORDSTROM, Jeffrey L
;  APPLICANT:  PERICLE, Federica
;  APPLICANT:  ROLLAND, Alain
;  APPLICANT:  RALSTON, Robert
;  TITLE OF INVENTION: Interferon Alpha Plasmids and Delivery Systems, and Methods of Ma
;  TITLE OF INVENTION:  Using the Same
;  FILE REFERENCE: 273/082 (GM15-1USC1)
;  CURRENT APPLICATION NUMBER: US/10/136,837
;  CURRENT FILING DATE:  2002-04-29
;  PRIOR APPLICATION NUMBER: US 09/268,135
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 5966
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Mouse IL-12 pIN0961
US-10-136-837-3

  Query Match             3.0%;  Score 30;  DB 7;  Length 5966;
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  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db       5342 CAGCTTCTTCATCAGGGACATCATCAAACC 5371


RESULT 95
US-10-511-237-2
; Sequence 2, Application US/10511237
; Publication No. US20050233457A1
; GENERAL INFORMATION:
;  APPLICANT: Block, Andreas
;  TITLE OF INVENTION: Recombinant Viral Vectors for the Tetracycline-regulated Expressi
;  TITLE OF INVENTION:  Genes
;  FILE REFERENCE: 66741-043
;  CURRENT APPLICATION NUMBER: US/10/511,237
;  CURRENT FILING DATE:  2004-10-12
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 11458
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Adenoviral expression plasmid pAd.3r.mscIL-12 for regulated
;   OTHER INFORMATION: expression of murine IL-12
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (327)..(713)
;   OTHER INFORMATION: VP16
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (714)..(1352)
;   OTHER INFORMATION: TetR
;   FEATURE:
;   NAME/KEY: Intron
;   LOCATION: (1353)..(1912)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: promoter
;   LOCATION: (1864)..(1902)
;   OTHER INFORMATION: TK-min
;   FEATURE:
;   NAME/KEY: protein_bind
;   LOCATION: (1913)..(2212)
;   OTHER INFORMATION: TetO7
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2213)..(2687)
;   OTHER INFORMATION: CMV-min + Intron
;   FEATURE:
;   NAME/KEY: promoter
;   LOCATION: (2226)..(2264)
;   OTHER INFORMATION: CMV-min
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (2688)..(4325)
;   OTHER INFORMATION: Murine single-chain IL-12
US-10-511-237-2

  Query Match             3.0%;  Score 30;  DB 10;  Length 11458;
  Best Local Similarity   100.0%;  Pred. No. 0.00011;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGGGACATCATCAAACC 707
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Db       3362 CAGCTTCTTCATCAGGGACATCATCAAACC 3391


RESULT 96
US-09-917-265-85
; Sequence 85, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREO
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 85
;   LENGTH: 28
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-917-265-85

  Query Match             2.8%;  Score 28;  DB 3;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.0012;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCT 28
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Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCT 28
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RESULT 97
US-10-821-670-85
; Sequence 85, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 85
;   LENGTH: 28
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-10-821-670-85

  Query Match             2.8%;  Score 28;  DB 9;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.0012;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCT 28
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Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCT 28


RESULT 98
US-09-917-265-87
; Sequence 87, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 87
;   LENGTH: 37
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-917-265-87

  Query Match             2.8%;  Score 28;  DB 3;  Length 37;
  Best Local Similarity   100.0%;  Pred. No. 0.0012;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCT 28
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Db         10 ATGCATCCTCAGCAGTTGGTCATCGCCT 37


RESULT 99
US-10-821-670-87
; Sequence 87, Application US/10821670
; Publication No. US20040248261A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/10/821,670
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 87
;   LENGTH: 37
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-10-821-670-87

  Query Match             2.8%;  Score 28;  DB 9;  Length 37;
  Best Local Similarity   100.0%;  Pred. No. 0.0012;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCATCCTCAGCAGTTGGTCATCGCCT 28
              ||||||||||||||||||||||||||||
Db         10 ATGCATCCTCAGCAGTTGGTCATCGCCT 37


RESULT 100
US-09-917-265-86/c
; Sequence 86, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREC
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 86
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-917-265-86

  Query Match             2.5%;  Score 25;  DB 3;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 0.047;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        961 AGCAACTGGGCATCCGTGTCCTGCA 985
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Db         25 AGCAACTGGGCATCCGTGTCCTGCA 1


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OM nucleic - nucleic search, using sw model

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Title: US-10-821-670A-29
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Scoring table: OLIGO_NUC
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8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	2.0	303	7	US-11-217-529-5663	Sequence 5663, Ap
c	2	18	1.8	960	6	US-10-471-571A-1285	Sequence 1285, Ap
	3	18	1.8	5934	7	US-11-313-450-13	Sequence 13, Appl
	4	18	1.8	6371	7	US-11-251-465-8	Sequence 8, Appli
c	5	17	1.7	862	6	US-10-953-349-15338	Sequence 15338, A
c	6	17	1.7	1000	7	US-11-233-726-17	Sequence 17, Appl
	7	17	1.7	1061	6	US-10-953-349-3012	Sequence 3012, Ap
	8	17	1.7	1498	6	US-10-953-349-9710	Sequence 9710, Ap
c	9	17	1.7	3228	7	US-11-217-529-190982	Sequence 190982,
c	10	16	1.6	231	6	US-10-471-571A-4869	Sequence 4869, Ap
	11	16	1.6	305	6	US-10-548-484-9	Sequence 9, Appli
	12	16	1.6	305	6	US-10-548-484-10	Sequence 10, Appl
	13	16	1.6	561	6	US-10-488-619-3012	Sequence 3012, Ap
c	14	16	1.6	577	6	US-10-953-349-38575	Sequence 38575, A
	15	16	1.6	634	6	US-10-953-349-39182	Sequence 39182, A
	16	16	1.6	726	6	US-10-548-484-16	Sequence 16, Appl
	17	16	1.6	742	6	US-10-196-749-359	Sequence 359, App
c	18	16	1.6	921	6	US-10-471-571A-689	Sequence 689, App
c	19	16	1.6	945	7	US-11-217-529-79675	Sequence 79675, A
	20	16	1.6	1039	6	US-10-953-349-27059	Sequence 27059, A
	21	16	1.6	1083	7	US-11-217-529-4517	Sequence 4517, Ap
	22	16	1.6	1098	7	US-11-217-529-75941	Sequence 75941, A
c	23	16	1.6	1145	6	US-10-953-349-22082	Sequence 22082, A
	24	16	1.6	1226	6	US-10-953-349-9694	Sequence 9694, Ap
	25	16	1.6	1232	6	US-10-953-349-3568	Sequence 3568, Ap
c	26	16	1.6	1621	6	US-10-953-349-22615	Sequence 22615, A
	27	16	1.6	1747	6	US-10-953-349-33373	Sequence 33373, A
	28	16	1.6	1797	7	US-11-217-529-4576	Sequence 4576, Ap
c	29	16	1.6	1975	7	US-11-313-836-53	Sequence 53, Appl
c	30	16	1.6	2117	6	US-10-953-349-37153	Sequence 37153, A
	31	16	1.6	2270	7	US-11-293-697-1627	Sequence 1627, Ap
c	32	16	1.6	2278	7	US-11-293-697-928	Sequence 928, App
c	33	16	1.6	2324	7	US-11-293-697-1624	Sequence 1624, Ap
c	34	16	1.6	2538	7	US-11-293-697-1068	Sequence 1068, Ap
	35	16	1.6	2629	7	US-11-293-697-781	Sequence 781, App
c	36	16	1.6	2682	7	US-11-266-446-7	Sequence 7, Appli
c	37	16	1.6	2703	6	US-10-953-349-36221	Sequence 36221, A
c	38	16	1.6	2829	7	US-11-293-697-539	Sequence 539, App
	39	16	1.6	2846	6	US-10-505-928-444	Sequence 444, App
	40	16	1.6	2872	7	US-11-145-307A-3	Sequence 3, Appli
c	41	16	1.6	3271	6	US-10-953-349-5832	Sequence 5832, Ap
	42	16	1.6	5310	7	US-11-217-529-77298	Sequence 77298, A
c	43	16	1.6	6266	7	US-11-253-190-4	Sequence 4, Appli
c	44	16	1.6	12659	6	US-10-953-349-5546	Sequence 5546, Ap
c	45	16	1.6	151830	6	US-10-519-335-37	Sequence 37, Appl
c	46	15	1.5	20	7	US-11-266-409-12	Sequence 12, Appl
c	47	15	1.5	25	7	US-11-217-529-28477	Sequence 28477, A
c	48	15	1.5	25	7	US-11-217-529-94239	Sequence 94239, A
c	49	15	1.5	25	7	US-11-217-529-115861	Sequence 115861,
c	50	15	1.5	25	7	US-11-217-529-121503	Sequence 121503,
	51	15	1.5	209	6	US-10-857-260-37	Sequence 37, Appl
	52	15	1.5	261	7	US-11-217-529-4828	Sequence 4828, Ap
	53	15	1.5	277	7	US-11-301-554-899	Sequence 899, App
	54	15	1.5	354	7	US-11-217-529-82243	Sequence 82243, A
	55	15	1.5	423	7	US-11-217-529-80395	Sequence 80395, A
	56	15	1.5	456	6	US-10-488-619-382	Sequence 382, App
	57	15	1.5	489	7	US-11-217-529-4924	Sequence 4924, Ap
	58	15	1.5	498	6	US-10-471-571A-5447	Sequence 5447, Ap
c	59	15	1.5	506	6	US-10-473-173-325	Sequence 325, App
c	60	15	1.5	506	6	US-10-488-619-94	Sequence 94, Appl
	61	15	1.5	508	6	US-10-560-723-10	Sequence 10, Appl
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c	64	15	1.5	566	6	US-10-953-349-13816	Sequence 13816, A
c	65	15	1.5	605	6	US-10-953-349-15128	Sequence 15128, A
c	66	15	1.5	621	6	US-10-953-349-1547	Sequence 1547, Ap
	67	15	1.5	702	6	US-10-488-619-1757	Sequence 1757, Ap
c	68	15	1.5	723	7	US-11-217-529-78302	Sequence 78302, A
	69	15	1.5	734	6	US-10-953-349-30607	Sequence 30607, A
c	70	15	1.5	795	6	US-10-488-619-1758	Sequence 1758, Ap
c	71	15	1.5	798	6	US-10-953-349-3534	Sequence 3534, Ap
	72	15	1.5	843	7	US-11-217-529-970	Sequence 970, App
	73	15	1.5	852	6	US-10-953-349-25	Sequence 25, Appl
	74	15	1.5	865	6	US-10-953-349-39	Sequence 39, Appl
	75	15	1.5	880	6	US-10-953-349-5007	Sequence 5007, Ap
	76	15	1.5	922	6	US-10-953-349-15440	Sequence 15440, A
c	77	15	1.5	1021	6	US-10-953-349-12006	Sequence 12006, A
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	79	15	1.5	1077	7	US-11-217-529-173436	Sequence 173436,
	80	15	1.5	1089	7	US-11-217-529-6206	Sequence 6206, Ap
c	81	15	1.5	1101	6	US-10-953-349-32952	Sequence 32952, A
c	82	15	1.5	1122	6	US-10-953-349-31251	Sequence 31251, A
	83	15	1.5	1129	6	US-10-953-349-17431	Sequence 17431, A
c	84	15	1.5	1157	6	US-10-953-349-19240	Sequence 19240, A
c	85	15	1.5	1178	6	US-10-953-349-19188	Sequence 19188, A
c	86	15	1.5	1194	7	US-11-217-529-81713	Sequence 81713, A
c	87	15	1.5	1228	6	US-10-953-349-25037	Sequence 25037, A
	88	15	1.5	1243	6	US-10-953-349-37059	Sequence 37059, A
c	89	15	1.5	1244	6	US-10-953-349-21963	Sequence 21963, A
	90	15	1.5	1257	7	US-11-217-529-77875	Sequence 77875, A
c	91	15	1.5	1259	6	US-10-953-349-21887	Sequence 21887, A
	92	15	1.5	1262	6	US-10-953-349-28383	Sequence 28383, A
c	93	15	1.5	1290	7	US-11-217-529-191180	Sequence 191180,
	94	15	1.5	1301	6	US-10-953-349-5441	Sequence 5441, Ap
	95	15	1.5	1335	6	US-10-471-571A-569	Sequence 569, App
	96	15	1.5	1343	6	US-10-953-349-14176	Sequence 14176, A
	97	15	1.5	1344	6	US-10-953-349-29639	Sequence 29639, A
	98	15	1.5	1364	6	US-10-953-349-34749	Sequence 34749, A

c 99	15	1.5	1415	6	US-10-953-349-23846	Sequence 23846, A
c 100	15	1.5	1428	7	US-11-217-529-2039	Sequence 2039, Ap
c 101	15	1.5	1436	6	US-10-953-349-30996	Sequence 30996, A
102	15	1.5	1444	6	US-10-953-349-289	Sequence 289, App
c 103	15	1.5	1452	6	US-10-505-928-318	Sequence 318, App
c 104	15	1.5	1479	7	US-11-217-529-76855	Sequence 76855, A
c 105	15	1.5	1486	6	US-10-953-349-19870	Sequence 19870, A
106	15	1.5	1489	6	US-10-953-349-31882	Sequence 31882, A
c 107	15	1.5	1503	7	US-11-217-529-76539	Sequence 76539, A
108	15	1.5	1519	6	US-10-953-349-19905	Sequence 19905, A
c 109	15	1.5	1582	6	US-10-953-349-11557	Sequence 11557, A
110	15	1.5	1600	6	US-10-953-349-3805	Sequence 3805, Ap
111	15	1.5	1645	6	US-10-953-349-22110	Sequence 22110, A
c 112	15	1.5	1648	6	US-10-953-349-10297	Sequence 10297, A
113	15	1.5	1671	7	US-11-217-529-78801	Sequence 78801, A
114	15	1.5	1683	7	US-11-217-529-82600	Sequence 82600, A
115	15	1.5	1690	6	US-10-196-749-449	Sequence 449, App
116	15	1.5	1704	7	US-11-217-529-81313	Sequence 81313, A
117	15	1.5	1725	7	US-11-217-529-77188	Sequence 77188, A
c 118	15	1.5	1733	7	US-11-293-697-1577	Sequence 1577, Ap
c 119	15	1.5	1736	7	US-11-293-697-981	Sequence 981, App
120	15	1.5	1737	7	US-11-217-529-1440	Sequence 1440, Ap
121	15	1.5	1743	6	US-10-471-571A-4661	Sequence 4661, Ap
c 122	15	1.5	1758	6	US-10-953-349-3183	Sequence 3183, Ap
123	15	1.5	1767	7	US-11-217-529-6013	Sequence 6013, Ap
c 124	15	1.5	1785	7	US-11-217-529-81561	Sequence 81561, A
125	15	1.5	1838	6	US-10-953-349-37949	Sequence 37949, A
c 126	15	1.5	1843	6	US-10-511-937-620	Sequence 620, App
c 127	15	1.5	1889	6	US-10-953-349-7228	Sequence 7228, Ap
c 128	15	1.5	1915	6	US-10-953-349-11008	Sequence 11008, A
129	15	1.5	1949	7	US-11-293-697-89	Sequence 89, Appl
c 130	15	1.5	1962	7	US-11-217-529-82242	Sequence 82242, A
c 131	15	1.5	1974	7	US-11-217-529-80089	Sequence 80089, A
132	15	1.5	2035	6	US-10-511-937-2831	Sequence 2831, Ap
133	15	1.5	2045	6	US-10-953-349-40229	Sequence 40229, A
134	15	1.5	2046	6	US-10-471-571A-991	Sequence 991, App
c 135	15	1.5	2071	7	US-11-293-697-10	Sequence 10, Appl
c 136	15	1.5	2136	7	US-11-217-529-78809	Sequence 78809, A
c 137	15	1.5	2198	6	US-10-473-173-135	Sequence 135, App
c 138	15	1.5	2209	6	US-10-953-349-23348	Sequence 23348, A
c 139	15	1.5	2236	6	US-10-511-937-516	Sequence 516, App
c 140	15	1.5	2276	6	US-10-953-349-20232	Sequence 20232, A
c 141	15	1.5	2295	7	US-11-293-697-946	Sequence 946, App
c 142	15	1.5	2324	6	US-10-511-937-585	Sequence 585, App
143	15	1.5	2366	7	US-11-293-697-1960	Sequence 1960, Ap
c 144	15	1.5	2520	6	US-10-953-349-7725	Sequence 7725, Ap
c 145	15	1.5	2532	7	US-11-217-529-77060	Sequence 77060, A
c 146	15	1.5	2615	6	US-10-196-749-523	Sequence 523, App
147	15	1.5	2640	7	US-11-238-282-18	Sequence 18, Appl
148	15	1.5	2650	7	US-11-293-697-241	Sequence 241, App
149	15	1.5	2766	7	US-11-293-697-1119	Sequence 1119, Ap
150	15	1.5	2787	7	US-11-293-697-653	Sequence 653, App
c 151	15	1.5	2810	7	US-11-305-477-2	Sequence 2, Appli
152	15	1.5	2883	7	US-11-333-838-3	Sequence 3, Appli
c 153	15	1.5	2925	7	US-11-217-529-78225	Sequence 78225, A
c 154	15	1.5	2926	7	US-11-293-697-327	Sequence 327, App
c 155	15	1.5	2961	6	US-10-511-455-53	Sequence 53, Appl
c 156	15	1.5	2961	7	US-11-293-697-49	Sequence 49, Appl
157	15	1.5	3041	7	US-11-293-697-1534	Sequence 1534, Ap
c 158	15	1.5	3054	7	US-11-217-529-2509	Sequence 2509, Ap
c 159	15	1.5	3112	7	US-11-293-697-1458	Sequence 1458, Ap
160	15	1.5	3366	7	US-11-333-838-2	Sequence 2, Appli
c 161	15	1.5	3428	6	US-10-511-455-51	Sequence 51, Appl
162	15	1.5	3442	7	US-11-293-697-1578	Sequence 1578, Ap
163	15	1.5	3560	7	US-11-293-697-654	Sequence 654, App
c 164	15	1.5	3624	7	US-11-217-529-3816	Sequence 3816, Ap
165	15	1.5	3674	6	US-10-473-173-2	Sequence 2, Appli
c 166	15	1.5	4059	7	US-11-106-014-47	Sequence 47, Appl
167	15	1.5	4534	6	US-10-473-691B-1	Sequence 1, Appli
168	15	1.5	4573	6	US-10-505-928-409	Sequence 409, App
169	15	1.5	4585	6	US-10-505-928-47	Sequence 47, Appl
170	15	1.5	4686	7	US-11-217-529-3096	Sequence 3096, Ap
171	15	1.5	4842	6	US-10-196-749-289	Sequence 289, App
172	15	1.5	4863	7	US-11-217-529-2436	Sequence 2436, Ap
173	15	1.5	4995	7	US-11-217-529-2505	Sequence 2505, Ap
c 174	15	1.5	5262	7	US-11-217-529-76367	Sequence 76367, A
175	15	1.5	5515	6	US-10-524-021-1	Sequence 1, Appli
176	15	1.5	5711	6	US-10-480-434A-15	Sequence 15, Appl
c 177	15	1.5	5934	7	US-11-313-450-13	Sequence 13, Appl
c 178	15	1.5	5997	7	US-11-313-450-1	Sequence 1, Appli
c 179	15	1.5	6003	7	US-11-313-450-5	Sequence 5, Appli
c 180	15	1.5	6018	7	US-11-313-450-3	Sequence 3, Appli
181	15	1.5	6218	6	US-10-505-928-460	Sequence 460, App
c 182	15	1.5	6328	7	US-11-263-326-101	Sequence 101, App
c 183	15	1.5	6328	7	US-11-263-326-102	Sequence 102, App
c 184	15	1.5	6328	7	US-11-263-326-103	Sequence 103, App
c 185	15	1.5	6328	7	US-11-263-326-146	Sequence 146, App
c 186	15	1.5	6328	7	US-11-263-326-147	Sequence 147, App
c 187	15	1.5	6328	7	US-11-263-326-148	Sequence 148, App
c 188	15	1.5	6328	7	US-11-263-326-149	Sequence 149, App
c 189	15	1.5	6328	7	US-11-263-326-150	Sequence 150, App
c 190	15	1.5	6328	7	US-11-263-326-151	Sequence 151, App
c 191	15	1.5	6328	7	US-11-263-326-152	Sequence 152, App
c 192	15	1.5	6371	7	US-11-251-465-8	Sequence 8, Appli
c 193	15	1.5	6596	7	US-11-263-326-105	Sequence 105, App
c 194	15	1.5	6599	7	US-11-263-326-106	Sequence 106, App
c 195	15	1.5	6599	7	US-11-263-326-107	Sequence 107, App
c 196	15	1.5	6599	7	US-11-263-326-109	Sequence 109, App
c 197	15	1.5	6732	7	US-11-217-529-1872	Sequence 1872, Ap
c 198	15	1.5	7280	6	US-10-505-928-842	Sequence 842, App
199	15	1.5	8019	7	US-11-217-529-76544	Sequence 76544, A
c 200	15	1.5	8292	6	US-10-501-814-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-11-217-529-5663
; Sequence 5663, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5663
; LENGTH: 303
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5663

Query Match 2.0%; Score 20; DB 7; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         20 TCATCGCCTGGTTTTCCCTG 39
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Db         35 TCATCGCCTGGTTTTCCCTG 54
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RESULT 2
US-10-471-571A-1285/c
; Sequence 1285, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:

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;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 1285
;   LENGTH: 960
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-1285

  Query Match             1.8%;  Score 18;  DB 6;  Length 960;
  Best Local Similarity   100.0%;  Pred. No. 4.4;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        675 CAGCAGCTTCTTCATCAG 692
              ||||||||||||||||||
Db        142 CAGCAGCTTCTTCATCAG 125


RESULT 3
US-11-313-450-13
; Sequence 13, Application US/11313450
; Publication No. US20060110778A1
; GENERAL INFORMATION:
;  APPLICANT: Adorante, Joeseph S.
;  APPLICANT:  Ehring, George R.
;  TITLE OF INVENTION: High-Throughput Screens For Identifying
;  TITLE OF INVENTION:  Selective Persistent Sodium Channels Channel Blockers
;  FILE REFERENCE: 17407 CIP (AP)
;  CURRENT APPLICATION NUMBER: US/11/313,450
;  CURRENT FILING DATE:  2005-12-19
;  PRIOR APPLICATION NUMBER: 09/989797
;  PRIOR FILING DATE: 2001-11-20
;  PRIOR APPLICATION NUMBER: 60/252771
;  PRIOR FILING DATE: 2000-11-22
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 5934
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-313-450-13

  Query Match             1.8%;  Score 18;  DB 7;  Length 5934;
  Best Local Similarity   100.0%;  Pred. No. 4.6;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        316 AAAAAGGAAGATGGAATT 333
              ||||||||||||||||||
Db       4975 AAAAAGGAAGATGGAATT 4992


RESULT 4
US-11-251-465-8
; Sequence 8, Application US/11251465
; Publication No. US20060094061A1
; GENERAL INFORMATION:
;  APPLICANT: Brys, Reginald
;  APPLICANT:  Vandeghinste, Nick
;  APPLICANT:  Tomme, Peter
;  APPLICANT:  Klaassen, Hubertus
;  TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
;  TITLE OF INVENTION:  Same, Useful In The Treatment Of Joint Degenerative And
;  TITLE OF INVENTION:  Inflammatory Diseases
;  FILE REFERENCE: P30,172-A USA
;  CURRENT APPLICATION NUMBER: US/11/251,465
;  CURRENT FILING DATE:  2005-10-14
;  PRIOR APPLICATION NUMBER: 60/619,384
;  PRIOR FILING DATE: 2004-10-15
;  NUMBER OF SEQ ID NOS: 880
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
;   LENGTH: 6371
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-251-465-8

  Query Match             1.8%;  Score 18;  DB 7;  Length 6371;
  Best Local Similarity   100.0%;  Pred. No. 4.6;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        316 AAAAAGGAAGATGGAATT 333
              ||||||||||||||||||
Db       5023 AAAAAGGAAGATGGAATT 5040


RESULT 5
US-10-953-349-15338/c
; Sequence 15338, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15338
;   LENGTH: 862
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-15338

  Query Match             1.7%;  Score 17;  DB 6;  Length 862;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        942 CTACTATAGCTCATCCT 958
              |||||||||||||||||
Db        620 CTACTATAGCTCATCCT 604


RESULT 6
US-11-233-726-17/c
; Sequence 17, Application US/11233726
; Publication No. US20060090216A1
; GENERAL INFORMATION:
;  APPLICANT: APUYA, Nestor
;  APPLICANT:  KWOK, Shing
;  APPLICANT:  ALEXANDROV, Nickolai
;  APPLICANT:  TATARINOVA, Tatiana
;  APPLICANT:  FANG, Yiwen
;  APPLICANT:  PENNELL, Roger
;  APPLICANT:  LU, Yu-Ping
;  APPLICANT:  MEDRANO, Leonard
;  APPLICANT:  FELDMANN, Kenneth A.
;  APPLICANT:  COOK, Zhihong C.
;  TITLE OF INVENTION: Promoter, Promoter Control Elements, And Combinations, And Uses T
;  FILE REFERENCE: 2750-1619PUS2
;  CURRENT APPLICATION NUMBER: US/11/233,726
;  CURRENT FILING DATE:  2005-02-23
;  PRIOR APPLICATION NUMBER: 60/612,891
;  PRIOR FILING DATE: 2004-09-23
;  PRIOR APPLICATION NUMBER: 60/613,134
;  PRIOR FILING DATE: 2004-09-23
;  PRIOR APPLICATION NUMBER: 60/637,174
;  PRIOR FILING DATE: 2004-12-16
;  NUMBER OF SEQ ID NOS: 46
; SEQ ID NO 17
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;   LENGTH: 1000
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1000)
;   OTHER INFORMATION: Ceres Promoter construct YP0382 as found in Promoter Report #130
US-11-233-726-17

  Query Match             1.7%;  Score 17;  DB 7;  Length 1000;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        233 AAGTCAAAGAATTTGCA 249
              |||||||||||||||||
Db        623 AAGTCAAAGAATTTGCA 607


RESULT 7
US-10-953-349-3012
; Sequence 3012, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3012
;   LENGTH: 1061
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-3012

  Query Match             1.7%;  Score 17;  DB 6;  Length 1061;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        370 AAAAATAAGATCTTTCT 386
              |||||||||||||||||
Db         63 AAAAATAAGATCTTTCT 79


RESULT 8
US-10-953-349-9710
; Sequence 9710, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9710
;   LENGTH: 1498
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-9710

  Query Match             1.7%;  Score 17;  DB 6;  Length 1498;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        183 CTCTGACCAGAGCAGTG 199
              |||||||||||||||||
Db        553 CTCTGACCAGAGCAGTG 569


RESULT 9
US-11-217-529-190982/c
; Sequence 190982, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 190982
;   LENGTH: 3228
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-190982

  Query Match             1.7%;  Score 17;  DB 7;  Length 3228;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        156 TCCTGAAGAAGATGACA 172
              |||||||||||||||||
Db       1929 TCCTGAAGAAGATGACA 1913


RESULT 10
US-10-471-571A-4869/c
; Sequence 4869, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 4869
;   LENGTH: 231
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-4869

  Query Match             1.6%;  Score 16;  DB 6;  Length 231;
  Best Local Similarity   100.0%;  Pred. No. 49;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        678 CAGCTTCTTCATCAGG 693
              ||||||||||||||||
Db        178 CAGCTTCTTCATCAGG 163


RESULT 11
US-10-548-484-9
; Sequence 9, Application US/10548484
; Publication No. US20060107343A1
; GENERAL INFORMATION:
;  APPLICANT: Ishihara Sangyo Kaisha, Ltd.
;  TITLE OF INVENTION: Plant Cells And Plant Bodies With Modified Cell Growth, Developmer
;  TITLE OF INVENTION:  Differentiation
;  FILE REFERENCE: IS-09PCT
```

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;  CURRENT APPLICATION NUMBER: US/10/548,484
;  CURRENT FILING DATE:  2005-09-09
;  PRIOR APPLICATION NUMBER: JP 2003-66064
;  PRIOR FILING DATE: 2003-03-12
;  NUMBER OF SEQ ID NOS: 100
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 305
;   TYPE: DNA
;   ORGANISM: Oryza sativa
US-10-548-484-9

  Query Match             1.6%;  Score 16;  DB 6;  Length 305;
  Best Local Similarity   100.0%;  Pred. No. 49;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        160 GAAGAAGATGACATCA 175
              ||||||||||||||||
Db         55 GAAGAAGATGACATCA 70


RESULT 12
US-10-548-484-10
; Sequence 10, Application US/10548484
; Publication No. US20060107343A1
; GENERAL INFORMATION:
;  APPLICANT: Ishihara Sangyo Kaisha, Ltd.
;  TITLE OF INVENTION: Plant Cells And Plant Bodies With Modified Cell Growth, Developme
;  TITLE OF INVENTION:  Differentiation
;  FILE REFERENCE: IS-09PCT
;  CURRENT APPLICATION NUMBER: US/10/548,484
;  CURRENT FILING DATE:  2005-09-09
;  PRIOR APPLICATION NUMBER: JP 2003-66064
;  PRIOR FILING DATE: 2003-03-12
;  NUMBER OF SEQ ID NOS: 100
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 305
;   TYPE: DNA
;   ORGANISM: Oryza sativa
US-10-548-484-10

  Query Match             1.6%;  Score 16;  DB 6;  Length 305;
  Best Local Similarity   100.0%;  Pred. No. 49;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        160 GAAGAAGATGACATCA 175
              ||||||||||||||||
Db         55 GAAGAAGATGACATCA 70


RESULT 13
US-10-488-619-3012
; Sequence 3012, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3012
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-488-619-3012

  Query Match             1.6%;  Score 16;  DB 6;  Length 561;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        905 ACAAGGATGCCAAGAT 920
              ||||||||||||||||
Db        336 ACAAGGATGCCAAGAT 351


RESULT 14
US-10-953-349-38575/c
; Sequence 38575, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38575
;   LENGTH: 577
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-38575

  Query Match             1.6%;  Score 16;  DB 6;  Length 577;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        335 GGTCCACTGATATCTT 350
              ||||||||||||||||
Db        436 GGTCCACTGATATCTT 421


RESULT 15
US-10-953-349-39182
; Sequence 39182, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39182
;   LENGTH: 634
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-39182

  Query Match             1.6%;  Score 16;  DB 6;  Length 634;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        904 CACAAGGATGCCAAGA 919
              ||||||||||||||||
Db        281 CACAAGGATGCCAAGA 296


RESULT 16
US-10-548-484-16
; Sequence 16, Application US/10548484
; Publication No. US20060107343A1
; GENERAL INFORMATION:
;  APPLICANT: Ishihara Sangyo Kaisha, Ltd.
;  TITLE OF INVENTION: Plant Cells And Plant Bodies With Modified Cell Growth, Developme
;  TITLE OF INVENTION:  Differentiation
;  FILE REFERENCE: IS-09PCT
;  CURRENT APPLICATION NUMBER: US/10/548,484
;  CURRENT FILING DATE:  2005-09-09
```

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;  PRIOR APPLICATION NUMBER: JP 2003-66064
;  PRIOR FILING DATE: 2003-03-12
;  NUMBER OF SEQ ID NOS: 100
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 726
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (542)..(542)
;   OTHER INFORMATION: n stands for any base
US-10-548-484-16

  Query Match             1.6%;  Score 16;  DB 6;  Length 726;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        160 GAAGAAGATGACATCA 175
              ||||||||||||||||
Db        567 GAAGAAGATGACATCA 582


RESULT 17
US-10-196-749-359
; Sequence 359, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C340
;  CURRENT APPLICATION NUMBER: US/10/196,749
;  CURRENT FILING DATE:  2002-07-16
;  PRIOR APPLICATION NUMBER: 10/052586
;  PRIOR FILING DATE: 2002-01-15
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059266
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063120
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063121
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063486
;  PRIOR FILING DATE: 1997-10-21
;  PRIOR APPLICATION NUMBER: 60/063540
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063541
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063544
;  PRIOR FILING DATE: 1997-10-28
;  Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 359
;   LENGTH: 742
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-196-749-359

  Query Match             1.6%;  Score 16;  DB 6;  Length 742;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GAAGATGACATCACCT 178
              ||||||||||||||||
Db        361 GAAGATGACATCACCT 376


RESULT 18
US-10-471-571A-689/c
; Sequence 689, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 689
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-689

  Query Match             1.6%;  Score 16;  DB 6;  Length 921;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        677 GCAGCTTCTTCATCAG 692
              ||||||||||||||||
Db        398 GCAGCTTCTTCATCAG 383


RESULT 19
US-11-217-529-79675/c
; Sequence 79675, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79675
;   LENGTH: 945
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-79675

  Query Match             1.6%;  Score 16;  DB 7;  Length 945;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        675 CAGCAGCTTCTTCATC 690
              ||||||||||||||||
Db        214 CAGCAGCTTCTTCATC 199


RESULT 20
US-10-953-349-27059
```

; Sequence 27059, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27059
; LENGTH: 1039
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-953-349-27059

Query Match 1.6%; Score 16; DB 6; Length 1039;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 445 AGTACCGATTTGAAAT 460
||||||||||||||||
Db 407 AGTACCGATTTGAAAT 422

RESULT 21
US-11-217-529-4517
; Sequence 4517, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4517
; LENGTH: 1083
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4517

Query Match 1.6%; Score 16; DB 7; Length 1083;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 AACTGGAGAAAAACGT 89
||||||||||||||||
Db 467 AACTGGAGAAAAACGT 482

RESULT 22
US-11-217-529-75941
; Sequence 75941, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75941
; LENGTH: 1098
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-75941

Query Match 1.6%; Score 16; DB 7; Length 1098;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 731 TGAAGCCATTAAAAAA 746
||||||||||||||||
Db 254 TGAAGCCATTAAAAAA 269

RESULT 23
US-10-953-349-22082/c
; Sequence 22082, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22082
; LENGTH: 1145
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-22082

Query Match 1.6%; Score 16; DB 6; Length 1145;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGCATCCTCAGCAGTT 17
||||||||||||||||
Db 473 TGCATCCTCAGCAGTT 458

RESULT 24
US-10-953-349-9694
; Sequence 9694, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9694
; LENGTH: 1226
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-9694

Query Match 1.6%; Score 16; DB 6; Length 1226;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 376 AAGATCTTTCTAAAAT 391

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              ||||||||||||||||
Db        973 AAGATCTTTCTAAAAT 988


RESULT 25
US-10-953-349-3568
; Sequence 3568, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3568
;   LENGTH: 1232
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-3568

  Query Match             1.6%;  Score 16;  DB 6;  Length 1232;
  Best Local Similarity   100.0%;  Pred. No. 51;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        669 CTACACCAGCAGCTTC 684
              ||||||||||||||||
Db        592 CTACACCAGCAGCTTC 607


RESULT 26
US-10-953-349-22615/c
; Sequence 22615, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22615
;   LENGTH: 1621
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-22615

  Query Match             1.6%;  Score 16;  DB 6;  Length 1621;
  Best Local Similarity   100.0%;  Pred. No. 51;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        802 TCCTACTTCTCCTTAA 817
              ||||||||||||||||
Db       1184 TCCTACTTCTCCTTAA 1169


RESULT 27
US-10-953-349-33373
; Sequence 33373, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33373
;   LENGTH: 1747
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-33373

  Query Match             1.6%;  Score 16;  DB 6;  Length 1747;
  Best Local Similarity   100.0%;  Pred. No. 51;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        467 TCAAAAGCAGCAGAGG 482
              ||||||||||||||||
Db       1268 TCAAAAGCAGCAGAGG 1283


RESULT 28
US-11-217-529-4576
; Sequence 4576, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4576
;   LENGTH: 1797
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-4576

  Query Match             1.6%;  Score 16;  DB 7;  Length 1797;
  Best Local Similarity   100.0%;  Pred. No. 51;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        816 AACATTTGGCGTACAG 831
              ||||||||||||||||
Db        729 AACATTTGGCGTACAG 744


RESULT 29
US-11-313-836-53/c
; Sequence 53, Application US/11313836
; Publication No. US20060116508A1
; GENERAL INFORMATION:
;  APPLICANT: Glucksman, Maria Alexandra
;  APPLICANT:  Williamson, Mark J.
;  APPLICANT:  Tsia, Fong-Ying
;  APPLICANT:  Rudolph-Owen, Laura A.
;  APPLICANT:  Kapeller-Libermann, Rosana
;  APPLICANT:  Meyers, Rachel E.
;  APPLICANT:  Chiang, Lillian Wei-Ming
;  APPLICANT:  Hunter, John Joseph
;  APPLICANT:  Wood, Andrew
;  APPLICANT:  Jenkins, Lorayne P.
;  TITLE OF INVENTION: NOVEL 27411, 23413, 22438, 23553,
;  TITLE OF INVENTION:  25278, 26212, NARC SC1, NARC 10A, NARC 1, NARC 12, NARC 13,
;  TITLE OF INVENTION:  NARC17, NARC 25, NARC 3, NARC 4, NARC 7, NARC 8, NARC 11,
;  TITLE OF INVENTION:  NARC 14A, NARC 15, NARC 16, NARC 19, NARC 20, NARC 26, NARC
;  TITLE OF INVENTION:  27, NARC 28, NARC 30, NARC 5, NARC 6, NARC 9, NARC 10C, NARC
;  TITLE OF INVENTION:  8B, NARC 9, NARC2A, NARC 16B, NARC 1C, NARC 1A, NARC 25,
;  TITLE OF INVENTION:  86604 AND 32222 MOLECULES AND USES THEREFOR
;  FILE REFERENCE: MPI03-062OMNIM
;  CURRENT APPLICATION NUMBER: US/11/313,836
```

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;  CURRENT FILING DATE:  2005-12-21
;  PRIOR APPLICATION NUMBER: US/10/426,776
;  PRIOR FILING DATE: 2003-04-30
;  PRIOR APPLICATION NUMBER: 10/229,662
;  PRIOR FILING DATE: 2002-08-28
;  PRIOR APPLICATION NUMBER: 09/795,691
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: 60/185,517
;  PRIOR FILING DATE: 2000-02-28
;  PRIOR APPLICATION NUMBER: 10/105,992
;  PRIOR FILING DATE: 2002-03-25
;  PRIOR APPLICATION NUMBER: 09/406,045
;  PRIOR FILING DATE: 1999-09-27
;  PRIOR APPLICATION NUMBER: 10/314,881
;  PRIOR FILING DATE: 2002-12-09
;  PRIOR APPLICATION NUMBER: 09/773,426
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 09/495,823
;  PRIOR FILING DATE: 2000-01-31
;  PRIOR APPLICATION NUMBER: 09/692,785
;  PRIOR FILING DATE: 2000-10-20
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53
;    LENGTH: 1975
;    TYPE: DNA
;    ORGANISM: Homo Sapiens
US-11-313-836-53

  Query Match             1.6%;  Score 16;  DB 7;  Length 1975;
  Best Local Similarity   100.0%;  Pred. No. 51;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        475 AGCAGAGGCTCCTCTG 490
              ||||||||||||||||
Db        225 AGCAGAGGCTCCTCTG 210


RESULT 30
US-10-953-349-37153/c
; Sequence 37153, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37153
;    LENGTH: 2117
;    TYPE: DNA
;    ORGANISM: Zea mays subsp. mays
US-10-953-349-37153

  Query Match             1.6%;  Score 16;  DB 6;  Length 2117;
  Best Local Similarity   100.0%;  Pred. No. 52;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        868 CTCTCCGTGGACAAGA 883
              ||||||||||||||||
Db       1588 CTCTCCGTGGACAAGA 1573


RESULT 31
US-11-293-697-1627
; Sequence 1627, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1627
;    LENGTH: 2270
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-11-293-697-1627

  Query Match             1.6%;  Score 16;  DB 7;  Length 2270;
  Best Local Similarity   100.0%;  Pred. No. 52;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        901 TGCCACAAGGATGCCA 916
              ||||||||||||||||
Db       1151 TGCCACAAGGATGCCA 1166


RESULT 32
US-11-293-697-928/c
; Sequence 928, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 928
;    LENGTH: 2278
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-11-293-697-928

  Query Match             1.6%;  Score 16;  DB 7;  Length 2278;
  Best Local Similarity   100.0%;  Pred. No. 52;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        475 AGCAGAGGCTCCTCTG 490
              ||||||||||||||||
Db        442 AGCAGAGGCTCCTCTG 427


RESULT 33
US-11-293-697-1624/c
; Sequence 1624, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1624
;    LENGTH: 2324
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-11-293-697-1624

  Query Match             1.6%;  Score 16;  DB 7;  Length 2324;
```

```
  Best Local Similarity   100.0%;  Pred. No. 52;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        947 ATAGCTCATCCTGGAG 962
              ||||||||||||||||
Db       1957 ATAGCTCATCCTGGAG 1942


RESULT 34
US-11-293-697-1068/c
; Sequence 1068, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1068
;   LENGTH: 2538
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-1068

  Query Match             1.6%;  Score 16;  DB 7;  Length 2538;
  Best Local Similarity   100.0%;  Pred. No. 52;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        365 AATCCAAAAATAAGAT 380
              ||||||||||||||||
Db       2405 AATCCAAAAATAAGAT 2390


RESULT 35
US-11-293-697-781
; Sequence 781, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/11/293,697
;  CURRENT FILING DATE:  2005-12-05
;  PRIOR APPLICATION NUMBER: US/10/108,260
;  PRIOR FILING DATE: 2002-03-28
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 781
;   LENGTH: 2629
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-293-697-781

  Query Match             1.6%;  Score 16;  DB 7;  Length 2629;
  Best Local Similarity   100.0%;  Pred. No. 52;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         38 TGGTTTTGCTGGCACC 53
              ||||||||||||||||
Db        622 TGGTTTTGCTGGCACC 637


RESULT 36
US-11-266-446-7/c
; Sequence 7, Application US/11266446
; Publication No. US20060112452A1
; GENERAL INFORMATION:
;  APPLICANT: Keetman, Ulrich
;  APPLICANT:  Duwenig, Elke
;  APPLICANT:  Loyall, Linda P
;  APPLICANT:  Herbers, Karin
;  APPLICANT:  Hillebrand, Helke
;  TITLE OF INVENTION: EXPRESSION CASSETTES FOR SEED-PREFERENTIAL EXPRESSION IN PLANTS
;  FILE REFERENCE: 12810-00165-US
;  CURRENT APPLICATION NUMBER: US/11/266,446
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04026295.8
;  PRIOR FILING DATE: 2004-11-05
;  PRIOR APPLICATION NUMBER: EP 04029024.9
;  PRIOR FILING DATE: 2004-12-08
;  PRIOR APPLICATION NUMBER: EP 05002262.3
;  PRIOR FILING DATE: 2005-02-03
;  PRIOR APPLICATION NUMBER: EP 05002850.5
;  PRIOR FILING DATE: 2005-02-11
;  NUMBER OF SEQ ID NOS: 156
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
;   LENGTH: 2682
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (93)..(2387)
;   OTHER INFORMATION: coding for 5-methyltetrahydro-pteroyltriglutamate homocysteine
;   OTHER INFORMATION: methyltransferase (At5g17920)
US-11-266-446-7

  Query Match             1.6%;  Score 16;  DB 7;  Length 2682;
  Best Local Similarity   100.0%;  Pred. No. 52;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        868 CTCTCCGTGGACAAGA 883
              ||||||||||||||||
Db       1562 CTCTCCGTGGACAAGA 1547


RESULT 37
US-10-953-349-36221/c
; Sequence 36221, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36221
;   LENGTH: 2703
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-36221

  Query Match             1.6%;  Score 16;  DB 6;  Length 2703;
  Best Local Similarity   100.0%;  Pred. No. 52;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        174 CACCTGGACCTCTGAC 189
              ||||||||||||||||
Db       1550 CACCTGGACCTCTGAC 1535


RESULT 38
US-11-293-697-539/c
; Sequence 539, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: H1-A0106
```

; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 539
; LENGTH: 2829
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-539

Query Match 1.6%; Score 16; DB 7; Length 2829;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 360 GAAAGAATCCAAAAAT 375
||||||||||||||||
Db 330 GAAAGAATCCAAAAAT 315

RESULT 39
US-10-505-928-444
; Sequence 444, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 444
; LENGTH: 2846
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-444

Query Match 1.6%; Score 16; DB 6; Length 2846;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 845 ACAACAGAGAAAAGAA 860
||||||||||||||||
Db 599 ACAACAGAGAAAAGAA 614

RESULT 40
US-11-145-307A-3
; Sequence 3, Application US/11145307A
; Publication No. US20060094035A1
; GENERAL INFORMATION:
; APPLICANT: Arcturus Bioscience, Inc.
; APPLICANT: Erlander, Mark G.
; APPLICANT: Ma, Xiao-Jun
; TITLE OF INVENTION: Identification of Tumors
; FILE REFERENCE: 022041-002020US
; CURRENT APPLICATION NUMBER: US/11/145,307A
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 60/577,084
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2872
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-145-307A-3

Query Match 1.6%; Score 16; DB 7; Length 2872;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 314 ACAAAAAGGAAGATGG 329
||||||||||||||||
Db 1864 ACAAAAAGGAAGATGG 1879

RESULT 41
US-10-953-349-5832/c
; Sequence 5832, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5832
; LENGTH: 3271
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5832

Query Match 1.6%; Score 16; DB 6; Length 3271;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 154 ACTCCTGAAGAAGATG 169
||||||||||||||||
Db 824 ACTCCTGAAGAAGATG 809

RESULT 42
US-11-217-529-77298
; Sequence 77298, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77298
; LENGTH: 5310
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77298

Query Match 1.6%; Score 16; DB 7; Length 5310;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 329 GAATTTGGTCCACTGA 344
||||||||||||||||
Db 4376 GAATTTGGTCCACTGA 4391

RESULT 43
US-11-253-190-4/c
; Sequence 4, Application US/11253190

```
; Publication No. US20060115839A1
; GENERAL INFORMATION:
;  APPLICANT: Halazonetis, Thanos D
;  TITLE OF INVENTION: METHODS OF IDENTIFYING AN AGENT THAT MODULATES AN INTERACTION
;  TITLE OF INVENTION:  BETWEEN 53BP1 AND HISTONE H3, AND USES THEREOF
;  FILE REFERENCE: HALA0001-100
;  CURRENT APPLICATION NUMBER: US/11/253,190
;  CURRENT FILING DATE:  2005-10-17
;  PRIOR APPLICATION NUMBER: US 60/620,461
;  PRIOR FILING DATE: 2004-10-19
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
;   LENGTH: 6266
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-253-190-4

  Query Match             1.6%;  Score 16;  DB 7;  Length 6266;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        179 GGACCTCTGACCAGAG 194
              ||||||||||||||||
Db       1220 GGACCTCTGACCAGAG 1205


RESULT 44
US-10-953-349-5546/c
; Sequence 5546, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5546
;   LENGTH: 12659
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-5546

  Query Match             1.6%;  Score 16;  DB 6;  Length 12659;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        214 GGTAAAACTCTGACCA 229
              ||||||||||||||||
Db       5793 GGTAAAACTCTGACCA 5778


RESULT 45
US-10-519-335-37/c
; Sequence 37, Application US/10519335
; Publication No. US20060099210A1
; GENERAL INFORMATION:
;  APPLICANT: Cavarec, Laurent
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Destenaves, Benoit
;  APPLICANT:  Gonthier, Catherine
;  APPLICANT:  Elias, Isabelle
;  TITLE OF INVENTION: NOVEL KCNQ POLYPEPTIDES, MODULATORS THEREOF, AND THEIR USES IN TH
;  TITLE OF INVENTION:  TREATMENT OF MENTAL DISORDERS
;  FILE REFERENCE: G-194US03PCT
;  CURRENT APPLICATION NUMBER: US/10/519,335
;  CURRENT FILING DATE:  2004-12-22
;  PRIOR APPLICATION NUMBER: US 60/391,359
;  PRIOR FILING DATE: 2002-06-25
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
;   LENGTH: 151830
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (10)..(10)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (60402)..(60402)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (61110)..(61110)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (98207)..(98207)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (98208)..(98208)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (98209)..(98209)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (98210)..(98210)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (98211)..(98211)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (99743)..(99743)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (108055)..(108055)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (109094)..(109094)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (109125)..(109125)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (118900)..(118900)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (119024)..(119052)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (119053)..(119112)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (119115)..(119121)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (119123)..(119123)
;   OTHER INFORMATION: n = a or c or g or t
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;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (141674)..(141674)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (142063)..(142063)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (142137)..(142137)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (142967)..(142967)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (143077)..(143077)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (143506)..(143506)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (143587)..(143587)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (143629)..(143629)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (149079)..(149079)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (5363)..(5363)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (8080)..(8080)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (10296)..(10296)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (14528)..(14528)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (15336)..(15336)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (15457)..(15457)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (16288)..(16288)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (16306)..(16307)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (16316)..(16316)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (16397)..(16397)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (56012)..(56012)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (57662)..(57662)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: 5'UTR
;   LOCATION: (1)..(54)
;   OTHER INFORMATION: exon 1
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (55)..(124)
;   OTHER INFORMATION: exon 1
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (91147)..(91244)
;   OTHER INFORMATION: exon 2
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (93669)..(93834)
;   OTHER INFORMATION: exon 3
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (96310)..(96422)
;   OTHER INFORMATION: exon 4
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (99546)..(99723)
;   OTHER INFORMATION: exon 5
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (125441)..(125605)

  Query Match             1.6%;  Score 16;  DB 6;  Length 151830;
  Best Local Similarity   100.0%;  Pred. No. 56;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        584 AGGAGGGCAGTGCCTG 599
              ||||||||||||||||
Db       8739 AGGAGGGCAGTGCCTG 8724


RESULT 46
US-11-266-409-12/c
; Sequence 12, Application US/11266409
; Publication No. US20060093578A1
; GENERAL INFORMATION:
;  APPLICANT: SUZUMURA, AKIO
;  TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATING MULTIPLE SCLEROSIS
;  FILE REFERENCE: 279847US40
;  CURRENT APPLICATION NUMBER: US/11/266,409
;  CURRENT FILING DATE:  2005-11-04
;  PRIOR APPLICATION NUMBER: US 60/624,851
;  PRIOR FILING DATE: 2004-11-04
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA
US-11-266-409-12

  Query Match             1.5%;  Score 15;  DB 7;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy        799 CATTCCTACTTCTCC 813
              ||||||||||||||
Db         17 CATTCCTACTTCTCC 3


RESULT 47
US-11-217-529-28477/c
; Sequence 28477, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28477
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-28477

  Query Match             1.5%;  Score 15;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        353 GGGAACAGAAAGAAT 367
              |||||||||||||||
Db         23 GGGAACAGAAAGAAT 9


RESULT 48
US-11-217-529-94239/c
; Sequence 94239, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 94239
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-94239

  Query Match             1.5%;  Score 15;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        916 AAGATCCGCGTGCAA 930
              |||||||||||||||
Db         24 AAGATCCGCGTGCAA 10


RESULT 49
US-11-217-529-115861/c
; Sequence 115861, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 115861
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-115861

  Query Match             1.5%;  Score 15;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        358 CAGAAAGAATCCAAA 372
              |||||||||||||||
Db         18 CAGAAAGAATCCAAA 4


RESULT 50
US-11-217-529-121503/c
; Sequence 121503, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 121503
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-121503

  Query Match             1.5%;  Score 15;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        811 TCCTTAACATTTGGC 825
              |||||||||||||||
Db         19 TCCTTAACATTTGGC 5


RESULT 51
US-10-857-260-37
; Sequence 37, Application US/10857260
; Publication No. US20060110742A1
```

; GENERAL INFORMATION:
; APPLICANT: Lyons, Leslie A.
; APPLICANT: Grahn, Robert
; APPLICANT: Erdman, Carolyn
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Carrier Tests for Polycystic Kidney Disease in the Cat
; FILE REFERENCE: 023070-146800US
; CURRENT APPLICATION NUMBER: US/10/857,260
; CURRENT FILING DATE: 2004-05-28
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 209
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human (Hsap) PKD1 exon 29
US-10-857-260-37

Query Match 1.5%; Score 15; DB 6; Length 209;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 422 CCTGCTGGTGGCTGA 436
||||||||||||||||
Db 27 CCTGCTGGTGGCTGA 41

RESULT 52
US-11-217-529-4828
; Sequence 4828, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4828
; LENGTH: 261
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4828

Query Match 1.5%; Score 15; DB 7; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 840 CAAGAACAACAGAGA 854
||||||||||||||||
Db 15 CAAGAACAACAGAGA 29

RESULT 53
US-11-301-554-899
; Sequence 899, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; CURRENT FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 899
; LENGTH: 277
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-301-554-899

Query Match 1.5%; Score 15; DB 7; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 737 CATTAAAAAATTCTC 751
||||||||||||||||
Db 10 CATTAAAAAATTCTC 24

RESULT 54
US-11-217-529-82243
; Sequence 82243, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82243
; LENGTH: 354
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus

```
US-11-217-529-82243

  Query Match             1.5%;  Score 15;  DB 7;  Length 354;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        854 AAAAGAAAGACAGAC 868
              |||||||||||||||
Db         19 AAAAGAAAGACAGAC 33


RESULT 55
US-11-217-529-80395
; Sequence 80395, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80395
;   LENGTH: 423
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-80395

  Query Match             1.5%;  Score 15;  DB 7;  Length 423;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        156 TCCTGAAGAAGATGA 170
              |||||||||||||||
Db        324 TCCTGAAGAAGATGA 338


RESULT 56
US-10-488-619-382
; Sequence 382, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 382
;   LENGTH: 456
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(456)
;   OTHER INFORMATION: n is g, c, a or t
US-10-488-619-382

  Query Match             1.5%;  Score 15;  DB 6;  Length 456;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        851 GAGAAAAGAAAGACA 865
              |||||||||||||||
Db        251 GAGAAAAGAAAGACA 265


RESULT 57
US-11-217-529-4924
; Sequence 4924, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4924
;   LENGTH: 489
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-4924

  Query Match             1.5%;  Score 15;  DB 7;  Length 489;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 CAGTTGGTCATCGCC 27
              |||||||||||||||
Db        178 CAGTTGGTCATCGCC 192


RESULT 58
US-10-471-571A-5447
; Sequence 5447, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 5447
;   LENGTH: 498
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-5447

  Query Match             1.5%;  Score 15;  DB 6;  Length 498;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        339 CACTGATATCTTAAG 353
              |||||||||||||||
Db        360 CACTGATATCTTAAG 374


RESULT 59
US-10-473-173-325/c
; Sequence 325, Application US/10473173
; Publication No. US20060088823A1
; GENERAL INFORMATION:
;  APPLICANT: VAN ANDEL INSTITUTE
```

```
;  TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell
;  TITLE OF INVENTION:  Carcinoma: Prognosis and Drug Target Identification
;  FILE REFERENCE: 38345-170094
;  CURRENT APPLICATION NUMBER: US/10/473,173
;  CURRENT FILING DATE:  2003-09-29
;  PRIOR APPLICATION NUMBER: US 60/279,411
;  PRIOR FILING DATE: 2001-03-29
;  NUMBER OF SEQ ID NOS: 498
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 325
;   LENGTH: 506
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-473-173-325

  Query Match             1.5%;  Score 15;  DB 6;  Length 506;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        543 AGTGGACAACAGGGA 557
              |||||||||||||||
Db        258 AGTGGACAACAGGGA 244


RESULT 60
US-10-488-619-94/c
; Sequence 94, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 94
;   LENGTH: 506
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-488-619-94

  Query Match             1.5%;  Score 15;  DB 6;  Length 506;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        543 AGTGGACAACAGGGA 557
              |||||||||||||||
Db        258 AGTGGACAACAGGGA 244


RESULT 61
US-10-560-723-10
; Sequence 10, Application US/10560723
; Publication No. US20060115821A1
; GENERAL INFORMATION:
;  APPLICANT: EXONHIT THERAPEUTICALS
;  TITLE OF INVENTION: PROSTATE SPECIFIC GENES AND THE USE THEREOF AS TARGETS FOR PROSTA
;  TITLE OF INVENTION:  CANCER THERAPY AND DIAGNOSIS
;  FILE REFERENCE: B0213WO
;  CURRENT APPLICATION NUMBER: US/10/560,723
;  CURRENT FILING DATE:  2005-12-15
;  NUMBER OF SEQ ID NOS: 185
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 508
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-560-723-10

  Query Match             1.5%;  Score 15;  DB 6;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        877 GACAAGACCTCAGCC 891
              |||||||||||||||
Db        261 GACAAGACCTCAGCC 275


RESULT 62
US-10-953-349-31038
; Sequence 31038, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31038
;   LENGTH: 525
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (511)..(511)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-31038

  Query Match             1.5%;  Score 15;  DB 6;  Length 525;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        883 ACCTCAGCCAAGGTC 897
              |||||||||||||||
Db        410 ACCTCAGCCAAGGTC 424


RESULT 63
US-11-217-529-174237/c
; Sequence 174237, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174237
;   LENGTH: 531
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-174237

  Query Match             1.5%;  Score 15;  DB 7;  Length 531;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        859 AAAGACAGACTCTCC 873
              |||||||||||||||
Db        261 AAAGACAGACTCTCC 247
```

RESULT 64
US-10-953-349-13816/c
; Sequence 13816, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13816
; LENGTH: 566
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-13816

Query Match 1.5%; Score 15; DB 6; Length 566;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 676 AGCAGCTTCTTCATC 690
||||||||||||||||
Db 255 AGCAGCTTCTTCATC 241

RESULT 65
US-10-953-349-15128/c
; Sequence 15128, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15128
; LENGTH: 605
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-15128

Query Match 1.5%; Score 15; DB 6; Length 605;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 276 AGGAGGCGAGGTTCT 290
||||||||||||||||
Db 134 AGGAGGCGAGGTTCT 120

RESULT 66
US-10-953-349-1547/c
; Sequence 1547, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1547
; LENGTH: 621
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1547

Query Match 1.5%; Score 15; DB 6; Length 621;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 159 TGAAGAAGATGACAT 173
||||||||||||||||
Db 148 TGAAGAAGATGACAT 134

RESULT 67
US-10-488-619-1757
; Sequence 1757, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations W
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1757
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1757

Query Match 1.5%; Score 15; DB 6; Length 702;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 829 CAGGTCCAGGGCAAG 843
||||||||||||||||
Db 41 CAGGTCCAGGGCAAG 55

RESULT 68
US-11-217-529-78302/c
; Sequence 78302, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78302
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78302

Query Match 1.5%; Score 15; DB 7; Length 723;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 358 CAGAAAGAATCCAAA 372
||||||||||||||||
Db 515 CAGAAAGAATCCAAA 501

```
RESULT 69
US-10-953-349-30607
; Sequence 30607, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30607
;   LENGTH: 734
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-10-953-349-30607

  Query Match             1.5%;  Score 15;  DB 6;  Length 734;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        250 GATGCTGGCCAGTAT 264
              |||||||||||||||
Db        328 GATGCTGGCCAGTAT 342


RESULT 70
US-10-488-619-1758/c
; Sequence 1758, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
;  APPLICANT: Greenlee, Winner and Sullivan, P.C.
;  TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
;  TITLE OF INVENTION:  Physiological Conditions, And Genotyping Arrays
;  FILE REFERENCE: 98-01 WO
;  CURRENT APPLICATION NUMBER: US/10/488,619
;  CURRENT FILING DATE:  2004-03-01
;  NUMBER OF SEQ ID NOS: 3040
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1758
;   LENGTH: 795
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(795)
;   OTHER INFORMATION: n is g, c, a or t
US-10-488-619-1758

  Query Match             1.5%;  Score 15;  DB 6;  Length 795;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        829 CAGGTCCAGGGCAAG 843
              |||||||||||||||
Db        726 CAGGTCCAGGGCAAG 712


RESULT 71
US-10-953-349-3534/c
; Sequence 3534, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3534
;   LENGTH: 798
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-3534

  Query Match             1.5%;  Score 15;  DB 6;  Length 798;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        677 GCAGCTTCTTCATCA 691
              |||||||||||||||
Db        577 GCAGCTTCTTCATCA 563


RESULT 72
US-11-217-529-970
; Sequence 970, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 970
;   LENGTH: 843
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-970

  Query Match             1.5%;  Score 15;  DB 7;  Length 843;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        852 AGAAAAGAAAGACAG 866
              |||||||||||||||
Db        480 AGAAAAGAAAGACAG 494


RESULT 73
US-10-953-349-25
; Sequence 25, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
;   LENGTH: 852
;   TYPE: DNA
;   ORGANISM: Brassica napus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (697)..(697)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (753)..(753)
```

```
;   OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-25

  Query Match             1.5%;  Score 15;  DB 6;  Length 852;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        314 ACAAAAAGGAAGATG 328
              |||||||||||||||
Db        547 ACAAAAAGGAAGATG 561


RESULT 74
US-10-953-349-39
; Sequence 39, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39
;   LENGTH: 865
;   TYPE: DNA
;   ORGANISM: Brassica napus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (529)..(529)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-39

  Query Match             1.5%;  Score 15;  DB 6;  Length 865;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        470 AAAGCAGCAGAGGCT 484
              |||||||||||||||
Db        678 AAAGCAGCAGAGGCT 692


RESULT 75
US-10-953-349-5007
; Sequence 5007, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5007
;   LENGTH: 880
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-5007

  Query Match             1.5%;  Score 15;  DB 6;  Length 880;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        156 TCCTGAAGAAGATGA 170
              |||||||||||||||
Db        478 TCCTGAAGAAGATGA 492


RESULT 76
US-10-953-349-15440
; Sequence 15440, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15440
;   LENGTH: 922
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-15440

  Query Match             1.5%;  Score 15;  DB 6;  Length 922;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        912 TGCCAAGATCCGCGT 926
              |||||||||||||||
Db        791 TGCCAAGATCCGCGT 805


RESULT 77
US-10-953-349-12006/c
; Sequence 12006, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12006
;   LENGTH: 1021
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (682)..(682)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (691)..(691)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (729)..(729)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (761)..(761)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (804)..(804)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-12006

  Query Match             1.5%;  Score 15;  DB 6;  Length 1021;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        477 CAGAGGCTCCTCTGA 491
              |||||||||||||||
Db         74 CAGAGGCTCCTCTGA 60
```

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RESULT 78
US-11-217-529-78549
; Sequence 78549, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78549
;   LENGTH: 1041
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-78549

  Query Match             1.5%;  Score 15;  DB 7;  Length 1041;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        729 ACTGAAGCCATTAAA 743
              |||||||||||||||
Db        376 ACTGAAGCCATTAAA 390


RESULT 79
US-11-217-529-173436
; Sequence 173436, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 173436
;   LENGTH: 1077
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-173436

  Query Match             1.5%;  Score 15;  DB 7;  Length 1077;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        232 CAAGTCAAAGAATTT 246
              |||||||||||||||
Db        283 CAAGTCAAAGAATTT 297


RESULT 80
US-11-217-529-6206
; Sequence 6206, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6206
;   LENGTH: 1089
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-6206

  Query Match             1.5%;  Score 15;  DB 7;  Length 1089;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        622 CCCATTGAAGTCGTG 636
              |||||||||||||||
Db        478 CCCATTGAAGTCGTG 492


RESULT 81
US-10-953-349-32952/c
; Sequence 32952, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32952
;   LENGTH: 1101
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-32952

  Query Match             1.5%;  Score 15;  DB 6;  Length 1101;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        877 GACAAGACCTCAGCC 891
              |||||||||||||||
Db       1092 GACAAGACCTCAGCC 1078


RESULT 82
US-10-953-349-31251/c
; Sequence 31251, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31251
```

```
;   LENGTH: 1122
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-10-953-349-31251

  Query Match             1.5%;  Score 15;  DB 6;  Length 1122;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        305 TCCTGATACACAAAA 319
              |||||||||||||||
Db       1044 TCCTGATACACAAAA 1030


RESULT 83
US-10-953-349-17431
; Sequence 17431, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17431
;   LENGTH: 1129
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-17431

  Query Match             1.5%;  Score 15;  DB 6;  Length 1129;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        155 CTCCTGAAGAAGATG 169
              |||||||||||||||
Db        893 CTCCTGAAGAAGATG 907


RESULT 84
US-10-953-349-19240/c
; Sequence 19240, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19240
;   LENGTH: 1157
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-19240

  Query Match             1.5%;  Score 15;  DB 6;  Length 1157;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        477 CAGAGGCTCCTCTGA 491
              |||||||||||||||
Db         74 CAGAGGCTCCTCTGA 60


RESULT 85
US-10-953-349-19188/c
; Sequence 19188, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19188
;   LENGTH: 1178
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-19188

  Query Match             1.5%;  Score 15;  DB 6;  Length 1178;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        239 AAGAATTTGCAGATG 253
              |||||||||||||||
Db        280 AAGAATTTGCAGATG 266


RESULT 86
US-11-217-529-81713/c
; Sequence 81713, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81713
;   LENGTH: 1194
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-81713

  Query Match             1.5%;  Score 15;  DB 7;  Length 1194;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        372 AAATAAGATCTTTCT 386
              |||||||||||||||
Db        719 AAATAAGATCTTTCT 705


RESULT 87
US-10-953-349-25037/c
; Sequence 25037, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25037
```

```
;   LENGTH: 1228
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-25037

  Query Match             1.5%;  Score 15;  DB 6;  Length 1228;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        239 AAGAATTTGCAGATG 253
              |||||||||||||||
Db        399 AAGAATTTGCAGATG 385


RESULT 88
US-10-953-349-37059
; Sequence 37059, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37059
;   LENGTH: 1243
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-37059

  Query Match             1.5%;  Score 15;  DB 6;  Length 1243;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        154 ACTCCTGAAGAAGAT 168
              |||||||||||||||
Db        823 ACTCCTGAAGAAGAT 837


RESULT 89
US-10-953-349-21963/c
; Sequence 21963, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21963
;   LENGTH: 1244
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-21963

  Query Match             1.5%;  Score 15;  DB 6;  Length 1244;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        790 AGCACCCCACATTCC 804
              |||||||||||||||
Db        362 AGCACCCCACATTCC 348


RESULT 90
US-11-217-529-77875
; Sequence 77875, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77875
;   LENGTH: 1257
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-77875

  Query Match             1.5%;  Score 15;  DB 7;  Length 1257;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        447 TACCGATTTGAAATT 461
              |||||||||||||||
Db       1017 TACCGATTTGAAATT 1031


RESULT 91
US-10-953-349-21887/c
; Sequence 21887, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21887
;   LENGTH: 1259
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-21887

  Query Match             1.5%;  Score 15;  DB 6;  Length 1259;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        211 TCTGGTAAAACTCTG 225
              |||||||||||||||
Db        137 TCTGGTAAAACTCTG 123


RESULT 92
US-10-953-349-28383
; Sequence 28383, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28383
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;   LENGTH: 1262
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-10-953-349-28383

  Query Match             1.5%;  Score 15;  DB 6;  Length 1262;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        154 ACTCCTGAAGAAGAT 168
              ||||||||||||||||
Db        831 ACTCCTGAAGAAGAT 845


RESULT 93
US-11-217-529-191180/c
; Sequence 191180, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 191180
;   LENGTH: 1290
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-191180

  Query Match             1.5%;  Score 15;  DB 7;  Length 1290;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        806 ACTTCTCCTTAACAT 820
              ||||||||||||||||
Db        571 ACTTCTCCTTAACAT 557


RESULT 94
US-10-953-349-5441
; Sequence 5441, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5441
;   LENGTH: 1301
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-5441

  Query Match             1.5%;  Score 15;  DB 6;  Length 1301;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        749 CTCGGCATGTGGAAG 763
              ||||||||||||||||
Db        878 CTCGGCATGTGGAAG 892


RESULT 95
US-10-471-571A-569
; Sequence 569, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: P026927WO
;  CURRENT APPLICATION NUMBER: US/10/471,571A
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: GB-0107661.1
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 5642
;  SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 569
;   LENGTH: 1335
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-471-571A-569

  Query Match             1.5%;  Score 15;  DB 6;  Length 1335;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 TCAGCAGTTGGTCAT 23
              ||||||||||||||||
Db        688 TCAGCAGTTGGTCAT 702


RESULT 96
US-10-953-349-14176
; Sequence 14176, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14176
;   LENGTH: 1343
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (84)..(84)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-14176

  Query Match             1.5%;  Score 15;  DB 6;  Length 1343;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        470 AAAGCAGCAGAGGCT 484
              ||||||||||||||||
Db        652 AAAGCAGCAGAGGCT 666


RESULT 97
US-10-953-349-29639
; Sequence 29639, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
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;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29639
;   LENGTH: 1344
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-10-953-349-29639

  Query Match             1.5%;  Score 15;  DB 6;  Length 1344;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        226 ACCATCCAAGTCAAA 240
              |||||||||||||||
Db        800 ACCATCCAAGTCAAA 814


RESULT 98
US-10-953-349-34749
; Sequence 34749, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34749
;   LENGTH: 1364
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-34749

  Query Match             1.5%;  Score 15;  DB 6;  Length 1364;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        158 CTGAAGAAGATGACA 172
              |||||||||||||||
Db        583 CTGAAGAAGATGACA 597


RESULT 99
US-10-953-349-23846/c
; Sequence 23846, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23846
;   LENGTH: 1415
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-23846

  Query Match             1.5%;  Score 15;  DB 6;  Length 1415;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        469 AAAAGCAGCAGAGGC 483
              |||||||||||||||
Db       1010 AAAAGCAGCAGAGGC 996


RESULT 100
US-11-217-529-2039/c
; Sequence 2039, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2039
;   LENGTH: 1428
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-2039

  Query Match             1.5%;  Score 15;  DB 7;  Length 1428;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        353 GGGAACAGAAAGAAT 367
              |||||||||||||||
Db       1051 GGGAACAGAAAGAAT 1037


Search completed: June  9, 2006, 23:43:16
Job time : 24.8366 secs
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 12, 2006, 15:14:42 ; Search time 4461.13 Seconds
(without alignments)
7073.997 Million cell updates/sec

Title: US-10-821-670A-30
Perfect score: 1761
Sequence: 1 MHPQQLVIAWFSLVLLAPPL.....QARDRYYSSSWSNWASVSCS 329

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/abss/ABSSWEB_spool/US10821670/runat_07062006_110102_26152/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss06h
-USER=US10821670_@CGN_1_1_5308_@runat_07062006_110102_26152 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
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8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		1761	100.0	987	2	AR595950	AR595950 Sequence
2	c	1761	100.0	987	2	AR595951	AR595951 Sequence
3		1761	100.0	990	2	AX076200	AX076200 Sequence
4		1761	100.0	990	2	AX076482	AX076482 Sequence
5		1761	100.0	4522	2	AX076209	AX076209 Sequence
6		1761	100.0	4522	2	AX076476	AX076476 Sequence
7		1757	99.8	985	2	AR595967	AR595967 Sequence
8	c	1757	99.8	985	2	AR595968	AR595968 Sequence
9		1756	99.7	990	14	FCU83184	U83184 Felis catus
10		1755	99.7	2193	2	AR242435	AR242435 Sequence
11		1755	99.7	2193	2	AR280203	AR280203 Sequence
12		1755	99.7	2193	2	AR322418	AR322418 Sequence
13		1747	99.2	1006	14	FCIL12P40	Y07762 Felis catus
14		1747	99.2	1599	2	AR595956	AR595956 Sequence
15	c	1747	99.2	1599	2	AR595957	AR595957 Sequence
16		1657	94.1	987	2	AR595969	AR595969 Sequence
17	c	1657	94.1	987	2	AR595970	AR595970 Sequence
18		1657	94.1	990	2	AR151071	AR151071 Sequence
19		1657	94.1	990	2	BD014663	BD014663 Process f
20		1657	94.1	990	2	E15017	E15017 Canine mRNA
21		1657	94.1	990	2	AR316470	AR316470 Sequence
22		1657	94.1	1599	2	AR595971	AR595971 Sequence
23	c	1657	94.1	1599	2	AR595972	AR595972 Sequence
24		1657	94.1	2267	2	AR596011	AR596011 Sequence
25	c	1657	94.1	2267	2	AR596012	AR596012 Sequence
26		1647	93.5	921	2	AR242436	AR242436 Sequence
27		1647	93.5	921	2	AR242437	AR242437 Sequence
28		1647	93.5	921	2	AR280204	AR280204 Sequence
29		1647	93.5	921	2	AR280205	AR280205 Sequence
30		1647	93.5	921	2	AR322419	AR322419 Sequence
31		1647	93.5	921	2	AR322420	AR322420 Sequence
32		1646	93.5	1015	14	CFU49100	U49100 Canis famil
33		1639	93.1	921	2	AR595948	AR595948 Sequence
34	c	1639	93.1	921	2	AR595949	AR595949 Sequence
35		1639	93.1	1533	2	AR595959	AR595959 Sequence
36	c	1639	93.1	1533	2	AR595960	AR595960 Sequence
37		1628	92.4	990	2	BD014653	BD014653 Process f
38		1624	92.2	990	2	AR151061	AR151061 Sequence
39		1624	92.2	990	2	AR316460	AR316460 Sequence
40		1622.5	92.1	2154	2	BD171281	BD171281 Novel can
41		1583	89.9	990	2	AX154603	AX154603 Sequence
42		1558	88.5	1626	8	AF401989	AF401989 Synthetic
43		1557	88.4	1058	14	ECIL12P40	Y11129 Equus cabal
44		1554	88.2	921	2	AR595965	AR595965 Sequence
45	c	1554	88.2	921	2	AR595966	AR595966 Sequence

ALIGNMENTS

RESULT 1
AR595950
LOCUS AR595950 987 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 29 from patent US 6818444.
ACCESSION AR595950
VERSION AR595950.1 GI:56646931
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 987)
AUTHORS Wonderling,R.S. and Boroughs,K.L.
TITLE Canine and feline proteins, nucleic acid molecules and uses thereof
JOURNAL Patent: US 6818444-A 29 16-NOV-2004;
Heska Corporation; Fort Collins, CO
FEATURES Location/Qualifiers
source 1. .987
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Alignment Scores:

Pred. No.:	2.11e-186	Length:	987
Score:	1761.00	Matches:	329
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0

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DB:                    2             Gaps:          0

US-10-821-670A-30 (1-329) x AR595950 (1-987)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
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Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
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Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
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Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
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Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
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Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
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Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
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Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
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Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
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Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
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Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
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Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
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Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
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Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987

RESULT 2
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AR595951/c
LOCUS       AR595951                 987 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 31 from patent US 6818444.
ACCESSION   AR595951
VERSION     AR595951.1  GI:56646932
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 31 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .987
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                2.11e-186      Length:          987
Score:                    1761.00        Matches:         329
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-30 (1-329) x AR595951 (1-987)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
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Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
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Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
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Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
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Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
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Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
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Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
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Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
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Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328
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Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
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Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
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Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
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Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
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Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGCAGT 1

RESULT 3
AX076200
LOCUS       AX076200                990 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 1 from Patent WO0104155.
ACCESSION   AX076200
VERSION     AX076200.1  GI:12710825
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 1 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
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ORIGIN

Alignment Scores:
Pred. No.:              2.12e-186       Length:         990
Score:                  1761.00         Matches:        329
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-10-821-670A-30 (1-329) x AX076200 (1-990)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuAlaProProLeu 20
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Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
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Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
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Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
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Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
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Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
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Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
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Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
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Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
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Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
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Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
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Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
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Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987

RESULT 4
AX076482
LOCUS       AX076482                990 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 8 from Patent WO0104280.
ACCESSION   AX076482
VERSION     AX076482.1  GI:12711034
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 8 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
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     source          1. .990
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Sequence coding for SEQ ID NO 2, IL-12 p40"
ORIGIN

Alignment Scores:
Pred. No.:                2.12e-186      Length:         990
Score:                    1761.00        Matches:        329
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              100.0%         Indels:         0
DB:                       2              Gaps:           0

US-10-821-670A-30 (1-329) x AX076482 (1-990)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
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Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
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Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
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Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
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Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
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Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987

RESULT 5
AX076209
LOCUS       AX076209               4522 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 10 from Patent WO0104155.
ACCESSION   AX076209
VERSION     AX076209.1  GI:12710834
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 10 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .4522
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Plasmid pMol-fil12p40"
ORIGIN

Alignment Scores:
Pred. No.:                1.92e-185      Length:         4522
Score:                    1761.00        Matches:        329
Percent Similarity:       100.0%         Conservative:   0
Best Local Similarity:    100.0%         Mismatches:     0
Query Match:              100.0%         Indels:         0
DB:                       2              Gaps:           0

US-10-821-670A-30 (1-329) x AX076209 (1-4522)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
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Db       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db       4007 AGCAACTGGGCATCCGTGTCCTGCAGT 4033

RESULT 6
AX076476
LOCUS       AX076476               4522 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 2 from Patent WO0104280.
ACCESSION   AX076476
VERSION     AX076476.1  GI:12711028
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 2 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .4522
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="IL-12p40"
ORIGIN

Alignment Scores:
Pred. No.:              1.92e-185      Length:         4522
Score:                  1761.00        Matches:        329
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0

DB:                     2              Gaps:           0

US-10-821-670A-30 (1-329) x AX076476 (1-4522)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db       4007 AGCAACTGGGCATCCGTGTCCTGCAGT 4033

RESULT 7
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AR595967
LOCUS       AR595967                985 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 55 from patent US 6818444.
ACCESSION   AR595967
VERSION     AR595967.1  GI:56646948
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 985)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 55 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .985
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                5.87e-186      Length:          985
Score:                    1757.00        Matches:         328
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              99.8%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-30 (1-329) x AR595967 (1-985)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984

RESULT 8
AR595968/c
LOCUS       AR595968                985 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 57 from patent US 6818444.
ACCESSION   AR595968
VERSION     AR595968.1  GI:56646949
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 985)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 57 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
     source          1. .985
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                5.87e-186      Length:          985
Score:                    1757.00        Matches:         328
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              99.8%          Indels:          0
DB:                       2              Gaps:            0

US-10-821-670A-30 (1-329) x AR595968 (1-985)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
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Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
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Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        321 SerAsnTrpAlaSerValSerCys 328
                |||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGC 2

RESULT 9
FCU83184
LOCUS       FCU83184                990 bp    mRNA    linear   MAM 16-JUL-1999
DEFINITION  Felis catus interleukin-12 p40 subunit (IL-12) mRNA, complete cds.
ACCESSION   U83184
VERSION     U83184.1  GI:2735050
KEYWORDS    .
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Nucleotide and predicted peptide sequence of feline interleukin-12
            (IL-12)
  JOURNAL   DNA Seq. 8 (1-2), 77-82 (1997)
   PUBMED   9522125
REFERENCE   2  (bases 1 to 990)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal
            Veterinary Medicine, University of Zurich, Winterthurerstrasse 260,
            Zurich, ZH 8057, Switzerland
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="Felis catus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
     CDS             1. .990
                     /note="cytokine"
                     /codon_start=1
                     /product="interleukin-12 p40 subunit"
                     /protein_id="AAB93835.1"
                     /db_xref="GI:2735051"
                     /translation="MHPQQLVIAWFSLVLLAPPLMAIWELEKNVYVVELDWHPDAPGE
                     MVVLTCDTPEEDDITWTSDQSSEVLGSGKTLTIQVKEFADAGQYTCHKGGEVLSHSFL
                     LIHKKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFTVKSSR
                     GSSDPQGVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPAAEESLPIEVVVDAIHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFGV
                     QVQGKNNREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSNWASVSCS"
ORIGIN

Alignment Scores:
Pred. No.:                7.65e-186       Length:          990
Score:                    1756.00         Matches:         328
Percent Similarity:       100.0%          Conservative:    1
Best Local Similarity:    99.7%           Mismatches:      0
Query Match:              99.7%           Indels:          0
DB:                       14              Gaps:            0

US-10-821-670A-30 (1-329) x FCU83184 (1-990)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||:::||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGTGACACGCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987

RESULT 10
AR242435
LOCUS       AR242435                2193 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 5 from patent US 6472509.
ACCESSION   AR242435
VERSION     AR242435.1  GI:27288852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2193)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 5 29-OCT-2002;
            Juridical Foundation: The Chemo-Seso-Therapeutic Research
            Institute; Kumamoto;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .2193
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.14e-185      Length:         2193
Score:                  1755.00        Matches:        328
Percent Similarity:     99.7%          Conservative:   0
Best Local Similarity:  99.7%          Mismatches:     1
Query Match:            99.7%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-30 (1-329) x AR242435 (1-2193)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||    ||||||||||||||||||||||||
Db         64 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTACCTGGTTTTGCTGGCACCTCCTCTC 123

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 183

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 243

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 303

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 363

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 423

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 483

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 543

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 603

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 663

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 723

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 783

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 843

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 903

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 963

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 1023

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db       1024 AGCAACTGGGCATCCGTGTCCTGCAGT 1050

RESULT 11
AR280203
LOCUS       AR280203                2193 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 5 from patent US 6518045.
ACCESSION   AR280203
VERSION     AR280203.1  GI:29715593
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2193)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 5 11-FEB-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research Institute;
            Kumamoto-ken;
            EPX;
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FEATURES             Location/Qualifiers
     source          1. .2193
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ORIGIN

Alignment Scores:
Pred. No.:              3.14e-185      Length:         2193
Score:                  1755.00        Matches:        328
Percent Similarity:     99.7%          Conservative:   0
Best Local Similarity:  99.7%          Mismatches:     1
Query Match:            99.7%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-30 (1-329) x AR280203 (1-2193)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
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Db         64 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTACCTGGTTTTGCTGGCACCTCCTCTC 123

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
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Db        124 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 183

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 243

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 303

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 363

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 423

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 483

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 543

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 603

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 663

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 723

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 783

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 843

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 903

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 963

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 1023

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db       1024 AGCAACTGGGCATCCGTGTCCTGCAGT 1050

RESULT 12
AR322418
LOCUS       AR322418                2193 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 5 from patent US 6566097.
ACCESSION   AR322418
VERSION     AR322418.1  GI:33708171
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2193)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 5 20-MAY-2003;
            Juridical Foundation The Chemo-Sero-Therapeutic Research
            Institute;;
            EPX;
FEATURES             Location/Qualifiers
     source          1. .2193
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ORIGIN

Alignment Scores:
Pred. No.:              3.14e-185      Length:         2193
Score:                  1755.00        Matches:        328
Percent Similarity:     99.7%          Conservative:   0
Best Local Similarity:  99.7%          Mismatches:     1
Query Match:            99.7%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-30 (1-329) x AR322418 (1-2193)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
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Db         64 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTACCTGGTTTTGCTGGCACCTCCTCTC 123

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
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Db        184 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 243

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
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Db        244 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 303

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
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Db        304 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 363

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
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Db        364 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 423

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
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Db        424 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 483

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
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Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
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Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
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Qy        321 SerAsnTrpAlaSerValSerCysSer 329
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Db       1024 AGCAACTGGGCATCCGTGTCCTGCAGT 1050

RESULT 13
FCIL12P40
LOCUS       FCIL12P40               1006 bp    mRNA    linear   MAM 18-APR-2005
DEFINITION  Felis catus mRNA for interleukin-12 p40 chain.
ACCESSION   Y07762
VERSION     Y07762.1  GI:2102664
KEYWORDS    interleukin-12 p40.
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
            Felinae; Felis.
REFERENCE   1
  AUTHORS   Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
  TITLE     Molecular cloning of cat interleukin-12
  JOURNAL   Immunogenetics 45 (6), 462-463 (1997)
   PUBMED   9089110
REFERENCE   2  (bases 1 to 1006)
  AUTHORS   Schijns,V.E.C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
            Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
            Utrecht, NETHERLANDS
FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:                7.93e-185       Length:          1006
Score:                    1747.00         Matches:         327
Percent Similarity:       99.4%           Conservative:    0
Best Local Similarity:    99.4%           Mismatches:      2
Query Match:              99.2%           Indels:          0
DB:                       14              Gaps:            0

US-10-821-670A-30 (1-329) x FCIL12P40 (1-1006)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
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Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
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Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

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Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
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Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

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Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
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Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
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Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660
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Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
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Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
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Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
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Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
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Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
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Qy        321 SerAsnTrpAlaSerValSerCysSer 329
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RESULT 14
AR595956
LOCUS       AR595956               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 38 from patent US 6818444.
ACCESSION   AR595956
VERSION     AR595956.1  GI:56646937
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 38 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:              1.56e-184      Length:         1599
Score:                  1747.00        Matches:        327
Percent Similarity:     99.4%          Conservative:   0
Best Local Similarity:  99.4%          Mismatches:     2
Query Match:            99.2%          Indels:         0
DB:                     2              Gaps:           0

US-10-821-670A-30 (1-329) x AR595956 (1-1599)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
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Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
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Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
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Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
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Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
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Qy        321 SerAsnTrpAlaSerValSerCysSer 329
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Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987

RESULT 15
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LOCUS       AR595957               1599 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 40 from patent US 6818444.
ACCESSION   AR595957
VERSION     AR595957.1  GI:56646938
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1599)
  AUTHORS   Wonderling,R.S. and Boroughs,K.L.
  TITLE     Canine and feline proteins, nucleic acid molecules and uses thereof
  JOURNAL   Patent: US 6818444-A 40 16-NOV-2004;
            Heska Corporation; Fort Collins, CO
FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
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Pred. No.:	1.56e-184	Length:	1599
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Percent Similarity:	99.4%	Conservative:	0
Best Local Similarity:	99.4%	Mismatches:	2
Query Match:	99.2%	Indels:	0
DB:	2	Gaps:	0

US-10-821-670A-30 (1-329) x AR595957 (1-1599)

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Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
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Db       1299 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 1240

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
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Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1179 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 1120

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db       1119 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 1060

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        999 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 940

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        939 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 880

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        879 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 820

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 760

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        759 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 640
```

```
Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||
Db        639 AGCAACTGGGCATCCGTGTCCTGCAGT 613
```

Search completed: June 13, 2006, 03:27:21
Job time : 4471.13 secs

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 9, 2006, 23:43:41 ; Search time 702.303 Seconds
(without alignments)
4899.317 Million cell updates/sec

Title: US-10-821-670A-30
Perfect score: 1761
Sequence: 1 MHPQQLVIAWFSLVLLAPPL.....QARDRYYSSSWSNWASVSCS 329

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10821670/runat_07062006_110100_26141/app_query.fasta_1
-DB=N_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05h
-USER=US10821670_@CGN_1_1_2027_@runat_07062006_110100_26141 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1761	100.0	987	6	ABK98944	Abk98944 Feline in
c 2	1761	100.0	987	6	ABK98945	Abk98945 Feline in
3	1761	100.0	987	14	ADV34682	Adv34682 Feline si
c 4	1761	100.0	987	14	ADV34684	Adv34684 Feline si
5	1761	100.0	990	4	AAF26082	Aaf26082 Feline IL
6	1761	100.0	990	4	AAF26085	Aaf26085 Feline IL
7	1761	100.0	4522	4	AAF26076	Aaf26076 Feline IL
8	1761	100.0	4522	4	AAF26094	Aaf26094 Plasmid p
c 9	1757	99.8	985	6	ABK98962	Abk98962 Feline in
10	1757	99.8	985	6	ABK98961	Abk98961 Feline in
11	1757	99.8	985	14	ADV34707	Adv34707 Feline N-
c 12	1757	99.8	985	14	ADV34709	Adv34709 Feline N-
13	1755	99.7	2193	2	AAV56625	Aav56625 Feline FL
14	1747	99.2	1599	6	ABK98950	Abk98950 Feline in
c 15	1747	99.2	1599	6	ABK98951	Abk98951 Feline in
16	1747	99.2	1599	14	ADV34691	Adv34691 Feline si
c 17	1747	99.2	1599	14	ADV34693	Adv34693 Feline si
18	1657	94.1	987	6	ABK98963	Abk98963 Canine in
c 19	1657	94.1	987	6	ABK98964	Abk98964 Canine in
c 20	1657	94.1	987	14	ADV34712	Adv34712 Canine si
21	1657	94.1	987	14	ADV34710	Adv34710 Canine si
22	1657	94.1	990	2	AAV13817	Aav13817 Canine IL
23	1657	94.1	990	2	AAX03162	Aax03162 Nucleic a
24	1657	94.1	990	2	AAX35625	Aax35625 Nucleic a
25	1657	94.1	990	4	AAI64388	Aai64388 Canine co
26	1657	94.1	1599	6	ABK98965	Abk98965 Canine in
c 27	1657	94.1	1599	6	ABK98966	Abk98966 Canine in
c 28	1657	94.1	1599	14	ADV34715	Adv34715 Canine si
29	1657	94.1	1599	14	ADV34713	Adv34713 Canine si
c 30	1657	94.1	2267	6	ABK99006	Abk99006 Canine in
31	1657	94.1	2267	6	ABK99005	Abk99005 Canine in
32	1657	94.1	2267	14	ADV34757	Adv34757 Canine si
c 33	1657	94.1	2267	14	ADV34759	Adv34759 Canine si
34	1647	93.5	921	2	AAV56627	Aav56627 Feline FL
35	1647	93.5	921	2	AAV56626	Aav56626 Feline FL
36	1646	93.5	1015	13	ADT04849	Adt04849 Canine in
37	1639	93.1	921	6	ABK98942	Abk98942 Feline in
c 38	1639	93.1	921	6	ABK98943	Abk98943 Feline in
c 39	1639	93.1	921	14	ADV34681	Adv34681 Feline si
40	1639	93.1	921	14	ADV34679	Adv34679 Feline si
c 41	1639	93.1	1533	6	ABK98954	Abk98954 Feline in
42	1639	93.1	1533	6	ABK98953	Abk98953 Feline in
c 43	1639	93.1	1533	14	ADV34697	Adv34697 Feline si
44	1639	93.1	1533	14	ADV34695	Adv34695 Feline si
45	1628	92.4	990	2	AAV13816	Aav13816 Canine IL

ALIGNMENTS

RESULT 1
ABK98944
ID ABK98944 standard; cDNA; 987 BP.
XX
AC ABK98944;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p40-987 coding strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX

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PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69303.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 1; Page 51-53; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 987 BP; 283 A; 250 C; 246 G; 208 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              8.78e-167      Length:          987
Score:                  1761.00        Matches:         329
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            100.0%         Indels:          0
DB:                     6              Gaps:            0

US-10-821-670A-30 (1-329) x ABK98944 (1-987)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987

RESULT 2
ABK98945/c
ID   ABK98945 standard; cDNA; 987 BP.
XX
AC   ABK98945;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p40-987 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 3; Page 54; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
```

```
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 987 BP; 208 A; 246 C; 250 G; 283 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                8.78e-167      Length:          987
Score:                    1761.00        Matches:         329
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       6              Gaps:            0

US-10-821-670A-30 (1-329) x ABK98945 (1-987)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGCAGT 1

RESULT 3
ADV34682
ID   ADV34682 standard; cDNA; 987 BP.
XX
AC   ADV34682;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12p40 full-length cDNA, nFeIL-12p40 987.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .987
FT                   /*tag=  a
FT                   /product= "PFeIL-12p40 329 protein "
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34683.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 23; SEQ ID NO 29; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12p40 subunit protein
CC   encoding full-length cDNA.
XX
SQ   Sequence 987 BP; 283 A; 250 C; 246 G; 208 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.:              8.78e-167       Length:         987
Score:                  1761.00         Matches:        329
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-30 (1-329) x ADV34682 (1-987)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987

RESULT 4
ADV34684/c
ID   ADV34684 standard; DNA; 987 BP.
XX
AC   ADV34684;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline single chain IL-12p40 complementary DNA, nFeIL-12p40 987.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 31; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline single chain IL-12p40 subunit full-length
CC   complementary DNA.
XX
SQ   Sequence 987 BP; 208 A; 246 C; 250 G; 283 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              8.78e-167       Length:         987
Score:                  1761.00         Matches:        329
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     14              Gaps:           0

US-10-821-670A-30 (1-329) x ADV34684 (1-987)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
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Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
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Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGCAGT 1
```

RESULT 5
AAF26082
ID AAF26082 standard; DNA; 990 BP.
XX
AC AAF26082;
XX
DT 24-APR-2001 (first entry)
XX
DE Feline IL-12p40 encoding DNA SEQ ID 8.
XX
KW Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS Felis sp.
XX

PN WO200104280-A2.
XX
PD 18-JAN-2001.
XX
PF 08-JUL-2000; 2000WO-DE002262.
XX
PR 08-JUL-1999; 99CH-00001258.
XX
PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA (UYZU-) UNIV ZUERICH.
XX
PI Leutenegger C, Schroff M, Wittig B, Lutz H;
XX
DR WPI; 2001-147190/15.
XX
PT Vaccine for treating or preventing lentivirus infection in cats, contains
PT nucleic acid sequence encoding viral protein under control of eukaryotic
PT promoter.
XX
PS Claim 14; Page 36; 37pp; German.
XX
CC This invention describes a novel vaccine (A) for prevention or treatment
CC of lentivirus infection in felines which comprises an immunizing nucleic
CC acid sequence (I) that contains, or comprises, at least part of a gene
CC encoding a protein (II) of the virus, under control of a eukaryotic
CC promoter functional in the relevant animal. (II) is especially the
CC envelope (env) protein. The invention also describes (1) vaccine (A)
CC containing an immunizing protein, or fragment, from a lentivirus plus at
CC least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC lentivirus protein, or fragment, especially derived from feline immune
CC deficiency virus (FIV), by expressing the corresponding nucleic acid
CC sequence in a host cell. The products of the invention have antiviral
CC activity. The vaccine (A) and related protein-based vaccines, are
CC particularly used to treat or prevent lentivirus infections in domestic
CC cats, especially feline immune deficiency virus (FIV). Vaccination with
CC (A) allows differentiation between vaccinated and infected animals, from
CC the antibody status. The vaccines may be formulated with an adjuvant
CC (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC immune response, particularly a Th1 response
XX
SQ Sequence 990 BP; 283 A; 249 C; 248 G; 210 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	8.82e-167	Length:	990
Score:	1761.00	Matches:	329
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	4	Gaps:	0

US-10-821-670A-30 (1-329) x AAF26082 (1-990)

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Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
                |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
```

RESULT 6
AAF26085
ID AAF26085 standard; DNA; 990 BP.
XX
AC AAF26085;
XX
DT 24-APR-2001 (first entry)
XX
DE Feline IL-12p40 encoding DNA.
XX
KW Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS Felis sp.
XX
PN WO200104155-A2.
XX
PD 18-JAN-2001.
XX
PF 08-JUL-2000; 2000WO-DE002263.
XX
PR 08-JUL-1999; 99CH-00001259.
XX
PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA (UYZU-) UNIV ZUERICH.
PA (REGC) UNIV CALIFORNIA.
XX
PI Lutz H, Leutenegger C, Pedersen N, Schroff M, Wittig B;
XX
DR WPI; 2001-147178/15.
XX
PT Recombinant feline interleukin-12, useful as immunostimulant and for
PT treating e.g. viral infections in cats, and related nucleic acid
PT constructs.
XX
PS Claim 3; Page 30; 35pp; German.
XX
CC This invention describes a novel feline interleukin-12 (fIL-12)
CC polypeptide (I) that is expressed, by recombinant gene expression in
CC eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC of subunits p35 and p40. These proteins are formed so that, in equimolar
CC concentrations and in presence of an immunizing antigen, they can be
CC administered to carnivores, particularly domestic cats. The invention
CC also describes a nucleic acid construct (II) encoding fIL-12 containing
CC sequences at least 95% identical with the p40- and p35-encoding sequences
CC (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC as immunostimulants for immunization against infectious diseases and/or
CC for treating infections or tumors in felines, especially domestic cats.
CC The products of the invention have immunostimulatory, antiviral and
CC antitumor activity. Nucleic acid constructs that encode (II) are useful
CC as adjuvants for prophylactic immunization against viral diseases and for
CC treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC is useful for carnivores, and particularly domestic cats in the
CC following: (i) as immunostimulant, for preventative or therapeutic use;
CC and (ii) treating tumors and autoimmune diseases, or diseases associated
CC with a Th1 defect, especially pre-existing infections by feline immune
CC deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ Sequence 990 BP; 283 A; 249 C; 248 G; 210 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	8.82e-167	Length:	990
Score:	1761.00	Matches:	329
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	4	Gaps:	0

US-10-821-670A-30 (1-329) x AAF26085 (1-990)

```
Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
```

```
Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
```

RESULT 7
AAF26076
ID AAF26076 standard; DNA; 4522 BP.
XX
AC AAF26076;
XX
DT 24-APR-2001 (first entry)
XX
DE Feline IL-12p40 encoding DNA SEQ ID 2.
XX
KW Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS Felis sp.
XX
PN WO200104280-A2.
XX
PD 18-JAN-2001.
XX
PF 08-JUL-2000; 2000WO-DE002262.
XX
PR 08-JUL-1999; 99CH-00001258.
XX
PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA (UYZU-) UNIV ZUERICH.
XX
PI Leutenegger C, Schroff M, Wittig B, Lutz H;
XX
DR WPI; 2001-147190/15.
XX
PT Vaccine for treating or preventing lentivirus infection in cats, contains
PT nucleic acid sequence encoding viral protein under control of eukaryotic
PT promoter.
XX
PS Disclosure; Page 29-31; 37pp; German.
XX
CC This invention describes a novel vaccine (A) for prevention or treatment
CC of lentivirus infection in felines which comprises an immunizing nucleic
CC acid sequence (I) that contains, or comprises, at least part of a gene
CC encoding a protein (II) of the virus, under control of a eukaryotic
CC promoter functional in the relevant animal. (II) is especially the
CC envelope (env) protein. The invention also describes (1) vaccine (A)
CC containing an immunizing protein, or fragment, from a lentivirus plus at
CC least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC lentivirus protein, or fragment, especially derived from feline immune
CC deficiency virus (FIV), by expressing the corresponding nucleic acid
CC sequence in a host cell. The products of the invention have antiviral
CC activity. The vaccine (A) and related protein-based vaccines, are
CC particularly used to treat or prevent lentivirus infections in domestic
CC cats, especially feline immune deficiency virus (FIV). Vaccination with
CC (A) allows differentiation between vaccinated and infected animals, from
CC the antibody status. The vaccines may be formulated with an adjuvant
CC (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC immune response, particularly a Th1 response
XX
SQ Sequence 4522 BP; 1180 A; 1126 C; 1106 G; 1110 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.82e-166	Length:	4522
Score:	1761.00	Matches:	329
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	4	Gaps:	0

US-10-821-670A-30 (1-329) x AAF26076 (1-4522)

```
Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db       4007 AGCAACTGGGCATCCGTGTCCTGCAGT 4033
```

RESULT 8
AAF26094
ID AAF26094 standard; DNA; 4522 BP.
XX
AC AAF26094;
XX
DT 24-APR-2001 (first entry)
XX
DE Plasmid pMol-fil12p40 DNA SEQ ID 10.
XX
KW Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS Synthetic.
XX
PN WO200104155-A2.
XX
PD 18-JAN-2001.
XX
PF 08-JUL-2000; 2000WO-DE002263.
XX
PR 08-JUL-1999; 99CH-00001259.
XX
PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA (UYZU-) UNIV ZUERICH.
PA (REGC) UNIV CALIFORNIA.
XX
PI Lutz H, Leutenegger C, Pedersen N, Schroff M, Wittig B;
XX
DR WPI; 2001-147178/15.
XX
PT Recombinant feline interleukin-12, useful as immunostimulant and for
PT treating e.g. viral infections in cats, and related nucleic acid
PT constructs.
XX
PS Example 1c; Page 33-35; 35pp; German.
XX
CC This invention describes a novel feline interleukin-12 (fIL-12)
CC polypeptide (I) that is expressed, by recombinant gene expression in
CC eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC of subunits p35 and p40. These proteins are formed so that, in equimolar
CC concentrations and in presence of an immunizing antigen, they can be
CC administered to carnivores, particularly domestic cats. The invention
CC also describes a nucleic acid construct (II) encoding fIL-12 containing
CC sequences at least 95% identical with the p40- and p35-encoding sequences
CC (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC as immunostimulants for immunization against infectious diseases and/or
CC for treating infections or tumors in felines, especially domestic cats.
CC The products of the invention have immunostimulatory, antiviral and
CC antitumor activity. Nucleic acid constructs that encode (II) are useful
CC as adjuvants for prophylactic immunization against viral diseases and for
CC treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC is useful for carnivores, and particularly domestic cats in the
CC following: (i) as immunostimulant, for preventative or therapeutic use;
CC and (ii) treating tumors and autoimmune diseases, or diseases associated
CC with a Th1 defect, especially pre-existing infections by feline immune
CC deficiency virus (FIV), feline leukemia virus and corona virus
XX
SQ Sequence 4522 BP; 1180 A; 1126 C; 1106 G; 1110 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.82e-166	Length:	4522
Score:	1761.00	Matches:	329
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	4	Gaps:	0

US-10-821-670A-30 (1-329) x AAF26094 (1-4522)

```
Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706
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```
Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db       4007 AGCAACTGGGCATCCGTGTCCTGCAGT 4033
```

RESULT 9
ABK98962/c
ID ABK98962 standard; cDNA; 985 BP.
XX
AC ABK98962;
XX
DT 21-OCT-2002 (first entry)
XX
DE Feline interleukin-12 nFeIL-12p40-N985 complementary strand.
XX
KW Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW tumour development; inflammatory disease; graft rejection; ss.
XX
OS Felis catus.
XX
PN US2002052030-A1.
XX
PD 02-MAY-2002.
XX
PF 27-JUL-2001; 2001US-00917265.
XX
PR 04-AUG-2000; 2000US-0223016P.
XX
PA (WOND/) WONDERLING R S.
PA (BORO/) BOROUGHS K L.
XX
PI Wonderling RS, Boroughs KL;
XX
DR WPI; 2002-573554/61.
XX
PT Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT chain and canine IL-12 single chain proteins, useful for treating and
PT preventing autoimmune diseases, inflammatory diseases and/or graft
PT rejection in animals.
XX
PS Example 3; Page 75-76; 106pp; English.
XX
CC The present invention discloses new feline interleukin 18 (IL-18), feline
CC caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC proteins. A composition comprising a feline IL-18, feline caspase-1,
CC feline IL-12 single chain or canine IL-12 single chain proteins, a
CC nucleic acid encoding these proteins, mimetopes of these proteins,
CC multimeric forms of these proteins, an antibody against these proteins,
CC or an inhibitor identified by its ability to inhibit the activity of
CC these proteins, can be used to treat or prevent autoimmune diseases,
CC allergic reactions, infectious diseases, tumour development, inflammatory
CC diseases and/or graft rejection in animals. The present nucleic acid
CC sequence represents a feline interleukin 12 DNA sequence, as described in
CC the invention
XX
SQ Sequence 985 BP; 207 A; 245 C; 250 G; 283 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.21e-166	Length:	985
Score:	1757.00	Matches:	328
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	99.8%	Indels:	0
DB:	6	Gaps:	0

US-10-821-670A-30 (1-329) x ABK98962 (1-985)

```
Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86
```

```
Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGC 2

RESULT 10
ABK98961
ID   ABK98961 standard; cDNA; 985 BP.
XX
AC   ABK98961;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12p40-N985 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69311.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Example 3; Page 73-74; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 985 BP; 283 A; 250 C; 245 G; 207 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.21e-166       Length:         985
Score:                  1757.00         Matches:        328
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            99.8%           Indels:         0
DB:                     6               Gaps:           0

US-10-821-670A-30 (1-329) x ABK98961 (1-985)
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```
Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984

RESULT 11
ADV34707
ID   ADV34707 standard; cDNA; 985 BP.
XX
AC   ADV34707;
```

```
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline N-terminal IL-12p40 protein encoding cDNA, nFeIL-12p40-N985.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; gene; ss.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .984
FT                   /*tag=  a
FT                   /product= "PCaIL-12P40-N328 protein"
FT                   /partial
FT                   /note= "No stop codon"
XX
PN   US2004248261-A1.
XX
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
DR   P-PSDB; ADV34708.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Claim 24; SEQ ID NO 55; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline N-terminal single chain IL-12p40 protein
CC   encoding cDNA.
XX
SQ   Sequence 985 BP; 283 A; 250 C; 245 G; 207 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.21e-166      Length:         985
Score:                  1757.00        Matches:        328
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            99.8%          Indels:         0
DB:                     14             Gaps:           0

US-10-821-670A-30 (1-329) x ADV34707 (1-985)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGC 984

RESULT 12
ADV34709/c
ID   ADV34709 standard; DNA; 985 BP.
XX
AC   ADV34709;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Feline N-terminal IL-12p40 protein complementary DNA, nFeIL-12p40-N985.
XX
KW   DNA purification; p35; p40; IL; interleukin; casp; caspase; vaccine;
KW   infectious disease; antimicrobial; ds.
XX
OS   Felis catus.
XX
PN   US2004248261-A1.
XX
```

```
PD   09-DEC-2004.
XX
PF   09-APR-2004; 2004US-00821670.
XX
PR   04-AUG-2000; 2000US-0223016P.
PR   27-JUL-2001; 2001US-00917265.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2005-020565/02.
XX
PT   New nucleic acid molecule comprising a sequence encoding a feline p35 or
PT   p40 subunit protein and a nucleic acid linker, useful in preparing a
PT   vaccine against infectious diseases in feline animals.
XX
PS   Example 3; SEQ ID NO 57; 103pp; English.
XX
CC   The present invention relates to the feline interleukin (IL)-12p35 or p40
CC   subunit protein and their encoding nucleic acid molecules and a nucleic
CC   acid linker. The invention also provides the feline caspase (casp)-1,
CC   feline IL-18 single chain and canine IL-12 single chain proteins and
CC   their nucleic acid molecules. The nucleic acid molecule is useful in
CC   preparing a vaccine against infectious diseases in feline animals. The
CC   present sequence is the feline N-terminal single chain IL-12p40
CC   complementary DNA.
XX
SQ   Sequence 985 BP; 207 A; 245 C; 250 G; 283 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.21e-166      Length:         985
Score:                  1757.00        Matches:        328
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            99.8%          Indels:         0
DB:                     14             Gaps:           0

US-10-821-670A-30 (1-329) x ADV34709 (1-985)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        321 SerAsnTrpAlaSerValSerCys 328
              |||||||||||||||||||||||
Db         25 AGCAACTGGGCATCCGTGTCCTGC 2

RESULT 13
AAV56625
ID   AAV56625 standard; cDNA; 2193 BP.
XX
AC   AAV56625;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp40 cDNA.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             64. .1053
FT                   /*tag=  a
FT   sig_peptide     64. .129
FT                   /*tag=  b
FT   mat_peptide     130. .1050
FT                   /*tag=  c
FT                   /product= "FLAFp40"
FT                   /note= "feline cytokine"
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP001824.
XX
PR   04-JUN-1996;   96JP-00165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Imamura T,  Maeda H,  Fujiyasu T,  Imagawa Y,  Tokiyoshi S;
XX
```

```
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76173.
XX
PT   Novel feline cytokine protein - useful for treating feline auto:immune
PT   diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS   Claim 19; Page 52-54; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine protein, FLAFp40. This
CC   protein can be used in the production of a FLAFp35/FLAFp40 heterodimer
CC   which can potentiate the cytotoxic activity of feline cytotoxic T
CC   lymphocyte cells. Such proteins are used for treatment of feline
CC   autoimmune diseases e.g. as caused by feline herpes virus or feline
CC   calcivirus
XX
SQ   Sequence 2193 BP; 680 A; 451 C; 493 G; 569 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.03e-165      Length:          2193
Score:                  1755.00        Matches:         328
Percent Similarity:     99.7%          Conservative:    0
Best Local Similarity:  99.7%          Mismatches:      1
Query Match:            99.7%          Indels:          0
DB:                     2              Gaps:            0

US-10-821-670A-30 (1-329) x AAV56625 (1-2193)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||
Db         64 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTACCTGGTTTTGCTGGCACCTCCTCTC 123

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 183

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 243

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 303

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 363

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 423

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 483

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 543

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 603

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 663

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 723

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        724 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 783

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 843

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 903

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 963

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 1023

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||||
Db       1024 AGCAACTGGGCATCCGTGTCCTGCAGT 1050

RESULT 14
ABK98950
ID   ABK98950 standard; cDNA; 1599 BP.
XX
AC   ABK98950;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1599 coding strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; gene; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
DR   P-PSDB; ABG69306.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 58-60; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
```

```
XX
SQ   Sequence 1599 BP; 460 A; 402 C; 380 G; 357 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              4.27e-165      Length:          1599
Score:                  1747.00        Matches:         327
Percent Similarity:     99.4%          Conservative:    0
Best Local Similarity:  99.4%          Mismatches:      2
Query Match:            99.2%          Indels:          0
DB:                     6              Gaps:            0

US-10-821-670A-30 (1-329) x ABK98950 (1-1599)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987

RESULT 15
ABK98951/c
ID   ABK98951 standard; cDNA; 1599 BP.
XX
AC   ABK98951;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Feline interleukin-12 nFeIL-12-1599 complementary strand.
XX
KW   Feline interleukin 18; IL-18; feline caspase-1; feline IL-12; cat; dog;
KW   canine IL-12; autoimmune disease; allergic reaction; infectious disease;
KW   tumour development; inflammatory disease; graft rejection; ss.
XX
OS   Felis catus.
XX
PN   US2002052030-A1.
XX
PD   02-MAY-2002.
XX
PF   27-JUL-2001; 2001US-00917265.
XX
PR   04-AUG-2000; 2000US-0223016P.
XX
PA   (WOND/) WONDERLING R S.
PA   (BORO/) BOROUGHS K L.
XX
PI   Wonderling RS,  Boroughs KL;
XX
DR   WPI; 2002-573554/61.
XX
PT   Feline interleukin 18 (IL-18), feline caspase-1, feline IL-12 single
PT   chain and canine IL-12 single chain proteins, useful for treating and
PT   preventing autoimmune diseases, inflammatory diseases and/or graft
PT   rejection in animals.
XX
PS   Claim 6; Page 61-62; 106pp; English.
XX
CC   The present invention discloses new feline interleukin 18 (IL-18), feline
CC   caspase-1, feline IL-12 single chain and canine IL-12 single chain
CC   proteins. A composition comprising a feline IL-18, feline caspase-1,
CC   feline IL-12 single chain or canine IL-12 single chain proteins, a
CC   nucleic acid encoding these proteins, mimetopes of these proteins,
CC   multimeric forms of these proteins, an antibody against these proteins,
CC   or an inhibitor identified by its ability to inhibit the activity of
CC   these proteins, can be used to treat or prevent autoimmune diseases,
CC   allergic reactions, infectious diseases, tumour development, inflammatory
CC   diseases and/or graft rejection in animals. The present nucleic acid
CC   sequence represents a feline interleukin 12 DNA sequence, as described in
CC   the invention
XX
SQ   Sequence 1599 BP; 357 A; 380 C; 402 G; 460 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              4.27e-165      Length:          1599
Score:                  1747.00        Matches:         327
Percent Similarity:     99.4%          Conservative:    0
Best Local Similarity:  99.4%          Mismatches:      2
Query Match:            99.2%          Indels:          0
DB:                     6              Gaps:            0

US-10-821-670A-30 (1-329) x ABK98951 (1-1599)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
```

```
Db       1599 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 1540

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 1420

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy         81 GluPheAlaAspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1359 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 1300

Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1299 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 1240

Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1179 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 1120

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db       1119 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 1060

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        999 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 940

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        939 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 880

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        879 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 820

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 760

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        759 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 640

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||||||||||||||||||||||||
Db        639 AGCAACTGGGCATCCGTGTCCTGCAGT 613


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Run on: June 10, 2006, 00:20:47 ; Search time 4032.45 Seconds
(without alignments)
6843.525 Million cell updates/sec

Title: US-10-821-670A-30
Perfect score: 1761
Sequence: 1 MHPQQLVIAWFSLVLLAPPL.....QARDRYYSSSWSNWASVSCS 329

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10821670/runat_07062006_110104_26172/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
-USER=US10821670_@CGN_1_1_27300_@runat_07062006_110104_26172 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1176.5	66.8	1839	6	AK162981	AK162981 Mus muscu
	2	1163.5	66.1	2908	6	AK155593	AK155593 Mus muscu
	3	1111.5	63.1	735	5	CD559605	CD559605 AGENCOURT
	4	1111.5	63.1	756	5	CK130264	CK130264 AGENCOURT
	5	1098.5	62.4	747	5	CD559607	CD559607 AGENCOURT
	6	1084	61.6	772	5	CD559604	CD559604 AGENCOURT
	7	981.5	55.7	745	5	CD559602	CD559602 AGENCOURT
c	8	965	54.8	785	5	CD559448	CD559448 AGENCOURT
c	9	963.5	54.7	736	5	CD559453	CD559453 AGENCOURT
c	10	960.5	54.5	772	5	CD559450	CD559450 AGENCOURT
c	11	955.5	54.3	762	5	CD559451	CD559451 AGENCOURT
c	12	906.5	51.5	766	5	CD559449	CD559449 AGENCOURT
c	13	898.5	51.0	754	5	CD559452	CD559452 AGENCOURT
c	14	824	46.8	725	5	CD559454	CD559454 AGENCOURT
	15	781	44.3	724	5	CD559603	CD559603 AGENCOURT
	16	776.5	44.1	1042	5	CD559606	CD559606 AGENCOURT
	17	759.5	43.1	649	5	CJ134671	CJ134671 CJ134671
	18	580.5	33.0	475	7	BF704417	BF704417 MI-P-E6-a
	19	506.5	28.8	417	8	CO949904	CO949904 UMC-pd12c
	20	461	26.2	387	4	BY167742	BY167742 BY167742
	21	452	25.7	432	4	BY154173	BY154173 BY154173
	22	425	24.1	423	4	BY218447	BY218447 BY218447
	23	412	23.4	375	4	BY222535	BY222535 BY222535
	24	406	23.1	346	4	BY164658	BY164658 BY164658
	25	394	22.4	355	4	BY221814	BY221814 BY221814
	26	378	21.5	535	11	AZ441303	AZ441303 1M0232M24
	27	365	20.7	700	12	CE093997	CE093997 tigr-gss-
c	28	351	19.9	569	11	AZ853726	AZ853726 2M0157M01
	29	346.5	19.7	252	10	DV799576	DV799576 est_t_tru
	30	277	15.7	666	4	BY749553	BY749553 BY749553
c	31	229.5	13.0	812	10	DT349218	DT349218 JGI_CAAX1
	32	192.5	10.9	755	10	DV591060	DV591060 AGENCOURT
	33	191.5	10.9	748	10	DV593962	DV593962 AGENCOURT
	34	189	10.7	705	8	CX261472	CX261472 1314997 N
	35	184	10.4	1277	14	DQ037702	DQ037702 Homo sapi
	36	182.5	10.4	2548	6	AK046337	AK046337 Mus muscu
	37	182	10.3	1277	14	DQ037703	DQ037703 Pan trogl
	38	181.5	10.3	1118	14	AY403646	AY403646 Mus muscu
	39	181.5	10.3	1881	6	AK137026	AK137026 Mus muscu
	40	180.5	10.2	2373	6	AK141197	AK141197 Mus muscu
	41	180	10.2	850	3	BU291084	BU291084 603603708
	42	177.5	10.1	709	4	CA344594	CA344594 675030 NC
c	43	177	10.1	665	4	CA062264	CA062264 ssalrgb52
c	44	177	10.1	689	10	DW558518	DW558518 EST_ssal_
	45	176	10.0	1008	4	BX364435	BX364435 BX364435

ALIGNMENTS

RESULT 1
AK162981
LOCUS AK162981 1839 bp mRNA linear HTC 21-SEP-2005
DEFINITION Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430014H12 product:interleukin 12b, full insert sequence.
ACCESSION AK162981
VERSION AK162981.1 GI:74188061
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,

Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

PUBMED 11076861

REFERENCE 4

AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

CONSRTM RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409 (6821), 685-690 (2001)

PUBMED 11217851

REFERENCE 5

AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420 (6915), 563-573 (2002)

PUBMED 12466851

REFERENCE 6

AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE The transcriptional landscape of the mammalian genome

JOURNAL Science 309 (5740), 1559-1563 (2005)

PUBMED 16141072

REFERENCE 7

AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.

CONSRTM RIKEN Genome Exploration Research Group

TITLE Antisense transcription in the mammalian transcriptome

JOURNAL Science 309 (5740), 1564-1566 (2005)

PUBMED 16141073

REFERENCE 8 (bases 1 to 1839)

AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

```
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                     /mol_type="mRNA"
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     CDS             58. .1065
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                     (MGD|MGI:96540 GB|M86671, evidence: BLASTN, 100%,
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                     /protein_id="BAE37146.1"
                     /db_xref="GI:74188062"
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                     TVNLTCDTPEEDDITWTSDQRHGVIGSGKTLTITVKEFLDAGQYTCHKGGETLSHSHL
                     LLHKKENGIWSTEILKNFKNKTFLKCEAPNYSGRFTCSWLVQRNMDLKFNIKSSSSSP
                     DSRAVTCGMASLSAEKVTLDQRDYEKYSVSCQEDVTCPTAEETLPIELALEARQQNKY
                     ENYSTSFFIRDIIKPDPPKNLQMKPLKNSQVEVSWEYPDSWSTPHSYFSLKFFVRIQR
                     KKEKMKETEEGCNQKGAFLVEKTSTEVQCKGGNVCVQAQDRYYNSSCSKWACVPCRVR
                     S"
ORIGIN

Alignment Scores:
Pred. No.:              2.13e-120       Length:         1839
Score:                  1176.50         Matches:        225
Percent Similarity:     78.0%           Conservative:   37
Best Local Similarity:  67.0%           Mismatches:     61
Query Match:            66.8%           Indels:         13
DB:                     6               Gaps:           4

US-10-821-670A-30 (1-329) x AK162981 (1-1839)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
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Db         58 ATGTGTCCTCAGAAGCTAACCATCTCCTGGTTTGCCATCGTTTTGCTGGTGTCTCCACTC 117

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||:::|||||||||||||||:::|||||||||||||||:::|||||   ||||||
Db        118 ATGGCCATGTGGGAGCTGGAGAAAGACGTTTATGTTGTAGAGGTGGACTGGACTCCCGAT 177

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||   |||   |||||||||:::|||||||||||||||||||||||||||
Db        178 GCCCCTGGAGAAACAGTGAACCTCACCTGTGACACGCCTGAAGAAGATGACATCACCTGG 237

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
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Qy        101 PheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGln 120
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Db        409 AAAAATTTCAAAAACAAGACTTTCCTGAAGTGTGAAGCACCAAATTACTCCGGACGGTTC 468

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
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Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
                 |||   |||   :::   ||||||||||||   |||:::||||||||||||||||||
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Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
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Db        649 CCAACTGCCGAGGAGACCCTGCCCATTGAACTGGCGTTGGAAGCACGGCAGCAGAATAAA 708

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
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Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
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Db        769 AACTTGCAGATGAAGCCTTTGAAGAACTCACAG---GTGGAGGTCAGCTGGGAGTACCCT 825

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              |||:::|||||||||||||||||||||||||||||||   |||   |||::::::|||
Db        826 GACTCCTGGAGCACTCCCCATTCCTACTTCTCCCTCAAGTTCTTTGTTCGAATCCAGCGC 885

Qy        281 LysAsnAsnArgGluLys----------------------LysAspArgLeuSerVal 292
              |||       :::   |||                     |||           |||
Db        886 AAGAAAGAAAAGATGAAGGAGACAGAGGAGGGGGTGTAACCAGAAAGGTGCGTTCCTCGTA 945

Qy        293 AspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaArg 312
              :::|||||||||   :::|||   |||   |||         :::   ||||||||||:::
Db        946 GAGAAGACATCTACCGAAGTCCAATGC---AAAGGCGGGAATGTCTGCGTGCAAGCTCAG 1002

Qy        313 AspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 328
              ||||||||||||:::||||||   |||   ||||||   |||   |||
Db       1003 GATCGCTATTACAATTCCTCATGCAGCAAGTGGGCATGTGTTCCCTGC 1050

RESULT 2
AK155593
LOCUS       AK155593               2908 bp    mRNA    linear   HTC 21-SEP-2005
DEFINITION  Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN
            full-length enriched library, clone:F730005O03 product:interleukin
            12b, full insert sequence.
ACCESSION   AK155593
VERSION     AK155593.1  GI:74212721
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
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Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

CONSRTM RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409 (6821), 685-690 (2001)

PUBMED 11217851

REFERENCE 5

AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420 (6915), 563-573 (2002)

PUBMED 12466851

REFERENCE 6

AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.

CONSRTM FANTOM Consortium

TITLE The transcriptional landscape of the mammalian genome

JOURNAL Science 309 (5740), 1559-1563 (2005)

PUBMED 16141072

REFERENCE 7

AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.

CONSRTM RIKEN Genome Exploration Research Group

TITLE Antisense transcription in the mammalian transcriptome

JOURNAL Science 309 (5740), 1564-1566 (2005)

PUBMED 16141073

REFERENCE 8 (bases 1 to 2908)

AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

source 1. .2908
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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/cell_type="B6-derived CD11 +ve dendritic cells"
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                     putative"
ORIGIN

Alignment Scores:
Pred. No.:              1.21e-118       Length:         2908
Score:                  1163.50         Matches:        225
Percent Similarity:     77.7%           Conservative:   37
Best Local Similarity:  66.8%           Mismatches:     61
Query Match:            66.1%           Indels:         14
DB:                     6               Gaps:           4

US-10-821-670A-30 (1-329) x AK155593 (1-2908)

Qy          1 MetHisProGlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeu 20
              |||   ||||||:::|||   |||:::||||||:::::|||||||||       ||||||
Db        461 ATGTGTCCTCAGAAGCTAACCATCTCCTGGTTTGCCATCGTTTTGCTGGTGTCTCCACTC 520

Qy         21 MetAlaIleTrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAsp 40
              ||||||:::|||||||||||||||:::|||||||||||||||:::||||||   ||||||
Db        521 ATGGCCATGTGGGAGCTGGAGAAAGACGTTTATGTTGTAGAGGTGGACTGGACTCCCGAT 580

Qy         41 AlaProGlyGluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrp 60
              ||||||||||||   |||   ||||||||||:::||||||||||||||||||||||||||
Db        581 GCCCCTGGAGAAACAGTGAACCTCACCTGTGACACGCCTGAAGAAGATGACATCACCTGG 640

Qy         61 ThrSerAspGlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLys 80
              ||||||||||||          ||:::|||||||||||||||||||||||   ||||||
Db        641 ACCTCAGACCAGAGACATGGAGTCATAGGCTCTGGAAAGACCCTGACCATCACTGTCAAA 700

Qy         81 GluPheAlaAspAlaGlyGln-TyrThrCysHisLysGlyGlyGluValLeuSerHisSe 100
              ||||||   |||||||||||| ||||||||||||||||||||   ||||||||||
Db        701 GAGTTTCTAGATGCTGGCCAGCTACACCTGCCACAAAGGAGGCGAGACTCTGAGCCACTC 760

Qy        100 rPheLeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGl 120
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Db        761 ACATCTGCTGCTCCACAAGAAGGAAAATGGAATTTGGTCCACTGAAATTTTA-------- 812

Qy        120 nLysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPh 140
               |||      |||||||||   ||||||||||||||||||   ||||||||||||||||
Db        813 -AAAAATTTCAAAAACAAGACTTTCCTGAAGTGTGAAGCACCAAATTACTCCGGACGGTT 871

Qy        140 eThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerAr 160
              |||||||   ||||||         :::   ||||||||||||   :::||||||||
Db        872 CACGTGCTCATGGCTGGTGCAAAGAAACATGGACTTGAAGTTCAACATCAAGAGCAGTAG 931

Qy        160 gGlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVa 180
              |||   |||   :::   ||||||||||||   |||:::||||||||||||||||||||
Db        932 CAGTTCCCCTGACTCTCGGGCAGTGACATGTGGAATGGCGTCTCTGTCTGCAGAGAAGGT 991

Qy        180 lArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCy 200
              |   :::|||   |||||||||:::||||||:::|||   |||||||||         ||
Db        992 CACACTGGACCAAAGGGACTATGAGAAGTATTCAGTGTCCTGCCAGGAGGATGTCACCTG 1051

Qy        200 sProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLy 220
              ||||   |||||||||:::|||||||||||:::   ::::::|||      :::   ||
Db       1052 CCCAACTGCCGAGGAGACCCTGCCCATTGAACTGGCGTTGGAAGCACGGCAGCAGAATAA 1111

Qy        220 sTyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLy 240
              ||||||||||||::::::||||||||||||||||||||||||||||||||||||||||||
Db       1112 ATATGAGAACTACAGCACCAGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAA 1171

Qy        240 sAsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPr 260
              ||||||||||:::|||||||||||||||||:::   |||||||||||||||||||||||
Db       1172 GAACTTGCAGATGAAGCCTTTGAAGAACTCACAG---GTGGAGGTCAGCTGGGAGTACCC 1228

Qy        260 oAspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGl 280
              ||||:::|||||||||||||||||||||||||||||||   |||   |||::::::|||
Db       1229 TGACTCCTGGAGCACTCCCCATTCCTACTTCTCCCTCAAGTTCTTTGTTCGAATCCAGCG 1288

Qy        280 yLysAsnAsnArgGluLys----------------------LysAspArgLeuSerVa 292
```

```
              |||      :::   |||                              |||          ||
Db       1289 CAAGAAAGAAAAGATGAAGGAGACAGAGGAGGGGGTGTAACCAGAAAGGTGCGTTCCTCGT 1348

Qy        292 lAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAlaAr 312
              |:::|||||||||   :::|||   |||   |||          :::   |||||||||::
Db       1349 AGAGAAGACATCTACCGAAGTCCAATGC---AAAGGCGGGAATGTCTGCGTGCAAGCTCA 1405

Qy        312 gAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCys 328
              :||||||||||||:::||||||   |||   ||||||   |||   |||
Db       1406 GGATCGCTATTACAATTCCTCATGCAGCAAGTGGGCATGTGTTCCCTGC 1454

RESULT 3
CD559605
LOCUS       CD559605                735 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496534 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971870 5', mRNA sequence.
ACCESSION   CD559605
VERSION     CD559605.2  GI:38558937
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 735)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585673.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 01
            High quality sequence stop: 709.
FEATURES             Location/Qualifiers
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                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              1.08e-113       Length:         735
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Score:                 1111.50       Matches:       206
Percent Similarity:    94.5%         Conservative:  18
Best Local Similarity: 86.9%         Mismatches:    12
Query Match:           63.1%         Indels:        1
DB:                    5             Gaps:          1

US-10-821-670A-30 (1-329) x CD559605 (1-735)

Qy          4 GlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeuMetAlaIle 23
              |||||||||||||||:::|||||||||||||||   ||||||   ||||||:::||||||
Db         26 CAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTCGTGGCCATA 85

Qy         24 TrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaProGly 43
              |||||||||:::|||:::|||||||||||||||||||||:::|||||||||||||||
Db         86 TGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCTGGA 145

Qy         44 GluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSerAsp 63
              ||||||||||||||||||||:::|||||||||||||||   ||||||||||||   |||
Db        146 GAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTGGAC 205

Qy         64 GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheAla 83
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 CAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTTGGA 265

Qy         84 AspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeuLeu 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        266 GATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTGCTG 325

Qy        104 IleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGluSer 123
              :::||||||||||||||||||||||||||||||||||||||||||:::::||||||||||
Db        326 CTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAACCC 385

Qy        124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrp 143
              |||||||||   ||||||:::||||||||||||||||||||||||||||||||||||||
Db        386 AAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGG 445

Qy        144 TrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSer 163
              |||||||||   ||||||||||||||   |||:::||||||||||||||||||||||||
Db        446 TGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAGAGCAGCAGAGGCTCTTCT 505

Qy        164 AspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAsp 183
              ||||||||||||||||||||||||||||||||||||||:::||||||   |||
Db        506 GACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGAC 565

Qy        184 AsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAla 203
              |||::::::|||   :::|||:::|||||||||||||||   ||||||||||||||||||
Db        566 AACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCT 622

Qy        204 GluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsn 223
              ||||||||||||||||||||||:::||||||||||:::||||||||||||||||||||||
Db        623 GAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAAC 682

Qy        224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 TACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 733

RESULT 4
CK130264
LOCUS       CK130264                 756 bp    mRNA    linear   EST 02-DEC-2003
DEFINITION  AGENCOURT_14496566 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971871 5', mRNA sequence.
ACCESSION   CK130264
VERSION     CK130264.1  GI:38622200
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 756)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 02
            High quality sequence start: 5
            High quality sequence stop: 731.
FEATURES              Location/Qualifiers
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                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:6971871"
                      /tissue_type="mixed"
                      /lab_host="DH5A (T1 phage-resistant)"
                      /clone_lib="NIH_MGC_195"
                      /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                      loxP-HindIII; Clones from this library have been
                      PCR-amplified using gene-specific primers to contain the
                      complete open reading frame (based on known gene sequences
                      available from NCBI's RefSeq). Template for PCR is cDNA
                      derived from either pooled cytoplasmic polyA RNA from 30
                      cells lines or pooled total RNA from 10 different tissues
                      (from BD Biosciences/Clontech and Washington University).
                      PCR products are directionally cloned into the loxP sites
                      of the pDNR-Dual vector. Library constructed by Dr.
                      Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                      Expression Laboratory, Research Technology Program, SAIC
                      Frederick, NCI-Frederick, Frederick, MD 21702). For
                      information on which gene each clone represents, please
                      visit our anonymous ftp site at
                      ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                      a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:             1.13e-113     Length:        756
Score:                 1111.50       Matches:       206
Percent Similarity:    94.1%         Conservative:  18
Best Local Similarity: 86.6%         Mismatches:    13
Query Match:           63.1%         Indels:        1
DB:                    5             Gaps:          1

US-10-821-670A-30 (1-329) x CK130264 (1-756)

Qy          4 GlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeuMetAlaIle 23
              |||||||||||||||:::|||||||||||||||   ||||||   ||||||:::||||||
Db         43 CAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTCGTGGCCATA 102

Qy         24 TrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaProGly 43
              |||||||||:::|||:::|||||||||||||||||||||:::|||||||||||||||
Db        103 TGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCTGGA 162

Qy         44 GluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSerAsp 63
              ||||||||||||||||||||:::|||||||||||||||   ||||||||||||   |||
Db        163 GAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTGGAC 222

Qy         64 GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheAla 83
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        223 CAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTTGGA 282

Qy         84 AspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeuLeu 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        283 GATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTGCTG 342
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Qy        104 IleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGluSer 123
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Db        343 CTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAACCC 402

Qy        124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrp 143
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Db        403 AAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGG 462

Qy        144 TrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSer 163
              |||||||||   ||||||||||||||   |||:::||||||||||||||||||||||||
Db        463 TGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCT 522

Qy        164 AspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAsp 183
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Db        523 GACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGAC 582

Qy        184 AsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAla 203
              |||::::::|||   :::|||:::|||||||||||||||   ||||||||||||||||||
Db        583 AACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCT 639

Qy        204 GluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsn 223
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Db        640 GAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAAC 699

Qy        224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsn 241
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Db        700 TACACCAGCAGCTTCTTCATCAGGGACATCATCNAACCTGACCCACCCAAGAAC 753

RESULT 5
CD559607
LOCUS       CD559607                747 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14497061 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971868 5', mRNA sequence.
ACCESSION   CD559607
VERSION     CD559607.2  GI:38558941
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 747)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585675.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: g  column: 11
            High quality sequence start: 14
            High quality sequence stop: 671.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:6971868"
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                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              3.19e-112       Length:         747
Score:                  1098.50         Matches:        203
Percent Similarity:     93.7%           Conservative:   19
Best Local Similarity:  85.7%           Mismatches:     14
Query Match:            62.4%           Indels:         1
DB:                     5               Gaps:           1

US-10-821-670A-30 (1-329) x CD559607 (1-747)

Qy          4 GlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeuMetAlaIle 23
              ||||||||||||||:::||||||||||||||   ||||||   ||||||:::||||||
Db         38 CAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTCGTGGCCATA 97

Qy         24 TrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaProGly 43
              |||||||||:::|||:::||||||||||||||||||||||:::|||||||||||||||
Db         98 TGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCTGGA 157

Qy         44 GluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSerAsp 63
              ||||||||||||||||||:::|||||||||||||||   ||||||||||||   |||
Db        158 GAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTGGAC 217

Qy         64 GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheAla 83
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 CAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTTGGA 277

Qy         84 AspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeuLeu 103
              |||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        278 GATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTGCTG 337

Qy        104 IleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGluSer 123
              :::||||||||||||||||||||||||||||||||||||||||||||:::::|||||||||
Db        338 CTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAACCC 397

Qy        124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrp 143
              |||||||||   ||||||:::||||||||||||||||||||||||||||||||||||||
Db        398 AAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGG 457

Qy        144 TrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSer 163
              |||||||||   ||||||||||||||   |||:::||||||||||||||||||||||||
Db        458 TGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCT 517

Qy        164 AspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAsp 183
              ||||||||||||||||||||||||||||||||||||||||||:::||||||   |||
Db        518 GACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGAC 577

Qy        184 AsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAla 203
              |||::::::|||   :::|||:::|||||||||||||||   ||||||||||||||||||
Db        578 AACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCT 634

Qy        204 GluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsn 223
              ||||||||||||||||||||||:::||||||   :::||||||||:::||||||||||
Db        635 GAGGAGAGTCTGCCCATTGAGGTCATGGTGGATTGCGTTCACAAGCTCCAGTATGAAAAC 694

Qy        224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
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Db        695 TACACCCGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAA 745
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RESULT 6
CD559604
LOCUS       CD559604                772 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496598 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971872 5', mRNA sequence.
ACCESSION   CD559604
VERSION     CD559604.2  GI:38558934
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 772)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585672.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 03
            High quality sequence start: 13
            High quality sequence stop: 750.
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                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              1.42e-110      Length:         772
Score:                  1084.00        Matches:        204
Percent Similarity:     93.7%          Conservative:   18
Best Local Similarity:  86.1%          Mismatches:     14
Query Match:            61.6%          Indels:         2
DB:                     5              Gaps:           1

US-10-821-670A-30 (1-329) x CD559604 (1-772)

Qy          4 GlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeuMetAlaIle 23

Db        447 CAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTCGTGGCCATA 506

Qy         24 TrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaProGly 43

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Qy         44 GluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSerAsp 63

Db        567 GAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTGGAC 626

Qy         64 GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheAla 83

Db        627 CAGAGCAGTGAGGTCCTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTTGGA 686

Qy         84 AspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeuLeu 103

Db        687 GATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTGCTG 746

Qy        104 IleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGluSer 123

Db        747 CTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAACCC 806

Qy        124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrp 143

Db        807 AAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGG 866

Qy        144 TrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSer 163

Db        867 TGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCT 926

Qy        164 AspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAsp 183

Db        927 GACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGAC 986

Qy        184 AsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAla 203

Db        987 AACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCT 1043

Qy        204 GluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsn 223

Db       1044 GAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAAC 1103

Qy        224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240

Db       1104 TACACCAGCAGCTTCTTCATCAGGGACATCATCAA-CCTGACCAACCCAAA 1153

RESULT 7
CD559602
LOCUS       CD559602                745 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496684 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971874 5', mRNA sequence.
ACCESSION   CD559602
VERSION     CD559602.2  GI:38558930
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 745)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585670.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: IRBK2  row: h  column: 05
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FEATURES             Location/Qualifiers
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                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              4.34e-99        Length:         745
Score:                  981.50          Matches:        189
Percent Similarity:     90.2%           Conservative:   23
Best Local Similarity:  80.4%           Mismatches:     20
Query Match:            55.7%           Indels:         4
DB:                     5               Gaps:           3

US-10-821-670A-30 (1-329) x CD559602 (1-745)

Qy          4 GlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeuMetAlaIle 23
              ||||||||||||||:::|||||||||||||||   ||||||   ||||||:::||||||
Db         15 CAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTCGTGGCCATA 74

Qy         24 TrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaProGly 43
              |||||||||:::|||:::|||||||||||||||||||||||:::|||||||||||||||
Db         75 TGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCTGGA 134

Qy         44 GluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSerAsp 63
              ||||||||||||||||||||:::|||||||||||||||   ||||||||||||   |||
Db        135 GAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTGGAC 194

Qy         64 GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheAla 83
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        195 CAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTTGGA 254

Qy         84 AspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeuLeu 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        255 GATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTGCTG 314

Qy        104 IleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGluSer 123
              :::|||||||||||||||||||||||||||||||||||||:::::|||||||||
Db        315 CTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAACCC 374

Qy        124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrp 143
              |||||||||   ||||||:::|||||||||||||||||||||||||||||||||||||||
Db        375 AAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGG 434

Qy        144 TrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSer 163
              |||||||||   ||||||||||||||   |||:::||||||||||||||||||||||||
Db        435 TGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCT 494

Qy        164 AspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAsp 183
              ||||||||||||||||||||||||||||||||||||||||||:::||||||   |||
Db        495 GACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGAC 554

Qy        184 AsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAla 203
              |||::::::|||   :::|||:::|||||||||||||||   ||||||||||||||||||
Db        555 AACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCT 611

Qy        204 GluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsn 223
              ||||||||||||||||||||||:::|||||||||   |||||||||      :::
Db        612 GAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGT-CACAAGCTCATGTTGAAAATA 670

Qy        224 TyrThrSerSerPhePheIleArgAspIleIleLysProAspPro 238
              :::         ||||||:::   :::   ::::::   ||||||
Db        671 CAC---CACGGCTTCTTTCTCTGAAAT---CTTCAATCTGACCCA 709

RESULT 8
CD559448/c
LOCUS       CD559448                785 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496712 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971874 5', mRNA sequence.
ACCESSION   CD559448
VERSION     CD559448.2  GI:38453466
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 785)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585516.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 05
            High quality sequence stop: 696.
FEATURES             Location/Qualifiers
     source          1. .785
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971874"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
```

Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	3.34e-97	Length:	785
Score:	965.00	Matches:	187
Percent Similarity:	89.9%	Conservative:	18
Best Local Similarity:	82.0%	Mismatches:	22
Query Match:	54.8%	Indels:	3
DB:	5	Gaps:	1

US-10-821-670A-30 (1-329) x CD559448 (1-785)

```
Qy        102 LeuLeuIleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLys 121
              |||         :::|||||||||||||   ||||||||||||   |||::::::||||||
Db        771 CTCTGCTGCTCACAAAAGGAAGATGGAAT-TGGTCCACTGATAT-TTAAAGGACCAGAAA 714

Qy        122 GluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThr 141
              |||   ||||||||   ||||||:::||||||||||||||||||||||||||||||||||
Db        713 GAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACC 654

Qy        142 CysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGly 161
              ||||||||||||||   ||||||||||||||   |||:::||||||||||||||||||||
Db        653 TGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGC 594

Qy        162 SerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArg 181
              |||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        593 TCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGA 534

Qy        182 ValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysPro 201
              ||||||::::::|||   :::|||:::||||||||||||||   ||||||||||||
Db        533 GGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCA 477

Qy        202 AlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyr 221
              |||||||||||||||||||||||||||:::|||||||||:::||||||||||||||||
Db        476 GCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTAT 417

Qy        222 GluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLysAsn 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        416 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAAC 357

Qy        242 LeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAsp 261
              ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        356 TTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGAC 297

Qy        262 ThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLys 281
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        296 ACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAG 237

Qy        282 AsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValValCys 301
              :::   ||||||||||||||||||:::      ||||||||||||||   |||:::|||
Db        236 AGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGC 177

Qy        302 HisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSer 321
              |||:::|||   |||   |||:::|||:::||||||||||||||||||||||||||||
Db        176 CGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGC 117

Qy        322 AsnTrpAlaSerValSerCysSer 329
              ||||||||||||   ||||||
Db        116 GAATGGGCATCTGTGCCCTGCAGT 93
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RESULT 9
CD559453/c

LOCUS	CD559453 736 bp mRNA linear EST 19-NOV-2003
DEFINITION	AGENCOURT_14497154 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971869 5', mRNA sequence.
ACCESSION	CD559453
VERSION	CD559453.2 GI:38453475
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 736)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	On Jun 10, 2003 this sequence version replaced gi:31585521. Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cgapbs-r@mail.nih.gov Tissue Procurement: Narayan Bhat cDNA Library Preparation: Bhat Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: IRBK2 row: g column: 12 High quality sequence stop: 683.
FEATURES	Location/Qualifiers
source	1. .736 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6971869" /tissue_type="mixed" /lab_host="DH5A (T1 phage-resistant)" /clone_lib="NIH_MGC_195" /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	4.47e-97	Length:	736
Score:	963.50	Matches:	182
Percent Similarity:	91.3%	Conservative:	17
Best Local Similarity:	83.5%	Mismatches:	18
Query Match:	54.7%	Indels:	2
DB:	5	Gaps:	1

US-10-821-670A-30 (1-329) x CD559453 (1-736)

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Qy        112 TrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLysCys 131
              ||||||||||||   |||::::::|||||||||   |||||||||   ||||||:::|||
Db        727 TGGTCCACTGATAT-TTAAAGGACCAGAAAGAACCCAAAAATAAGACCTTTCTAAGATGC 669

Qy        132 GluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThrAsp 151
              ||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db        668 GAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGACAATCAGTACTGAT 609

Qy        152 LeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCysGly 171
              |||   |||:::|||||||||||||||||||||||||||||||||||||||||||||||
Db        608 TTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGGGTGACGTGCGGA 549
```

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Qy        172 AlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyrThr 191
Db        548 GCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAACAAGGAGTAT---GAGTACTCA 492

Qy        192 ValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGluVal 211
Db        491 GTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTC 432

Qy        212 ValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIleArg 231
Db        431 ATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGG 372

Qy        232 AspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSerArg 251
Db        371 GACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCTCGG 312

Qy        252 HisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPheSer 271
Db        311 CAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACATTCCTACTTCTCC 252

Qy        272 LeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeuSer 291
Db        251 CTGACATTCTGCGTTCAGGTCCAGGGCAAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTC 192

Qy        292 ValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGlnAla 311
Db        191 ACGGACAAGACCTCAGCCACGGTCATCTGCCGCAAAAATGCCAGCATTAGCGTGCGGGCC 132

Qy        312 ArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSer 329
Db        131 CAGGACCGCTACTATAGCTCATCTTGGAGCGAATGGGCATCTGTGCCCTGCAGT 78
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RESULT 10
CD559450/c

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LOCUS       CD559450                772 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496612 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971872 5', mRNA sequence.
ACCESSION   CD559450
VERSION     CD559450.2  GI:38453469
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 772)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585518.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 03
            High quality sequence start: 2
            High quality sequence stop: 753.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971872"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN
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Alignment Scores:

Pred. No.:	1.04e-96	Length:	772
Score:	960.50	Matches:	185
Percent Similarity:	90.6%	Conservative:	18
Best Local Similarity:	82.6%	Mismatches:	20
Query Match:	54.5%	Indels:	3
DB:	5	Gaps:	1

US-10-821-670A-30 (1-329) x CD559450 (1-772)

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Qy        106 LysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsn 125
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Qy        126 LysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeu 145
Db        710 AAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTG 651

Qy        146 ThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSerAspPro 165
Db        650 ACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCTGACCCC 591

Qy        166 GlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArg 185
Db        590 CAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAACAAG 531

Qy        186 AspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGlu 205
Db        530 GAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCTGAGGAG 474

Qy        206 SerLeuProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThr 225
Db        473 AGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACC 414

Qy        226 SerSerPhePheIleArgAspIleIleLysProAspProProLysAsnLeuGlnLeuLys 245
Db        413 AGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAG 354

Qy        246 ProLeuLysAsnSerArgHisValGluValSerTrpGluTyrProAspThrTrpSerThr 265
Db        353 CCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACT 294

Qy        266 ProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGlu 285
Db        293 CCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGCAAGAGAGAA 234

Qy        286 LysLysAspArgLeuSerValAspLysThrSerAlaLysValValCysHisLysAspAla 305
Db        233 AAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGCAAAAATGCC 174

Qy        306 LysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSer 325
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Db        173 AGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAATGGGCATCT 114

Qy        326 ValSerCysSer 329
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Db        113 GTGCCCTGCAGT 102

RESULT 11
CD559451/c
LOCUS       CD559451                762 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496580 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971871 5', mRNA sequence.
ACCESSION   CD559451
VERSION     CD559451.2  GI:38453471
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585519.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 02
            High quality sequence start: 38
            High quality sequence stop: 761.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
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                     /clone="IMAGE:6971871"
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                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              3.72e-96        Length:         762
Score:                  955.50          Matches:        184
Percent Similarity:     90.5%           Conservative:   17
Best Local Similarity:  82.9%           Mismatches:     20
Query Match:            54.3%           Indels:         3

DB:                     5               Gaps:           1

US-10-821-670A-30 (1-329) x CD559451 (1-762)

Qy        108 GluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIle 127
              ||||||||   ||||||||||||   |||::::::||||||||   ||||||||
Db        759 GAAGATGGAAT-TGGTCCACTGATAT-TTAAAGGACCAGAAAGAACCCAAAAATAAGACC 702

Qy        128 PheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAla 147
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        701 TCTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGACA 642

Qy        148 IleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGly 167
              ||||||||||||||   |||:::||||||||||||||||||||||||||||||||||||
Db        641 ATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGG 582

Qy        168 ValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyr 187
              ||||||||||||||||||||||||||||||:::||||||   ||||||::::::|||
Db        581 GTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAACAAGGAGTAT 522

Qy        188 LysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeu 207
              :::|||:::||||||||||||||   ||||||||||||||||||||||||||||||||
Db        521 ---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCTGAGGAGAGTCTG 465

Qy        208 ProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSer 227
              ||||||||||||:::||||||||:::||||||||||||||||||||||||||||||||||
Db        464 CCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACCAGCAGC 405

Qy        228 PhePheIleArgAspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeu 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        404 TTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTA 345

Qy        248 LysAsnSerArgHisValGluValSerTrpGluTyrProAspThrTrpSerThrProHis 267
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db        344 AAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACAT 285

Qy        268 SerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLys 287
              ||||||||||||||||||||   ||||||||||||||||:::   ||||||||||||
Db        284 TCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGCAAGAGAGAAAAGAAA 225

Qy        288 AspArgLeuSerValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIle 307
              ||||||:::      ||||||||||||||   |||:::|||   |||:::|||   |||
Db        224 GATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGCAAAAATGCCAGCATT 165

Qy        308 ArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSer 327
              |||:::|||:::||||||||||||||||||||||||||||   ||||||||||||
Db        164 AGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAATGGGCATCTGTGCCC 105

Qy        328 CysSer 329
              ||||||
Db        104 TGCAGT 99

RESULT 12
CD559449/c
LOCUS       CD559449                766 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496649 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971873 5', mRNA sequence.
ACCESSION   CD559449
VERSION     CD559449.2  GI:38453467
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 766)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585517.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
```

Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: h column: 04
High quality sequence stop: 641.

FEATURES Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:6971873"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	1.19e-90	Length:	766
Score:	906.50	Matches:	169
Percent Similarity:	91.1%	Conservative:	15
Best Local Similarity:	83.7%	Mismatches:	17
Query Match:	51.5%	Indels:	1
DB:	5	Gaps:	1

US-10-821-670A-30 (1-329) x CD559449 (1-766)

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Qy        128 PheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAla 147
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Db        693 TTTCTAAGATGCGAGGCCAAGAAGTATTCTGGACGTTTCACCTGGTGGTGGCTGACGACA 634

Qy        148 IleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGly 167
              |||||||||||||||   |||:::|||||||||||||||||||||||||||||||||||
Db        633 ATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCTGACCCCCAAGGG 574

Qy        168 ValThrCysGlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyr 187
              |||||||||||||||||||||||||||||||:::||||||   ||||||::::::|||
Db        573 GTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGAGGGGACAACAAGGAGTAT 514

Qy        188 LysLysTyrThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeu 207
                 :::|||:::|||||||||||||||   ||||||||||||||||||||||||||||||
Db        513 ---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGCTGAGGAGAGTCTG 457

Qy        208 ProIleGluValValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSer 227
              ||||||||||||:::|||||||||:::|||||||||||||||||||||||||||||||||
Db        456 CCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACCAGCAGC 397

Qy        228 PhePheIleArgAspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeu 247
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Db        396 TTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTA 337

Qy        248 LysAsnSerArgHisValGluValSerTrpGluTyrProAspThrTrpSerThrProHis 267
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db        336 AAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACAT 277

Qy        268 SerTyrPheSerLeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLys 287
              ||||||||||||||||||||   ||||||||||||||||||:::   ||||||||||||
Db        276 TCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAGAGCAAGAGAGAAAAGAAA 217

Qy        288 AspArgLeuSerValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIle 307
              |||||:::      ||||||||||||||   |||:::|||   |||:::|||   |||
Db        216 GATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGCCGCAAAAATGCCAGCATT 157

Qy        308 ArgValGlnAlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSer 327
              |||:::|||:::||||||||||||||||||||||||||||   ||||||||||||
Db        156 AGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGCGAATGGGCATCTGTGCCC 97

Qy        328 CysSer 329
              ||||||
Db         96 TGCAGT 91
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RESULT 13
CD559452/c

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LOCUS       CD559452                754 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496548 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971870 5', mRNA sequence.
ACCESSION   CD559452
VERSION     CD559452.2  GI:38453473
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 754)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585520.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 01
            High quality sequence start: 130
            High quality sequence stop: 572.
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                    /clone="IMAGE:6971870"
                    /tissue_type="mixed"
                    /lab_host="DH5A (T1 phage-resistant)"
                    /clone_lib="NIH_MGC_195"
                    /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                    loxP-HindIII; Clones from this library have been
                    PCR-amplified using gene-specific primers to contain the
                    complete open reading frame (based on known gene sequences
                    available from NCBI's RefSeq). Template for PCR is cDNA
                    derived from either pooled cytoplasmic polyA RNA from 30
                    cells lines or pooled total RNA from 10 different tissues
                    (from BD Biosciences/Clontech and Washington University).
                    PCR products are directionally cloned into the loxP sites
                    of the pDNR-Dual vector. Library constructed by Dr.
                    Narayan Bhat, Earl Bere III and Hongling Liao (Gene
```

Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	9.2e-90	Length:	754
Score:	898.50	Matches:	172
Percent Similarity:	86.3%	Conservative:	17
Best Local Similarity:	78.5%	Mismatches:	29
Query Match:	51.0%	Indels:	2
DB:	5	Gaps:	1

US-10-821-670A-30 (1-329) x CD559452 (1-754)

```
Qy        111 IleTrpSerThrAspIleLeuArgGluGlnLysGluSerLysAsnLysIlePheLeuLys 130
              |||||||||   |||   |||::::::|||||||||   |||||||||   ||||||:::
Db        750 ATTTGGTCCAATGATAT-TTAAAGGACCAGAAAGAACCCAAAAATAAGACCTTTCTAAGA 692

Qy        131 CysGluAlaLysAsnTyrSerGlyArgPheThrCysTrpTrpLeuThrAlaIleSerThr 150
              ||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db        691 TGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGGTGGCTGACGACAATCAGTACT 632

Qy        151 AspLeuLysPheThrValLysSerSerArgGlySerSerAspProGlnGlyValThrCys 170
              ||||||   |||:::|||||||||||||||||||       ||||||||||||||||||||
Db        631 GATTTGACATTCAGTGTCAAGAGCAGCAGAGGCTTTTTTGACCCCCAAGGGGTGACGTGC 572

Qy        171 GlyAlaAlaThrLeuSerAlaGluLysValArgValAspAsnArgAspTyrLysLysTyr 190
              ||||||||||||||   ||||||:::||||||   ||||||::::::|||   :::|||
Db        571 GGAGCTGCTACACTCTTTGCAGAGAGAGTCAGAGGGGACAACAAGGAGTAT---GAGTAC 515

Qy        191 ThrValGluCysGlnGluGlySerAlaCysProAlaAlaGluGluSerLeuProIleGlu 210
              :::|||||||||||||   ||||||||||||||   ||||||||||||||||||||||
Db        514 TCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCAGCTGGTGAGGAGAGTTTGCCCATTGAG 455

Qy        211 ValValValAspAlaIleHisLysLeuLysTyrGluAsnTyrThrSerSerPhePheIle 230
              |||:::|||||||||:::|||||||||||||||||||||||||||||||   |||||||||
Db        454 GTCATGGTGGATGCCGTTCACAAGCTCAAGTATGAAAACTACACCAGCAGGTTTTTCATC 395

Qy        231 ArgAspIleIleLysProAspProProLysAsnLeuGlnLeuLysProLeuLysAsnSer 250
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Db        394 AGGGACATCATCAAACCTGACCCACCCAAGAACTTGCAGCTGAAGCCATTAAAGAATTCT 335

Qy        251 ArgHisValGluValSerTrpGluTyrProAspThrTrpSerThrProHisSerTyrPhe 270
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Db        334 TGGCAGGTGGAGGTCAGCTGGGAGTACCCTGACACCTGGAGTACTCCACATTCCTAATTT 275

Qy        271 SerLeuThrPheGlyValGlnValGlnGlyLysAsnAsnArgGluLysLysAspArgLeu 290
              ||||||||||||   ||||||||||||||||:::   ||||||||||||||||||:::
Db        274 TCCCTGACATTTTGCGTTCAGGTTCAGGGCAAGAGCAAGAGAGAAAAGAAAGATAGAGTT 215

Qy        291 SerValAspLysThrSerAlaLysValValCysHisLysAspAlaLysIleArgValGln 310
              |||||||||   |||   |||:::|||   |||:::|||   |||   |||:::
Db        214 TTCACGGACAAGACCTTAGCCACGGTCATTTGCCGCAAAAATGCCAGCATTAGCGTGCGG 155

Qy        311 AlaArgAspArgTyrTyrSerSerSerTrpSerAsnTrpAlaSerValSerCysSer 329
              |||:::|||||||||||||||||   ||||||   ||||||   |||   ||||||
Db        154 GCCCAGGACCGGTACTATAGCTCATTTTGGAGCGAATGGGCATTTGTGCCCTGCAGT 98
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RESULT 14
CD559454/c

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LOCUS       CD559454                725 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14497089 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971868 5', mRNA sequence.
ACCESSION   CD559454
VERSION     CD559454.2  GI:38453478
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 725)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585522.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: g  column: 11
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            High quality sequence stop: 573.
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                      /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                      loxP-HindIII; Clones from this library have been
                      PCR-amplified using gene-specific primers to contain the
                      complete open reading frame (based on known gene sequences
                      available from NCBI's RefSeq). Template for PCR is cDNA
                      derived from either pooled cytoplasmic polyA RNA from 30
                      cells lines or pooled total RNA from 10 different tissues
                      (from BD Biosciences/Clontech and Washington University).
                      PCR products are directionally cloned into the loxP sites
                      of the pDNR-Dual vector. Library constructed by Dr.
                      Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                      Expression Laboratory, Research Technology Program, SAIC
                      Frederick, NCI-Frederick, Frederick, MD 21702). For
                      information on which gene each clone represents, please
                      visit our anonymous ftp site at
                      ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                      a Note: this is a NIH_MGC Library."
ORIGIN
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Alignment Scores:

Pred. No.:	2.01e-81	Length:	725
Score:	824.00	Matches:	165
Percent Similarity:	86.1%	Conservative:	15
Best Local Similarity:	78.9%	Mismatches:	27
Query Match:	46.8%	Indels:	3
DB:	5	Gaps:	2

US-10-821-670A-30 (1-329) x CD559454 (1-725)

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Qy        121 LysGluSerLysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
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Db        722 AAAGAACCAAAAATAAAGCTTTTT---AAGATGGGGGCCAAGAAGTATTTGGGAAGTTTC 666

Qy        141 ThrCysTrpTrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArg 160
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Db        665 CCTCGCTGTCGGCTGACGACAATCAGTACTGATTG-AACTTCAGTGTCAAAAGCAGCAGA 607

Qy        161 GlySerSerAspProGlnGlyValThrCysGlyAlaAlaThrLeuSerAlaGluLysVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::|||
Db        606 GGTTCCTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 547

Qy        181 ArgValAspAsnArgAspTyrLysLysTyrThrValGluCysGlnGluGlySerAlaCys 200
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                |||   ||||||::::::|||   :::|||:::|||||||||||||||   |||||||||
Db        546 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 490

Qy        201 ProAlaAlaGluGluSerLeuProIleGluValValValAspAlaIleHisLysLeuLys 220
              ||||||||||||||||||||||||||||||||:::||||||||:::|||||||||||||
Db        489 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 430

Qy        221 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 240
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Db        429 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 370

Qy        241 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGluTyrPro 260
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Db        369 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 310

Qy        261 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheGlyValGlnValGlnGly 280
              ||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        309 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 250

Qy        281 LysAsnAsnArgGluLysLysAspArgLeuSerValAspLysThrSerAlaLysValVal 300
              |||:::   ||||||||||||||||||:::      ||||||||||||||   |||:::
Db        249 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 190

Qy        301 CysHisLysAspAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerSerTrp 320
              |||   |||:::|||   |||   |||:::|||:::|||||||||||||||||||||||
Db        189 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 130

Qy        321 SerAsnTrpAlaSerValSerCysSer 329
              |||   ||||||||||||   ||||||
Db        129 AGCGAATGGGCATCTGTGCCCTGCAGT 103

RESULT 15
CD559603
LOCUS       CD559603                724 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496630 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971873 5', mRNA sequence.
ACCESSION   CD559603
VERSION     CD559603.2  GI:38558932
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 724)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585671.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: h  column: 04
            High quality sequence stop: 525.
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                     /clone="IMAGE:6971873"
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                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:                1.35e-76        Length:          724
Score:                    781.00          Matches:         143
Percent Similarity:       93.9%           Conservative:    11
Best Local Similarity:    87.2%           Mismatches:      10
Query Match:              44.3%           Indels:          0
DB:                       5               Gaps:            0

US-10-821-670A-30 (1-329) x CD559603 (1-724)

Qy          4 GlnGlnLeuValIleAlaTrpPheSerLeuValLeuLeuAlaProProLeuMetAlaIle 23
              |||||||||||||||:::|||||||||||||||||   ||||||   ||||||:::||||||
Db         23 CAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTCGTGGCCATA 82

Qy         24 TrpGluLeuGluLysAsnValTyrValValGluLeuAspTrpHisProAspAlaProGly 43
              |||||||||:::|||:::|||||||||||||||||||||||||:::|||||||||||||||
Db         83 TGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCCCCTGGA 142

Qy         44 GluMetValValLeuThrCysAsnThrProGluGluAspAspIleThrTrpThrSerAsp 63
              ||||||||||||||||||||:::|||||||||||||||   ||||||||||||   |||
Db        143 GAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACCTTGGAC 202

Qy         64 GlnSerSerGluValLeuGlySerGlyLysThrLeuThrIleGlnValLysGluPheAla 83
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 CAGAGCAGTGAGGTCCTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAGTTTGGA 262

Qy         84 AspAlaGlyGlnTyrThrCysHisLysGlyGlyGluValLeuSerHisSerPheLeuLeu 103
              |||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        263 GATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTCCTGCTG 322

Qy        104 IleHisLysLysGluAspGlyIleTrpSerThrAspIleLeuArgGluGlnLysGluSer 123
              :::|||||||||||||||||||||||||||||||||||||||||||:::::|||||||||
Db        323 CTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAAGAACCC 382

Qy        124 LysAsnLysIlePheLeuLysCysGluAlaLysAsnTyrSerGlyArgPheThrCysTrp 143
              ||||||||   ||||||:::|||||||||||||||||||||||||||||||||||||||
Db        383 AAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACCTGCTGG 442

Qy        144 TrpLeuThrAlaIleSerThrAspLeuLysPheThrValLysSerSerArgGlySerSer 163
              |||||||||   ||||||||||||||||   |||:::|||||||||||||||||||||||
Db        443 TGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGCTCTTCT 502

Qy        164 AspProGlnGly 167
              ||||||||||||
Db        503 GACCCCCAAGGG 514


Search completed: June 10, 2006, 10:30:46
Job time : 4038.45 secs
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